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July 28, 2003, 15:59:01; Search time 4746.96 Seconds (without alignments) 10471.464 Million cell updates/sec
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1708
1 GACGCTTCTGATCTCCAGAG.......GCCTAGAATAAACACCCAAA 1708
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                     2054640 seqs, 14551402878 residues
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Listing first 45 summaries
                                                   OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	

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Result No.	Score	Query	Length	DB	ID	ត	
T	21.	94.	1741	101	259	AF259981 R	Rattus no
	1278	74.	73	9 (	AR210324	AR210324 Se	dnence
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no on	* **	37.	675	_	AL/31698 AL669906	AL/31698 M AL669906 Mu	Mouse DNA Mus muscu
10		32.	126		AX076919	AX076919 Se	Sequence
11	561.4	32.9	1266	ဖြ	AX464186 AF083500	AX464186 Sequence AF083500 Homo sar	quence mo sapi
13	561.4	32.	29		AR210322	AR210322 Se	dneuce
c 14	561.4	32.	29		AR210323	AR210323 Se	Sequence
16	561.4	32.	42		AF U/4504 AF 100780	AFU/4604 HO AF100780 HO	mo sapi
17		32.	45		BC017782	BC017782 Ho	Homo sapi
18	528.8	31.	841		AR210338	AR210338 Se	dneuce
200	501.2	29.	73		AR210337 ac126895	AR210337 Se	quence
10	195.8	11.	0726		AL139352	AL139352 Hu	man DNA
22	168	9.	8		NVI271167	AJ271167 NO	tophtha
23	163.8	o	7.7		AR018957	AR018957 Se	dnence
25	163.8	. 0	2.		AR130891	AR130891 Se	quence
56	163.8	6	2		AX206708	AX206708 Se	dneuce
27	163.8	م م	7.7		111636	111636 Segu	squence 1
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31	163.8	o	ნ ი		AR119211 AP151276	AR119211 Se	Sequence
3 6	· 10	. 9.	2267		AX206706	AX206706 Se	Sequence
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45		. 0	320	9	AR201286	AR201286 Se	Sequence
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ACCESSION VERSION KEYWORDS	N AF2	259981 259981.1	GI:77	3978	0		
SOURCE	_	Q	norvegicus norvegicus ta; Metazoa a; Eutheria		Chordata; Craniata; Rođentia; Sciurogna	Vertebrata; thi; Muridae;	Euteleostomi; Murinae;
REFERENCE		Rattus. 1 (bases 7hang P	1 to 1741)	41)		D TO H Damaga	F.
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Coffey, R.J., Pardee, A.B. and Liang, P.
Identification of rCop-1, a new member of the CCN ps a negative regulator for cell transformation Mol. Cell. Biol. 18 (10), 6131-6141 (1998)
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9742130
2 (bases 1 to 1741)
Liang, P.
Liang, P.
Direct Submission
Submitted (24-App. 2000) Cell Biology, Vanderbilt-In Center, 649 MRB II, Nashville, TN 37232, USA
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Page 3

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                                                                                  TTCCTGATCTGAGAACACCCTGCCCGGCTGGGA------AGAATTTTCTGGGA
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                               CTGCCCCGAG#GGGTATGTGACCAGGGAGTGA---CACCGGCGATCCAGCGCTCCACGGC
                                                                        GCAAGGACAC@AACTTTCTGCCCTTGTCACTCCTGCCTGATGCTCCTTGTCCAAA
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                                                                                                                       Unclassified.

1 (bases 1 to 1734)

Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,

Barence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.

WISP Polypeptides and nucleic acids encoding same

Patent: US 6387657-A 18·14-MAY-2002;
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No. 0;
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Sequence 18 from patent
AR210325
AR210325.1 GI:21512526
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88.5%;
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Best Local Similarity 88.5
Matches 1520; Conservative
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AF100778  AF100778  Wis musculus connective tissue growth factor related protein WISP-2 (Wisp2) mRNA, complete cds.  AF100778  AF100778  AF100778  AF100778  AF100778  AF100778  Mus musculus.  Mus musculus.  Mus musculus.  Mus musculus.  Mus musculus.  Mus musculus.  Eukaryots, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Musculus.  Mus musculus.  Mus musculus.  Mus musculus.  Eukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Musculus.  I (bases 1 to 1734)  Eukaryots, Metanabe, M.F., Finley, G.G., Quirke, P., Goddard.A.D., Hillan, K.J., Gurmey, M.L., Bostelan, D. and Leovine, A.J. factor Colen, R.L., Melhem, M.F., Finley, G.G., Quirke, P., Goddard.A.D., Hillan, K.J., Gurmey, M.L., Bostelan, D. and Leovine, A.J. factor aberrantly expressed in human colon tunors of the connective tissue growth factor aberrantly expressed in human colon tunors  L Proc. Nall. Acad. Sci. U.S.A. 95 (25), 14717-14722 (1998)  E 99661931  E 1,134  E 2 (bases I to 1734)  E 2 (bases I to 1734)  E 343955  E 2 (bases I to 1734)  E 3443955  E 3 (bases I to 1734)  E 3 (bases I to 1734)  E 3 (bases I to 1734)  E 4 (bases I to 1734)  E 5 (bases I to 1734)  E 6 (bases I to 1734)  E 7 (bases I to 1734)  E 7 (bases I to 1734)  E 8 (bases I to 1734)  E 99661931  E 1,134  E	Local Similarity 88.5%; Pred. No. 0; DB 10; Length 1734; Local Similarity 88.5%; Pred. No. 0; DB 10; Length 1734; Local Similarity 88.5%; Pred. No. 0; DB 10; Indels 33; Gaps 11; DB 1520; Conservative 0; Mismatches 165; Indels 33; Gaps 11; CGCTCTGATCTCCAGAGGACCTGGGACAGGCCTTGGCAGGCCG 62
AF100778 LOCUS DEFINITION ACCESSION VERSION VERSION VERSION CONTROL ONGANISM CONTROL AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS TITLE JOURNAL MEDLINE GOUNT GENERAL TITLE JOURNAL GENERAL FEATURES SOUICE CDS CDS	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Consensus quality: 89474 bases at least Q40
consensus quality: 9422 bases at least Q30
Consensus quality: 96506 bases at least Q20
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Chemistry: Dye-terminator Big Dye: 100% of
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
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Center clone name: CH230-301E4
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Worley, K.C.
Direct Submission
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                        GAGCACAGCCTGGGGCCCCCTGCTCAACCACCTGTGGGCTGGGCATAGCCACCCCGAGTGTC 898
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Rattus norvegicus.
Rattus norvegicus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                            899 CAACCAGAACCGATTCTGCCAACTGGAGATCCAACGCCGCCTGTGTCTGCCCAGACCCTG
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 49 contings. The true order of the pieces
is not known and their order in this sequence record is
                                                                   arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Manhiney, E., Marwiniey, E., Marchal, T., Morbbat, K., Morgan, M., Morris, S.,
Moyer, M., Neal, D., Newtson, J., Newtson, N., Oguh, M., Okwuon, G.,
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Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
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Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O.,
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Mu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
Mang, S., Walliamson, A., Walczyk, R., Wooden, S., Worley, K.,
Direct Submission
AL Unpublished
CE J (bases I to 226303)
AL Unpublished
CE Submission
AL Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Submitted (17-Sep-2003)
CE S (bases)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 51 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (11-JUL-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jul 10, 2002 this sequence version replaced g1:17941885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990329 Consensus quality: 185950 bases at least Q40 Consensus quality: 193052 bases at least Q20 Consensus quality: 193076 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
Project Information
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Center clone name: CH230-7C10
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Direct Submission
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Archive, C., Bankenburg, K., Banks, T., Bunbaria, J., Benton, J., Birwage, K., Blankenburg, K., Bonnin, D., Buubay, C., Burch, P., Burkett, C., Burnell, K.L., Byrd, N.C., Cartor, R., Chen, Z., Chowdhry, I., Charistopoulos, C., Chen, R., Chen, Z., Chowdhry, I., Charistopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Doben, A.L., Ding, Y., Dinh, H. H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escetto, M., Falls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Foster, P., Ferraguto, D., Edwards, C., Elhaj, C., Hane, S., Hamilton, K., Harris, K., Hartis, C., Hartis, K., Harth, J., Joudah, S., Hernandez, O., Hodgson, A., Ghuson, R., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Korvah, J., Kartovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
                                                                                                                                                       44601 GCTGGGGATAAGGTC-TTGTTAGGACCAGACAGCAGATTGCCTGAAACTTCCAATTCCCT 44659
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            TCTCTGGTTCAGCCTGGAATTCTGGGTTCTCCTGGCTCATTCCTCAAAACATCCCTGTAC 1254
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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835 ATTGGAGCACAGCCCCCTGCTCCAACCACCTGTGGGCTGGGCATAGCCACCCGAG 894
112310 ATTGGAGCACAGGCCCCTGCTGCTCACCACCTGTGGGCTGGGCATAGCCACCAGG 112369 895 TGTCCAACCACAÂCCGATTCTGCCAACTGGAGATCCAAGGCGCCTGTGTCTGCCCAGAC 954 112849 112909 112669 1014 1074 1193 1311 1371 1431 ., Έ 1134 775 CGCAAGGACACĞAACTTTCTGCCCTTGTCACTCCTGCCTCTGCTGATGCTCCTTGTCCAA 834 112550 GIAGATGCTCTTCTCCCATGCTCTTGGCTGCAGTTAACTGCTCGCTTGGATTCACTGTGT 1135 AGAGCCACTGAGCGATCCCTGCTCTGTCTGAGGTA-GGCGGAGCAGGTGACCAGGTCCAG CCTGCCTGGCAGGCAGGAGCCACAGCTCATGGAACAGTGCTTTCTAAGGCCAACTGGGGA 1015 TGCGGATACAGGGCCTGCCATCCTCAGCAATGACCCTAGGACCAGGCCCTGGACTGCTG GTAGATGCTCTTGTCCTCTTGGCTGCAGTTAACTGTCCTGCTTGGATTCACTGTGT ACAAAAAGGACA-ÂCCAAAAAGACCTTTAAACCTAGGCTATACTGGGCAAACCTGGCCAC 3; Gaps Length 226303; 2710 142809: gap of unknown length
2810 149818: contig of 7009 bp in length
9819 149918: gap of unknown length
158719: contig of 8801 bp in length
8720 158819: gap of unknown length
8820 169868: contig of 11049 bp in length
9869 1880300: contig of 11042 bp in length
9869 1880390: contig of 10422 bp in length
9811 180490: gap of unknown length
9811 180490: gap of unknown length
9811 180490: gap of unknown length
9811 191372: gap of unknown length
9811 191373: gap of unknown length
9811 191373: gap of unknown length 5117 others Indels Query Match #51.6%; Score 881.8; DB 2; Best Local Similarity '98.4%; Pred. No. 2.2e-228; Matches 922; Conservative 0; Mismatches 12; /organism="Rattus norvegicus" /db\_xref="taxon:10116" /clone="CH230-7C10" 53353 c 52917 g 57041 t 158720 158820 169869 169969 191373 209668 209768 149819 149919 180391 191273 180491 57875 a 955 1075 1253 source BASE COUNT FEATURES qq qq g Ω qq ð g δ g ò g ò qq ò qq ò ò ò ò ò ò g ò

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Submitted (24-MAY-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On May 25, 2002 this sequence version replaced gi:21213601.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality) -

as compressions and repeats; all regions were ocvered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given

in the feature table with their source databases: Ems. EMBL: Sw.;

SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP

database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-161B3 is

from the RPCI-23 Mouse PAC Library

constructed by the group of Pieter de Jong.
                                                                                                112970 ACATGAAGAGATGAATCACACTGTCCTTAAGAAATTCCTCAAAGTCCAGGAACTTGAGCT 113029
                                                                                                                                                         TGGCAGGCCAGGGCCTTTCTCTTCAGCATGAGAAAGACAAGGGACAGCAGAGTACTCTCC 1671
ACATGAAGAGATGATCACACTGTCCTTAAGAAATTCCTGAAAGTCCAGGAACTTGAGCT 1551
                                                                                                                                                                                                                                                                                                                                                                           ROD 24-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                         AL731698 61072 bp DNA linear ROD 24-MAY-2003
Mouse DNA sequence from clone RP23-161B3 on chromosome 2, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 61072)
Wallis,J.
                                                                           TTGTATTTTCAGGAATGCACATCTCTTAAGCACTCGCAAAACAGGAAGGCTCCACACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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85.6%; Pred. No. 5.3e-164;
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                                                                                                                     TGTCCAACCAGAACCGATTCTGCCAACTGGAGATCCAACGCCGCGTGTGTCTGCCCAGAC
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AL669906.5 GI:21955520
HTG; HTGS_PHASE1; HTGS_CANCELLED.
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Ekkaryota; Metazoa; Chordata; Craniata; Manmalia: Eutheria; Rodentia; Sciurogna 1 (bases 1 to 216757) Sims, S. Direct Submission Submitted (23-JUL-2002) Wellcome Trust Cambridgeshire, CB10 15A, WK. E-mail enhunquery@sanger.ac.uk Clone requests: On Jul 25, 2002 this sequence version renter: Wellcome Trust Sanger and Center Center on Jul 25, 2002 this sequence version recenter wellcome Trust Sanger Institute Center code: SC Web Site: http://www.sanger.ac.uk Contact: humquery@sanger.ac.uk Contact: http://www.sanger.ac.uk Contact: name: bwl2702	Quality coverage: 6.29x in Q20 bases; sum-of-contigs Quality coverage: 5.90x in Q20 bases; sum-of-contigs Quality coverage: 5.90x in Q20 bases; agarose-fp	19 999 of 19 9999 of 19 99999 of 1
ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT		

PAT 22-FEB-2001

Euteleostomi;

and

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543 AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAAACCCAATTGCAGG
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                                                                                                                                                         for the treatment of
                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1266)
Botstein,D., Goddard,A., Gurney,A.L., Hillan,K.J., Roy,M.A.Wood,W.I.
                                                                                                                                                                                                                                                          Length 1266;
                                        linear
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                          Score 561.4; DB 6;
Pred. No. 2.2e-141;
; Mismatches 196;
                                       DNA
                                                                                                                                                         methods
                                                                                                                                                        Polypeptidic compositions and methods
Patent: WO 0105836-A 31 25-JAN-2001;
Genentech, Inc. (US)
                                                                                                                                                                                                                             242
                                   Sequence 31 from Patent W00105836. AX076919 AX076919.1 GI:13121575
                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                        Length 216757
                            others
                                                       Score 645; DB.2; Length 21
Pred. No. 5.8e-164;
0; Mismatches 115; Indels
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                            2003
/note="assembly_fragment:01318
                            u
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                 vector_side:right"
51573 c 51904 g
          clone_end:T7
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Best Local Similarity 85.6%;
Matches 804; Conservative
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20-JUN-2002
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Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.
WISP polypeptides and nucleic acids encoding same
Patent: US 6387657-A 13 14 MAY-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    ACGGTGTCCCACCATCCCCAGCTGGTGGCCCTGTGCCCTGGGCCTGATGGAAGATG
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Pred. No. 2.2e-141;
                                                                               DNA
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425 c 393 g
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/db_xref="c1:3462836"
/db_xref="c1:3462836"
/translation="MRGTPKTHILLAFSLLCLLSKVRTQLCPTPCTCPWPPPRCPLGVP
/translation="MRGTPKTHILLAFSLLCLLSKVRTQLCPTPCTCPWPPRCPLGVP
IVDGGGCGCRVCARRAGEPCDGLHVVDASQGIVCOPAGPGRGALCLLAEDDSSCEW
NGRLYREGEFFQPHGSIRCREDGGFTCVPLCSEDVRLPSWDCPHPRRVEVLGKCCPE
WYGGQGGGLGTQPLPAGGPQFSGLVSSLPPGYPCPEWSTAMGPCSTTCGLGMATRYSN
QNRFCRLETQRRLCLSRPCPPSRGRSPQNSAF"

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Pred. No. 2.2e-141;
0; Mismatches 196;
carboxy-terminal the CCN family"
                          /product="connective tissue
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1309 bp mRNA linear PRI 18-JUL-1998
Homo sapiens connective tissue growth factor-related protein
Precursor (CTS) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                  963 GCAGCCAGGAGECACAGCTCATGGAACAGTGCTTTCTA-AGGCCAACTGGGGATGCGGAT 1021
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precursor"
/protein_id="AAC26794.1"
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CT58, a new member of the connective tissue growth factor family, interacts with the breast cancer associated mucin MUC1
Unublished
2 (bases 1 to 1309)
Rowles, J. and Gendler, S.
Direct Submission
Submitted (2-10N-1998) Blochemistry and Molecular Biology, Mayo Clinic Scottsdale, 13400 E. Shea Blvd., Scottsdale, Az 85259, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi; Homo.
903 CAGAACCGATTOTGCCCAACTGGAGATCCAACGCCGCCTGTGTCTGCCCAGACCCTGCTG
                                                                                                                              CCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCAAGGA
                                                                                                               CACCAACTIT@TGCCCTTGTCACTCCTGCTGATGCTCCTTGTCCAAATTGGAGC
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Catarrhini; Hominidae;
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/db_xxef="taxon:9606"
/cell_line="HeLa"
1. .1309
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1309)
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7. .759
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Unclassified.

(December 1 to 1293)

Botstein, D.A., Cohen, R.L., Goddard, A.D., Gurney, A.L., Hillan, K.J., Lawrence, D.A., Levine, A.J., Pennica, D., Roy, M. Ann. and Wood, W.I. WISP polypeptides and nucleic acids encoding same patent: US 6387657-A 14 14-MAY-2002;

Location/Qualifiers
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/db\_xref="G1:3328192"
/translation="MRGTPKTHLLAFSLLCLLSKVRTQLCPTPCTCPWPPPRCPLGVP
LVLDGGGCRCWCARRLGEPCDGHVCDASOGIVCPGAGGGGGRGALCLLAEDDSSGEV
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QNRFCRLETQRRLCLSRPCFPSRGRSPQNSAF"
1 others 261

ACAGGCCTGCCATCCTCAGCAAATGACCCTAGGACCAGGCCCTGGACTGCTGGTAGATG 1081 3 GCAGCCAGGAGCCACAGCTCATGGAACAGTGCTTTCTA-AGGCCAACTGGGGATGCGGAT 1021 362 180 360 480 902 720 780 1139 302 422 482 240 542 300 602 662 420 722 782 540 842 900 099 840 9 TCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAG CGGCTGGGGGACCCTGCGACCAACTCCACGTCTGCGACGCCAGGCCTGGGTCTGC CAGCCTGGGGCAGCCCTGGCGGCCATGGGGCTGTGTGTCTTGGATGAGGATGACGGT AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGCCTTTAAACCCAATTGCAGG CGGCTGCCCAGCTGGGACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGC CCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCAAGGA CACCAACTITCTGCCCTTGTCACTCCTGCTCTGCTGATGCTCCTTGTCCAAATTGGAGC Gaps 5; Length Indels Score 561.4; DB 9; Pred. No. 2.2e-141; 0; Mismatches 196; 32.9%; 78.0%; Conservative 1 Similarity 701; Conserv Query Match Best Local S: Matches 701 1022 303 61 363 121 423 181 483 543 663 421 723 481 783 843 601 903 661 963 781 BASE COUNT ORIGIN q g ò g ò ò g ò g à g ò g ò g ò g õ g δ g ò g ò g ò g

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Nucleic acid sequences encoding rat heparin-induced CCN-like protein, used in methods to identify modulators or in diagnostic applications

WPI; 1999-562060/47. P-PSDB; AAY27434.

AAZ07517 AAZ07521 AAX76489 AAX16595

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AAH46952 AAH46936 AAA30048

Castellot JJ;

Human WISP-2 prote Connective tissue EGF-1ike homologue Human PRO261 CDNA Human WISP-2 prote Human WISP-2 prote Human WISP-2 prote Rat OST23 gene fra Rat HICP IGFBP dom Human tull-length Human immune/haema

Title: Perfect score:

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Heparin-induced CCN-like protein; HICP; cell-associated activity; ss; cardiovascular disorder; aberrant cell proliferation; fibrotic disorder.
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1 GACGCTTCTGATCTCCAGAG.......GCCTAGAATAAACACCCAAA 1708
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         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                               Agents that stimulate or inhibit HICP protein activity or expression, antisense HICP nucleic acid molecules and HICP antibodies, can be used to modulate cell-associated activity. HICP modulators can be used to treat disorders characterized by aberrant HICP protein activity or expression. Probes capable of hybridizing to HICP mRNA or antibodies specific for HICP can be used to detect HICP activity in a biological sample. HICP can be used to treat disorders, such as a cardiovascular or fibrotic disorder, characterized by aberrant cell proliferation.
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                        ncodes a rat heparin-induced CCN-like stimulate or inhibit HICP protein act
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                                                                                                                          100.0%; Score 1708; 100.0%; Pred. No. 0;
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                                                                                                          362 A; 486 C; 478
        English
                                                                                                                                         Conservative
                                                                                                                         Query Match
Best Local Similarity
Matches 1708; Conserv
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                                                                                                         Sequence 1708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-3 have homology to connective tissue growth factor (CTGE). Products from the present invention can be used to treat WISP-related disorders such as breast, ovarian, and colon cancer or melanoma. The products can be used to treat other diseases e.g. benign and malignant tumours, leukaemia and lymphoid malignancies, neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, and disorders, skin disorders, haematopolesis-related disorders, tissue-growth disorders, bone-related disorders und other wounds, connective tissue disorders, burns, incisions, and other wounds, connective tissue disorders, catabolic states, testicular-related disorders, and inflammatory, acception of the connective tissue disorders, and inclaimmatory, and incisions and other wounds, connective tissue disorders, and inclaimmatory, and incisions and other wounds, and inclaimmatory, and incisions and other wounds, inclaims and incipations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        can be used in the production of transgenic or knock-out animals.
Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anglogenic and immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The products
WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour; connective tissue growth factor; cancer; melanoma; arteriosclerosis; leukaemia; lymphoid malignancy; heematopolesis-related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion; kidney disorder; bone-related disorder; ostoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation; testicular-related disorder; anglogenesis; immunological disorder; ss.
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Roy MA, Wood WI;
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Pred. No. 0;
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Levine AJ,
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CC fibrotic disorder, characterized by aberrant cell proliferation. The CC present sequence represents the coding sequence of rat HICP.  XX  SQ Sequence 753 BP; 132 A; 235 C; 230 G; 156 T; 0 other;  Query Match 44.1%; Score 753; DB 20; Length 753;  Best Local Similarity 100.0%; Pred. No. 3.8e-216;  Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	y 249 ATGAGGGCAGCCCACTGATCCATCTTCTGGCCACTTCCTTC	0y 309 GTGTGCCCAGCTGTGCCGGACACCCTGTACCTGCGACACCACCCCGGTGCCCA 368	Qy 369 CAGGGGTACCCTGGTGCTGGATGCTTGTGCTGTAAAGTGTGCACGAGGTG 428	0y 429 GGGGAGTCCTGGGACCACCTGCACCCCAGCCAGGGCCTGGTTTGTCAGCCT 488	0y 489 GGGCAGGCCATGGGGCTGTGTGTCTCTTGATGAGGATGACGTACTGT 548	QY 549 GAGGTGAAFGGCCCAGGTACCTGGATGGAGACCTTTAAACCCAATTGCAGGGTCCTG 608	OY 609 TGCCGCTGTGATGACGGTGGCTTCACCTGCCTGCCGCTGTGCAGGATGTGCGGCTG 668	669 CCCAGCTGGGACTGCCCCAGGCCCGAAGAATACAGGTGCCAGGAAAGTGCTGCCCGAG	729		Db 541 CTTCTGCCCTTGTCCTGCTCCTGATGCTCCTTGTCCAAATTGGAGCACAGCC 600	0y 849 TGGGGCCCTGCTCAACCACTGTGGGCTGGCATAGCCACCGGGTGTCCAACCAGAAC 908	Oy 909 CGATTCTGCCAACTGGAGATCCAACGCCGCTGTGTCTGCCCAGACCCTGCCTG	969 AGGAGCCACAGCTCATGGAACAGTGCTTTCTAA 1001	Db 721 AGGAGCCACAGCMCATGGAACAGTGCTTTCTAA 753	SULT 4 207521	standard; cDNA;		DE Rat HICP mature polypeptide coding sequence.  XX  XW  XW  WM Hebarin-induced CCN-like protein: HICP: cell-associated activity: ss:
1313 GTGCTGGGGATAAGGTCAATGTTAGG-ACCAGACATGCCTGAAACTTCCAATTC   1371	1432 TCCTGACCTGAGACACCTGCCTGCGGGAGTATTCAGGGGCAGAATTCTCTGTGA 1491 	1492 ACATGAAGAT-GAATCACACTGTCCTTAAGAATTCCTGAAAGTCCAGGAACTTGAGC 1550 	1551 TTGTATTTCAGGAATGCACATCTCTTAAGCACTCGCAAAACAGGAAGGCTCCACACCT 1610 	1611 CTGGCAGGCCTTTCTTCTTCAGCATGAGAAAGACAAGGACAGCAGAGTACTCTC 1670 	1671 CTCTGGAGGACTAGTCTAGCTAGAATAAACACCCAAA 1708 	RESULT 3 AA207517 ID AA207517 standard: cDNA: 753 BP.		20 NOV 1999 (11SL entry) Rat HICP polypeptide coding sequence.	Heparin-induced CCN-like protein; HICP; cell-associated activity; ss; cardiovascular disorder; aberrant cell proliferation; fibrotic disorder.	Macus sp. W09947556-A2.	23-SEP-1999.	18-MAR-1999; 99WO-US05999. 19-MAR-1998; 98US-0044273.	(TUFT ) TUFTS COLLEGE. Castellot JJ:	WPI; 1999-562060/47. P-PSDB; AAY27434.	Nucleic acid sequences encoding rat heparin-induced CCN-like protein, used in methods to identify modulators or in diagnostic applications -		The invention provides a rat heparin-induced CCN-like protein (HICP) protein. Agents that stimulate or inhibit HICP protein activity or expression, antisense HICP inclosic and HICP antishadise	can be used to modulate cell-associated activity. HICP modulators can be used to treat disorders characterized by aberrant HICP protein activity	or expression. Probes capable of hybridizing to HICP MRNA or antibodies specific for HICP can be used to detect HICP can be used to treat disorders, such as a cardiovascular or sample. HICP can be used to treat disorders, such as a cardiovascular or

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                                                                                                                                                                                                                                                                                                                                                     protein. Agents that stimulate or inhibit HICP protein activity or can be used to modulate cell-associated activity. HICP modulate cell-associated activity. HICP modulators can be used to modulate cell-associated activity. HICP modulators can be used to treat disorders characterized by aberrant HICP protein activity or expression. Probes capable of hybridizing to HICP mRNA or antibodies specific for HICP can be used to detect HICP activity in a biological sample. HICP can be used to treat disorders, such as a cardiovascular or fibrotic disorder, characterized by aberrant cell proliferation. The present sequence represents the coding sequence of rat HICP mature
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cardiovascular disorder; aberrant cell proliferation; fibrotic disorder
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                                                                                                                                                                                                                                                                    acid sequences encoding rat heparin-induced CCN-like protein, methods to identify modulators or in diagnostic applications
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                           P-PSDB; AAY27440
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                                                                                                                                                                                                                                                                                                                                                                                                                       connective tissue growth factor; cancer; melanoma; arterioscierosis; leukaemia; lymphoid malignancy; haematopoiesis-related disorder: tissue-growth disorder; skin disorder; desmoplasia; flbrotic lesion; kidney disorder; bone-related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation; testicular-related disorder; anglogenesis; immunological disorder; ss.
                                                                        CTTGTCACTCCTGCCTCTGCTGATGCTCCTTGTCCAAATTGGAGCACACCTGGGGCCCC
                                                           Mouse WISP-2 protein complementary nucleotide sequence SEQ ID NO:18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 179-180; 284pp; English.
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Pennica D,
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97US-0063704.
98US-0073612.
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Levine AJ,
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29-OCT-1997;
03-FEB-1998;
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Lawrence DA,
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anglogenic and immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The products can be used in the production of transgenic or knock-out animals. Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
                                                                                                                                                             AACCGATTCTGCCAACTGGAGATCCAACGCCGCCTGTGTCTGCCCAGACCCTGCCA
                                                                                                                                                 GGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGGCCAGGGCCTGGTTTGTCAGCCT
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                                                                              Sequence 753 BP; 159 A; 229 C; 238 G; 127 T; 0 other;
                                                                                                    Score 657; DB 20;
Pred. No. 3.2e-187;
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                                          Human; growth factor-like protein; HGFLP; fisp-12; CTGF; PDGF family; connective tissue growth factor; platelet-derived growth factor; keloid; connective tissue disorder; cancer; ankylosing spondylitis; scleroderma; atherosclerosis; Dupuytren's conter; eosinophilic fascilitis; Felty syndrome; Goodpasture's disease; Hunter syndrome; Hurler syndrome; Marfan syndrome; nodular fascilitis; osteogenesis imperfecta; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 CACACACGACAGGCACCCCCTTGGTGGCCTTCACAGTTTCACCCTTCAGGCTCAAAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide encoding growth factor-like protein - useful preventing and treating connective tissue disorders and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                           rheumatoid arthritis; systemic lupus erythematosus; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1522 BP; 279 A; 496 C; 459 G; 288 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 583.4; DB 20;
Pred. No. 6.9e-165;
0; Mismatches 206;
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Best Local Similarity 77.6%;
Matches 747; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-080954/07.
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             growth
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                                                                                                                                                                                                                                                            CCTGGGCAAGTGCTGCCCTGAGTGGGTGTGCGGCCAAGGAGGGGGGACTGGGGACCCAGCC
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                        CCGGGTATGTGCACGGCGGCTGGGGGGGCCCTGCGACCACCTCCACGTCTGCGACGCCAG
                                               CCAGGGCCTGGTTTGTCAGCCTGGGGCAGGCCCTGGCGGCCATGGGGCTGTGTGTCTCTT
                                                            GGATGAGGATGAČGGTAGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGACCTT
                                                                                                                                               GTGCAGTGAGGATGTGCGGCTGCCCAGCTGGCCCACGCCCCCAAGAGAATACAGGT
                                                                                                                                                                                                           GCCAGGAAAGTGCTGCCCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGCG
                                                                                                                                                                                                                                                                                               CTCCACGCCCAAGGACACCAACTTTCTGCCCTTGTCACTCCTGCCTCTGCTGATGCTCC
                                                                                                                                                                                                                                                                                                            827 TIGICCAAATIGGAGCACAGCCTGGGGCCCCTGCTCAACCACCTGTGGGCTGGGCATAGC
                                                                                                                                                                                                                                                                                                                                                          CACCCGAGTGTCCAACCAGAACCGATTCTGCCAACTGGAGATCCAACGCCGCCTGTGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted protein; immunosuppressive; antiarthritic; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein encoding cDNA (clone Id HBODE48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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The invention provides novel human secreted proteins and polynucleotides encoding them. The secreted proteins can be expressed by standard recombinant methodology. The secreted proteins and polynucleotides are cused to prevent, treat or ameliorate a medical condition in e.g. humans, also be used in diagnosting a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme clinked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, byperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebroascular disorders e.g. cardiac arrest, cerebroascular disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and coular disorders e.g. corneal infection. The polypeptides can also be used at always and in chemotaxis. The polypeptides can also be used as a food additive or chemotaxis. The polypeptides can also be used as a food additive or sequence represents a human secreted protein encoding cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCAGGGCCCACAGGGGGG
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                                                                                                                                          3, Soppet DR, Olsen
Choi GH, Fiscella M;
                                                                                                                                                                                                                                                     17 isolated nucleic acid molecules encoding human secreted proteins, used to preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 566.8; DB 22; Length 1337; Pred. No. 6.5e-160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205;
                                                                                                                                          Birse CE,
Shi Y, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
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                                                                                                                                          KP,
DR,
                                                                                                                                            Baker Duan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.2%;
77.0%;
                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                         31-JAN-2000; 2000US-0179065.
04-FEB-2000; 2000US-0180628.
12-SEP-2000; 2000US-0231968.
                                                                                                                                        CA, Komatsoulis GA,
PA, Wei P, Ebner R,
Ruben SM, Barash SC;
             17-JAN-2001; 2001WO-US01431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 77.0
Matches 728; Conservative
                                                                                                                                                                                                        WPI; 2001-476220/51.
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                                                                                                                                          Rosen CA,
Moore PA,
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                                                                                                                                                      GGGACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGCCCCGAGTGGGTAT
                                                                                                                                                                                     CCCTTGTCACTCCTGCCTCTGCTGCTCCTTGTCCAAATTGGAGCACCAGCCTGGGGGCC
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                                                                                                                                                                                                                                                                                 ATGGCCGCAGGTACCTGGATGGAGACCTTTAAACCCAATTGCAGGGTCCTGTGCCGCT
                       ACGCCCCCTGTATCGGGAAGGGGAGCCTTCCAGCCCCACTGCAGCATCCGCTGCCGCT
                                              GTGATGACGGTGGCTTCACCTGCCGCGCTGTGCAGTGAGGATGTGCGGCTGCCCAGCT
                                                                                                        GTGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCAAGGACACCAACTTTCTG
                                                                                                                                                                                                                                    CCTGCTCAACCACCTGTGGGCTGGGCATAGCCACCCGAGTGTCCAACCAGAACCGATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                           CTCTTGGCTGCAGTTAACTGTCCTGCTTGGATTCACTGTGTAGAGC 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCTTGGCTGCAGGCAACACTTAGCTTGGGTCCACCATGCAGAAC 939
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DR,
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Moore PA, Wei P, Ebner R, Duan
Ni J, Ruben SM, Barash SC;
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2000US-0180628.
2000US-0231968.
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04-FEB-2000; 2
12-SEP-2000; 2
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The invention provides novel human secreted proteins and polynucleotides encoding them. The secreted proteins can be expressed by standard encoding them. The secreted proteins and polynucleotides are tecombinant methodology. The secreted proteins and polynucleotides are used to prevent, treat or ameliorate a medical condition in e.g. humans, also be used in diagnosing a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme clinked immunosorbend assays (ELISA). Disorders which are diagnosed or treated include autojmmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, serbovascular disorders e.g. cardiac arrest, serbovascular disorders e.g. cardiac arrest, oreneovascular disorders e.g. cardiac arrest, oreneovascular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, chemotaxis. The polypeptides can also be used as a food additive or present preservative to increase or decrease storage capabilities. The present
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                                                              17 isolated nucleic acid molecules encoding human secreted proteins,
                                                                                to preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 566.6; DB 22; Length 1352;
Pred. No. 7.5e-160;
0; Mismatches 209; Indels 10;
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Best Local Similarity 77.0%;
Matches 732; Conservative
               2001-476220/51.
                                                                                                               Claim 1; Page 415;
                               P-PSDB; AAB85526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246; PRO317; Unmour growth inhibitor; cancer; diagnosis; treatment; human; cell growth; proliferation; growth factor; ADEPT; antibody dependent enzyme mediated prodrug therapy; ss.
                                                                                                                                                                                                                                      CTTCTGCCGACTGGAGACCCAGCGCCGCTGTCCAGGCCCTGCCCACCCTCCAG
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                                                                                                                    TTCTGCCCTTGTCACTCCTGCTGCTGATGCTCCTTGTCCAAATTGGAGCACAGCCTG
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them are used for diagnosing a tumou: in a mammal. The antibodies are used for inhibiting the growth of tumour cells and identifying compounds that inhibit a biological or immunological activity of and/or expression of a PRO187, PRO513, PRO214, PRO211, PRO211, PRO520, PRO351, PRO246, or PRO317 polypeptide. The antibody can be used in antibody dependent enzyme mediated prodrug therapy (ADEPT) by conjugating the antibody to a prodrug-activating enzyme which converts a prodrug to an anti-cancer drug. The antibodies can be fluorescently labelled and monitored by light microscopy, flow cytometry or fluorimetry for diagnosis and prognosis of
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                                                                                                                                                        Length 1266;
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                                                                                                                                 Sequence 1266 BP; 216 A; 418 C; 390 G; 242 T; 0 other;
                                                                                                                                                         DB 21;
                                                                                                                                                       Query Match 32.9%; Score 561.4; DB 21;
Best Local Similarity 78.0%; Pred. No. 2.7e-158;
Matches 701; Conservative 0; Mismatches 196;
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CT-CTTCTCCATGCTCTTGGCTGCAGTTAACTGTCCTGCTTGGATTCACTGTAGAGC 1139
                                                                                                                                                muscle;
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         GTCCGTGCCCAGGCCCTTGCTGCAGCAACACTTTAGCTTGGGTCCACCATGCAGAAC
                                                                                                                              Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal mus adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deforge L, Desnoyers L, Filvaroff E, G
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                            CDNA sequence encoding for PRO261 polypeptide
                                                           AAS21403 standard; cDNA; 1266 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                breast, prostate, cervical
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99WO-US28551
99WO-US28564
99WO-US28565
99WO-US30095
99WO-US30095
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2000WO-US05601.
2000WO-US07377.
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2000WO-US14042
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2000WO-US04914
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Gerritsen ME, Goddard
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P-PSDB; AAU12331.
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18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
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01-MAR-2000;
20-MAR-2000;
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02-JUN-2000;
10-NOV-2000;
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06-JAN-2000;
11-FEB-2000;
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20-DEC-1999;
20-DEC-1999;
30-DEC-1999;
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30-MAR-2000;
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02-DEC-1999;
09-DEC-1999;
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02-DEC-1999
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PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bloactive molecules to cells expressing PRO polypeptides, to modulate blological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expressing in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor and properties are also useful to stimulate the release of tumour necrosis factor and properties are also useful to stimulate the release of tumour necrosis factor are also useful to stimulate the release of cartilage, the proliferation of chondrocytes, the proliferation of chondrocytes, the proliferation of inner ear utricular supporting cells of artilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCS), or the proliferation of endothellal cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptides confector VIIA. The ERO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
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28.0%; Pred. No. 2.7e-158;
1ve 0; Mismatches 196; Indels 2;
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                                                   ACAGGGCCTGCCATCCTCAGCAAATGACCCTAGGACCAGGCCCTGGACTGCTGGTAGATG 1081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to PRO proteins and coding sequences. The present sequence is the coding sequence for one such PRO protein. It was found that the PRO genes are amplified in the genome of tumour cells. The gene amplification is expected to be associated with the overexpression of the gene product and contributes to tumourigenesis. Therefore, antagonists of PRO proteins are useful for the treatment of benign or malignant tumours, leukaemias, lymphoid malignancies and other disorders such as neuronal, alial, astrocytal, hypothalamic, glandular, epithelial, inflammatory and immunologic disorders.
              724 CCCTCCAGGGTCGCAGTCCACAAAACAGTGCCTTCTAGAGCCGGGCTGGGAATGGGGGC
                                                                   New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533, useful for diagnosing and treating cancers -
                                                                                                                     ΜI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 561.4; DB 22; Length 1266;
Pred. No. 2.7e-158;
0; Mismatches 196; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roy
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                                                                                                                                                                                                                                                                                                                cancer;
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                                                                                                                                                                                                                                                                                                               tumour;
                                                                                                                                                                                                      ВР
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                                                                                                                                                                                                   AAF60368 standard; cDNA; 1266
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99WO-US23089.
99WO-US28214.
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78.0%;
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99WO-US20594.
99WO-US20944.
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                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                             Cytostatic; PRO protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goddard A,
                                                                                                                                                                                                                                                                                 PRO261 coding sequence
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05-OCT-1999;
29-NOV-1999;
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08-SEP-1999;
13-SEP-1999;
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                                TCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAG
                                                                       363 TGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGTAAAGTGTGTGCACGG
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The invention relates to novel human anglogenesis-associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, agonists or antagonists of a PRO protein, agonists or antagonists of a PRO protein, additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular, endothelial or additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular, endothelial or adjogenic disorder, or the expression level of a PRO gene within a PRO gene, treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid, or PRO nucleic acid; and methods of inhibiting or stimulating endothelial or and methods of inhibiting or stimulating endothelial or and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antagonist thereof. PRO nucleic acids, PRO protein, or an agonist or antagonist thereof. PRO nucleic acids, PRO proteins, antibodies against PRO proteins, productions and production of a PRO protein, and production of a produced angiogenic disorders, such as atherosclerosis, osteoporosis, myocardial infarction, hypertension, atherosclerosis, osteoporosis, myocardial infarction, hypertension, endometricosis, ulcers, wounds, cancer, Alabrimer's disease, funtington's endometricosis, ulcers, wounds, cancer, Alabrimer's disease, psoriasis, endometricosis, ulcers, wounds, cancer, Alabrimer's disease, psoriasis, endometricosis, ulcers, wounds, cancer, Alabrimer's disease, psoriasis, corceen libraries to isolate cDNAs with sequence identity to PRO proteins, to map genes encoding PRO proteins, to enadype genetit thereof to screen libraries to isolate cDNAs with sequence intentity to PRO proteins, of g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, wounds or cancer -
    arthritis;
| healing; ca
| screening;
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erk MR, Marsters
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NL, Hillan KJ, Kuo SS, Mark MR, M
Watanabe CK, Williams PM, Wood WI;
myocardial infarction; diabetic retinopathy; rheumatoid
Crohn's disease; psoriasis; endometriosis; ulcer; wound
Alzheimer's disease; Huntington's disease; stroke; drug
                                                               gene therapy; transgenic animal; ss.
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99US-0144758.
99US-0145698.
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P-PSDB; AAB53084.
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12-MAR-1999;
14-MAY-1999;
02-JUN-1999;
23-JUN-1999;
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08-SEP-1999;
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15-SEP-1999;
05-OCT-1999;
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26-JUL-1999;
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the development and screening of potential The present sequence represents a cDNA encoding a PRO
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                                                                     Length 1266
                                                                                              Indels
                                               Sequence 1266 BP; 216 A; 418 C; 390 G; 242 T; 0 other;
   animals useful for the development and screening of
                                                                      DB 22;
                                                                                              0; Mismatches 196;
                                                                     Score 561.4; DB 2;
Pred. No. 2.7e-158;
                                                                     32.9%;
             therapeutic agents. The p protein of the invention.
                                                                                   Best Local Similarity 78.0
Matches 701; Conservaltive
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RESULT 13 AAV29260

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963 GCAGCCAGGAGCCACAGCTCATGGAACAGTGCTTTCTA-AGGCCAACTGGGGATGCGGAT 1021
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 363 TGCCCACAGGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGTAAAGTGTGTGCACGG
                                                                                                                                                                     AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGCCTTTAAAACCCAATTGCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human WISP-2 protein nucleotide sequence SEQ ID NO:13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This nucleotide sequence codes for human connective tissue growth factor superfamily. It was discovered in a cDNA library dervor director superfamily. It was discovered in a cDNA library derived from human osteoblasts. The gene has also been identified in cDNA libraries from ovary, testis, heart, lung, skeletal muscle, adrenal medulla, adrenal cortex, thymus, prostate, small intestine and colon. A cDNA clone is deposited as ATCC 97756. Also provided are vectors, host cells and recombinant methods for producing croffs-3 polypeptides. CTGF-3 nucleic acid sequences or their fragments, e.g. primers or probes, can be used to diagnose diseases where CTGF-3 expression is enhanced, e.g. cancer, arthritis, throsis or atherosclerosis, or diseases where expression is decreased such as in osteoporosis. Discorders characterised by decreased or increased levels of CTGF-3 can be treated by administering CTGF-3 polypeptides and anti-CTGF-3 antibodies,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human connective tissue growth factor 3 gene - useful diagnosis and treatment of e.g. cancer, arthritis, fibrosis,
                                                                                                                                            tissue growth factor-3; CTGF-3; human; cancer; flbrosis; osteoporosis; diagnosis; therapy; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 561.4; DB 19; Length
Pred. No. 2.7e-158;
0; Mismatches 196; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1285 BP; 237 A; 418 C; 389 G; 241 T; 0 other;
                                                                                                             Human connective tissue growth factor-3 gene.
                                                                                                                                                                                                                                           Location/Qualifiers
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AAV29260 standard; DNA; 1285
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al Similarity 78.0%;
701; Conservative (
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P-PSDB; AAW37946.
                                                                                                                                                                                                        Homo sapiens
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                                                                        14-SEP-1998
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                                                                                                                                                Connective arthritis;
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963 GCAGCCAGGAGGCACAGCTCATGGAACAGTGCTTTCTA-AGGCCAACTGGGGATGCGGAT 1021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Growth factor; protein inhibitor; protease; damaged tissue; platelet-derived growth factor; PDGF; fibroblast growth factor; FGF; connective tissue derived growth factor; CTGF; chrysalin; VEGF; keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF; transforming growth factor TGF-beta; matrix metalloproteinase; MMP; granulocyte macrophage colony stimulating factor; GM-CSF; uPA; vascular endothelial growth factor; urokinase plasminogen activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1082 CT-CTTCTCCATGCTCTTGGCTGCAGTTAACTGTCCTGCTTGGATTCACTGTGTAGAGC 1139
                                                                                                                                                                                                                                                                                                                                                                             843 ACAGCCTGGGGCCCTGCTCAACCACCTGTGGGCTGGGCATAGCCACCGGATGTCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                           796 ACGGTGTCCACCATCCCCAGCTGGTGCCCTGTGCCTTGGCCCTGGGCTGATGGAAGATG
                                                                                                                                                                                                                  CGGCTGCCCAGCTGGGACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGC
                                                                                                                         CCCGAGTGGGTÄTGTGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCAAGGA
                                                                                                                                                                                                                                                                                   CACCAACTITICTGCCCTTGTCACTCCTGCTCTGCTGATGCTCCTTGTCCAAATTGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-3 have homology to connective tissue growth factor (CTGF).

Products from the present invention can be used to treat WISP-related disorders such as breast, ovarian, and colon cancer or melanoma. The products can be used to treat arteriosclerosis. The products can also be used to treat other diseases e.g. benign and malignant tumours, leavaemia and lymphoid malignancies, neuronal, glial, astrocytal, and purpothalamic and other glandular, marcophagal, epithelial, stromal, and blastocoelic disorders, haematopoissis-related disorders, tissue-growth disorders, bone-related disorders seconds, connective tissue disorders, and other wounds, connective tissue disorders, catabolic states, testicular-related disorders, and inflammatory, catabolic states, testicular-related disorders, and inflammatory, catabolic states, testicular-related disorders, and inflammatory, catabolic such immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of an bused in the products can be used for detection and diagnosis especially of an bused in the products.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAATGGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCCCACAGGGGGTACCCCTGGTGCTGGCTGTGGCTGCTGTAAAGTGTGTGCACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 561.4; DB 20; Length 1293;
Pred. No. 2.7e-158;
0; Mismatches 196; Indels 2;
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Wood WI;
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                                                                                                                                                                                                                                                                                   Gurney AL
Roy MA,
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Pennica D,
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lbodies can be used to induce
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Best Local Similarity 78.0%;
Matches 701; Conservative
                                                                                                                                         98US-0081695
                                                                                                                                                               97US-0063704
98US-0073612
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Levine AJ,
                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
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Lawrence DA,
WO9921998-A1
                                                                                           29-OCT-1998;
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The specification describes a pharmaceutical composition, comprising a growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent, i.e. a protease. The inhibitor agent, i.e. a protease. The inhibitor agent, i.e. a protease, that is upregulated in a damaged tissue such as a wound environment. Growth factors which are included in the composition of the invention are platelet-derived growth factor (PDGF), fibroblast growth factor (FGF), connective tissue derived growth factor (CGF), transforming growth factor (KGF), transforming growth factor (KGF), transforming growth factor (KGF), vascular endothelial growth factor (KGF), wascular endothelial growth composition of the invention include inhibitors of urokinase-type plasminogen activator (UPA) and matrix metalloproteinase (MMP). The composition is useful for the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers. The present sequence encodes a human corrective to the composition of the
                                                                                                                                                   Composition for the treatment of damaged tissue i.e. chronic wounds and dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
                                              Occleston NL;
                                           Mcintosh FS,
                                                                                                                                                                                                                                             Disclosure; Page 546; 572pp; English.
                                           Davies MJ, Huggins JP,
                                                                                   WPI; 2001-418351/44
P-PSDB; AAB84599.
(PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
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Sequence 1309 BP; 261 A; 418 C; 387 G; 242 T; 1 other;

2; CGGCTGGGGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCCAGGCCTGGTCTGC 240 422 303 TCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAG 362 CAGCCTGGGGCAGCCCTGGCGCCCATGGGGCTGTGTCTCTTGGATGAGGATGACGCT 542 543 AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAACCCAATTGCAGG 602 CGGCTGCCCAGGAGTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGC 722 CCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGGCGTCCACGGCGCAAGGA 782 GTCCTGTGCCGCTGTGACGGTGGCTTCACCTGCCTGCCGCTGTGCAGTGAGGATGTG TGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTGTAAAGTGTGTGCACGG 2; Gaps Query Match 32.9%; Score 561.4; DB 22; Length 1309; Best Local Similarity 78.0%; Pred. No. 2.7e-158; Matches 701; Conservative 0; Mismatches 196; Indels 2; 61 363 483 301 181 241 603 663 421 723 481 ð 셤 ò 셤 ð qq В ò g ò g ò ŏ ŏ g

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qa	601 A	601 AcGGCCTGGGGACCTGCGACCACCTGTGGGCTGGGCATGGCCACCGGGGTGTCCAAC 660
Qy	903	903 CAGAACCGATTCTGCCAACTGGAGATCCAACGCCGCTGTGTCTGCCCAGACCCTGCTG 962
qa	661 C	661 cadaaccecricieccaacieaadaccaacececcieiecrerecaagecererecea 720
Qy	963 6	963 GCAGCCAGGAGCCACAGCTCATGGAACAGTGCTTTCTA-AGGCCAACTGGGGATGCGGAT 1021
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qa	781 A	ACGITCICCACCATCCCCAGCTGTGGCCCTGTGCCTGGGCTCGTGGAGAGATG 840
Qy	1082 C	1082 CT-CTTCTCCATGCTCTTGGCTGCAGTTAACTGTCCTGCTTGGATTCACTGTGTAGAGC 1139
qa	841 G	841 GTCCGTGCCCAGGCCCTTGCTGCTGCAGCCAACACTTTAGCTTGGGTCCACCATGCAGAAC 899

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_NA:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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APPLICANT: Pennica, Diane APPLICANT: Noy, Margaret Ann APPLICANT: Nood, William I. APPLICANT: WOOG, William I. TITLE OF INVENTION: WASP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME CURRENT APPLICATION NUMBER: US/09/182,145B CURRENT APPLICATION NUMBER: US 60/063,704 EARLIER APPLICATION NUMBER: US 60/063,704 EARLIER FILING DATE: 1998-10-29 EARLIER FILING DATE: 1998-02-04 EARLIER FILING DATE: 1998-02-04 EARLIER FILING DATE: 1998-02-04 EARLIER FILING DATE: 1998-04-14 NUMBER OF SEQ ID NOS: 156 SEQ ID NO 14 LENGTH: 1293 TYPE: DNA ORGANISM: Homo Sapiens	Ouery Match 32.9%; Score 561.4; DB 4; Length 1293; Best Local Similarity 78.0%; Pred. No. 2.2e-152; Matches 701; Conservative 0; Mismatches 196; Indels 2; Gaps 2; Oy 243 GGTGACATGAGGGGCAGTCCATTCATGTTTTTTGGCCATTCTTTCT		OY 363 TGCCACAGGGGGTACCCCTGGTGCTGGTGGCTGTGGCTGTAAAGTGTGTGCACGG 422	QY 423 AGGCTGGGGAGT©CTGCGACCACCTGCATGCCTGCGACCCAGCCTGGTTTGT 482	A 83 CAGCCTGGGGCAGĞCCCTGGCGGCCATGGGGCTGTGTCTCTTGGATGACGATGACGGT 542	OY 543 AGCTGTGAGGTGAATGGCCGCAGGTACCTGGAGAGAGACCTTTAAACCCAATTGCAGG 602	AN 603 GTCCTGTGCCGCTGTGATGACGGTGGCTTCACCTGCCGCTGTGCAGTGAGGATGTG 662	QY 663 CGGCTGCCCAGCTGCCCACGCCCCAAGAATACAGGTGCCAGGAAAGTGCTGC 722 	Oy 723 CCCGAGTGGGTATGMGACCAGGGAGTGACAGGGGATCCAGGGCTCCAGGGCGAAGGA 782 1   1   1   1   1   1   1   1   1   1	QY         783 CACCAACTTTCTGC@CTTGTCACTCCTGCTGTGTGTCCTAGTGGAGC 842           1   1   1   1   1   1   1   1   1   1
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APPLICATION NUMBEŘ: US/07/752,427
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GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match $9.6%; Score 163.8; Best Local Similarity $3.5%; Pred. No. 2.1. Matches 392; Conservative 0; Mismatches
NAME: Wetherell, Dr. Ph.D., John W. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 31,678
RELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
INFORMATION FOR SEQ ID NO: SEGUENCE CHARACTERISTICS:
LENGTH: 2075 base
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194 361 421

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541 431 601 835

671

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Š Š	836 TIGGAGCACAGCCTGGGCCCCTGCTCACCTGTGGGCTGGGC	qa	195 GCGGCCGTCGGCCAGAACTGCAGCGGGCCGTGCCGGTGCCGGACGAGCGGCGCGCGG 254
3 8	CCASACCACAGAS I GOAGCCCC 161 I CCAAGACC I GI GGGCAI CICCACCCCGGGI /	. Оу	362 Greeccacagegegracecregerecresargecreregreergraaagrerecace 421
8 c	896 GICCAACCAATTCTGCCAACTGGAATTCCAACGCCGCCTGTGTCTGCCCAGACC 955  1111	qq	255 CFGCCGGGGGGGGGGGGGCTGCGGCTGCGGCTGCGGCGGCGG
ογ	956 CTGCCTGGCAGCC 968	Qy	422 GAGGCTGGGGGAGTCCTGCGACCACGTGTCTGCGACCCCAGCCAG
Q D	852 TTGCGAAGCTGAC 864	Qy	TCAGCCTGGGGCAGGCCCTGGCGGCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGG
RESULT	Υ Β - 1,003-30C	qa	375 TGACTTCGGCTCCCGGCCAACCGCAAGATCGGCGTGTGCACCGCCAAAGATGGTGC 431
Sec ;	US-U8-380-880-1; Sequence 1. Application US/08386680	· Oy	542 TAGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACTTTAAACCCAATTGCAG 601
	ent No. 5383270 WERAL INFORMATION: APPLICANT: Grotendorst Gary R	QQ	432 TCCCTGCATCTTCGGTGGTACGGTGTGTGCGCGGGGGGGTCCTTCCAGGGCAGCTGCAA 491
	APPLICANT: Bradham Jr., Douglas M., TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR NUMBER OF SEQUENCES: 2	QY	602 GGTCCTGTGCCGCTGTGATGACGGTGGCTTCACCTGCCTG
	CORRESPONDENCE ADDRESS: ADDRESSEE: Spensley Horn Jubas & Lubitz STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla	λ <sub>O</sub> qα	
	STATE: CA COUNTRY: US ZIP: 92037	QY	CCCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGGGCTCCACGGCGCAAGG
	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	qa	612 CGAGGAGTGGGGTGTGACGAGCCCAAGGACCAAACCGTGGTTGGGCCTGCCCTCGCGGC 671
	COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25	QQ	782 ACACCAACTTCTGCCCTTGTCACTCCTGCCTCTGCTGATGCTCCTTGTCCAAA 835
	CORRENT AFFILCATION DATA: APPLICATION NMBER: US/08/386,680 CLASSIFICATION: 435	Qy	836 TTGGAGCACAGCCTGGGGCCCTGACCACCTGTGGGCTGGGCATAGCCACCGGAGT 895
	PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/167,628 FILING DATE:	ογ	GTCCAACCAGGATTCTGCCAACTGGAGATCCAACGCCGCTGTGTGTTGCCCAGACC
	APPLICATION NUMBER: US/07/752,427 FILING DATE:	qa	792 TACCAATGACAACGCCTCCTGCAGGTAGAAAGCAGAGCCGCCTGTGCATGGTCAGGCC 851
	ATTORNEY/AGENT INFORMATION: NAME: Wetherell, Jr. Ph.D., REGISTRATION NUMBER: 31,678 REFERENCE/DOCKET NUMBER: PD-1294	ov da	956 CTGCCTGGCAGCC 968 
Ĥ	TELECOMMUNICATION INFORMATION: TELEPHONE: 619-455-5100 TELEFAX: 619-455-5110 INFORMATION FOR SEQ ID NO: 1:	RESULT US-08-	RESULT 9 US-08-459-717-1 : Sequence 1, Application US/08459717
		Pa 	Patent No. 5770209 GENERAL INFORMATION: APPLICANT: Grotendorst, Gary R.
	STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA		APPLICANT: Bradham Jr., Douglas M., TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR NIWABER OF SEGUENCES: 2
	3 E		CORRESPONDENCE ADDRESS: ADDRESSE: Spensley Horn Jubas & Lubitz
; ; us-0	# FALVAE: CDS ; LOCATION: 1301177		SIREET: 4225 EXECUTIVE SQUATE, SUITE 1400 CITY: La Jolla STATE: CA COUNTRY: US
Out Mat	Query Match Best Local Similarity 53.5%; Pred. No. 2.1e-37; Matches 392; Conservative 0; Mismatches 332; Indels 9; Gaps 2;		ZIP: 92037 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMpatible
oy B	242 CGGTGACATGAGGGGCACTCATCCATCTTCTGGCCACTTCCTTC		OFERATIOS 5151EM: P.C.DOS/MB-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: US/08/459,717 FILING DATE: 02-IN1-1995
٥y	302 CTCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCA 361	_	CLASSIFICATION: 536

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                                                                                                                                                                          Sequence 1, Application US/08712302
Patent No. 5783187
GENERAL INFORMATION:
APPLICANT: Cortendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: #PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,302
FILING DATE: 11-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 163.8; DB 1;
Pred. No. 2.1e-37;
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RELING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER; 31,678
REGISTRATION NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEPHONE: 619-455-5110
INFORMATION FOR SEG ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base Pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,680
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US/08/167,628
FILING DATE:
APPLICATION NUMBER: US/07/752,427
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Best Local Similarity 53.5%;
Matches 392; Conservative (
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 92037
COMPUTER READABLE FORM:
                                                           956 CTGCCTGGCAGCC
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130..1177
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 163.8; DB 1; Length
Pred. No. 2.1e-37;
0; Mismatches 332; Indels
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/752,427
FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: 19-455-5100
INFORMATION FOR SEQ ID NO: SEGUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.6%;
Best Local Similarity 53.5%;
Matches 392; Conservative
                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: 130..1177
US-08-459-717-1
                                                                                                                                                                                                                                                                linear
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CLONE: DB60R32
                                                                                                                                                                                                                                                                  TOPOLOGY: 11
MOLECULE TYPE:
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GCAGCTGGGCGAGCTGTGCACCGGGCGCACCCCTGCGACCCGCACAGGGCCTCTTCTG
                                                                                                            TCAGCCTGGGGCAGGCCCTGGGGGCCTTGGTGTGTCTCTTGGATGAGGATGACGG
                                                                                                                                       375 TGACTTCGGCTCCCCGGCCAACCGCAAGATCGGCGTGTG----CACCGCCAAAGATGGTGC
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APPLICANT: Bradham Jr., Douglas M.,
IITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
WIMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
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APPLICATION NUMBER: US/08/880,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08880031
Patent No. 5916756
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APPLICATION NUMBER: (FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                    Pred. No. 2.1e-37;
                                                                                                                                                                                                                                                                                                                                     Score 163.8;
                John
         NAME: Wetherell, Jr. Ph.D., JOJ
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-128
TELECOMMUNICATION INFORMATION:
TELEPRAX: 619-455-510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                   9.68;
53.58;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   Matches 392; Conservative
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130..1177
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MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: DB60R32
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                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                       LOCATION:
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US-08-880-031-1
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                                        482 TCAGCCTGGGGCAGGCCCTGGCGGCCATGGGGGCTGTGTGTCTTGGATGAGGATGACGG
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                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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CORRESPONDENCE ADDRESS;
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
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COMPUTER: IBM PC compati
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ZIP: 92037
COMPUTER READABLE FORM:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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                                                                                                                   Sequence 1, Application US/09097179

Patent No. 6149916

GENERAL INFORMATION:
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEFAX: 619-455-510
TELEFAX: 619-455-510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,680
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US/08/167,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/097,179
                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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956 CTGCCTGGCAGCC 968
                                 852 TIGCGAAGCIGAC 864
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LOCATION: 130..1177
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NAME: Clough, David W.
REGISTRATION NUMBER: 36,11
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                            Sequence 7, Application US/09142569 Patent No. 6413735 GENERAL INFORMATION:
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LENGTH: 2075 base pairs
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STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
            Best Local Similarity 53.5
Matches 392; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
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Pred. No. 2.1e-37;
0; Mismatches 332;
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEFAN: 619-455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 53.5%;
Matches 392; Conservative
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130..1177
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MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-09-080-715-1
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                            Molecules
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                                                                                                 Gerstein, Murray &
South Wacker Drive
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OTHER INFORMATION: "CTGF cDNA coding sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
APPLICANT: Lau, Lester F.
TITLE OF INVENTION: Extracellular Matrix Signalling
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,569
FILING DATE: 02-Apr-1999
CLASSIFICATION: CLASSIFICATION:
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                                                                                                                                                                    STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                 ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
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CDS
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; NAME/KEY:
; LOCATION:
PCT-US96-08140-1
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              GCGGCTGCCCAGGCACTGCCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTG
                                                                                                                                                              722 CCCCGAGTGGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCAAGG
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GENERAL INFORMATION:
APPLICANT: University of South Florida
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08140
FILING DATE: 30-MAY-1996
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NAME: Halle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07414/003W01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 619-678-5099
TELEFAX: 619-678-5099
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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  Length 2075;
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Pred. No. 2.1e-37;
0; Mismatches 332;
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 Query Match
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He: 97.1244 secs
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8368.853 Million cell updates/sec
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1 GACGCTTCTGATCTCCAGAG.......GCCTAGAATAAACACCCAAA 1708
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			d				
Result No.	ult No.	Score	Query Match	Length DB	DB	QI	Description
	-	1708	100.0	1708	15	US-10-010-408-1	Sequence 1, Appli
	7	1278	74.8	1734	15	US-10-112-267-17	Sequence 17, Appl
O	٣	1278	74.8	1734	15	US-10-112-267-18	18,
	4	753	44.1	753	15	US-10-010-408-3	٠.,
	Ŋ	681	39.9	681	15	US-10-010-408-12	H
	9	566.8	33.2	1337	11	US-09-915-582-30	30,
	7	566.6	33.2	1352	11	US-09-915-582-14	Sequence 14, Appl
	8	561.4	32.9	1266	14	US-10-137-866-319	319,
	6	561.4	32.9	1266	14	US-10-146-726-319	Sequence 319, App
	10	561.4	32.9	1266	14	US-10-146-727-319	319,
	11	561.4	32.9	1266	14	US-10-146-788-319	319,
	12	561.4	32.9	1266	14	US-10-152-380:319	319,
	13	561.4	32.9	1266	14	US-10-153-934-319	319,
	14	561.4	32.9	1266	15	US-10-028-072-319	319,
	15	561.4	32.9	1266	15	US-10-121-049-319	Sequence 319, App
	16	561.4	32.9	1266	15	US-10-123-904-319	319,

SEQUENCE CHARACTERISTICS:

		Sequence 319, App Sequence 319, App
10-140-470-31 10-175-746-31 10-176-918-31 10-137-865-31 10-140-474-31 10-140-474-31 10-143-114-31	10.142.419-31 10.142.422-31 10.142.422-31 10.121-050-31 10.141-755-31 10.143-032-31 10.123-236-31 10.123-236-31	-140-921- -121-23-292- -123-903- -124-819- -140-922- -140-922- -160-498- -124-824-
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## ALIGNMENTS

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UNABER OF SEQUENCES: 13

CORRESPONDES ACCEFIELD, LLP

STREET: 28 State Street

CITY: Boston

STRYTE: ABSCANDHESES:

COUNTRY: USA

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                                                                                                                                                                                                                                                            Sequence 17, Application US/10112267 Publication No. US20030068678A1 GENERAL INFORMATION:
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Goddard, Aurey
Gurney, Austin L.
Hillan, Kenneth J.
Lawrence, David A.
Levine, Arnold J.
Pennica, Diang,
Roy, Margaret. Ann
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LENGIH: 1708 base pairs
                                                  LOCATION: 249..1001 SEQUENCE DESCRIPTION: SEQ US-10-010-408-1
        TYPE: nucleic acid
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TOPOLOGY: linear
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'GENERAL INFORMATION:
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               SAME
                                                                                                              60/081,695
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               ENCODING
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APPLICANT: Wood, William I.

TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENTITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENTITLE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/10/112,267
CURRENT FILING DATE: 2002-03-27
PRIOR PELING DATE: EARLIER FILING DATE: 1998-10-29
PRIOR PELING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR PELING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR PELING DATE: EARLIER FILING DATE: 1998-02-04
PRIOR PILING DATE: EARLIER FILING DATE: 1998-02-04
PRIOR PILING DATE: EARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 17
                                                                       an
                                                                                           as
            ACIDS
                                                                                                                                                                                                  Score 1278; DB 15;
Pred. No. 0;
0; Mismatches 165;
                                                                                                                                                                                                   74.8%;
88.5%;
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Best Local Similarity 88.5
Matches 1520; Conservative
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David A. Dert	٥٨	599 CAGGTCTGTGCCGCTGTGATGACGGTGGCTTCACCTGCCTG
Conen, Audrey Goddard, Audrey Gurney, Austin L.	qa	B CAGGGTTTTGTGCCGCTGTGTTTTCACCTGCCTGCCGCTGTGTGTG
Hillan, Kenneth J. Lawrence, David A. Levine, Arnold J.	Qy Db	659 TGTGCGGCTGCCCAGCTGCGCCCCCAAGAGAATACAGGTGCCAGGAAGTG 718 
APPLICANT: ROY, MAIGHER Ann APPLICANT: Wood, William I. TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME	Qy Db	719 CTGCCCGGAGTÅGGTATGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGC 775 1008 CTGCCCCGAGTĞGGTGTGTGACCAGGCAGTGATGCAGCCGGCAATCCAGCCTCCTCAGC 949
	Oy Dp	776 GCAAGGACACCÂACTTTCTGCCCTTGTCACCTCTGCTGATGCTCCTTGTCCAAA 835
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704 PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612	oy Oy	836 TTGGAGCACAGGCTGGCGCCCTGCTCAACCACCTGTGGGCTGGGCATAGCCACCGAGT 895
PRIOR FILING DATE: BARLIER FILING DATE: 1998-02-04 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695 PRIOR FILING DATE: BARLIER FILING DATE: 1998-04-14	Qy	896 GTCCAACCAGAÄCGGATTCTGCCAACTGGAGATCCAACGCGCCTGTGTCTGCCCAGACC 955
LENGTH: 1734 TYPE: DNA TYPE: DNA MUS MUSCULUS	Oy Dp	956 CTGCCTGGCAGCGAGCCCACAGCTCATGGAACAGTGCTTTCTAAGGCCA-ACTGGGGA 1014
74.8%; Score 1278; DB 15; Length 1734; 88.5%; Pred. No. 0;	QQ Dp	1015 TGCGGATACAGGCCTGCCATCCTCAGCAAATGACCCTAGGACCAGGCCCTGGACTGCTG 1074
3 CGCTTCTGATCTCCAGAGACCCTGGGTACAGGGCCTTGGCAAGGCTGCAGCCC 62  11	VO du	1075 GTAGATGCTCTTÄTCCATGCTCTTGGCTGCAGTTAACTGTCCTGCTTGGATTCACTGTGT 1134 
NGGCTCC 	δγ	1135 AGAGCCACTGAGGATCCCTGCTCTCAGGTAGGGGGAGCAGGTGACCAGCTCCAGT 1194
	Qy Dp	1195 TCTCTGGTTCAGCCTGGAATTCTGGGTTCTCCTGGCTCATTCCTCAAAACATCCCTGT 1252 
CAAGGG	Oy D	1253 ACAAAAAGGACAAAAGACCTTTAAACCTAGGCTATACTGGGCAAACCTGGCCACC 1312 
	Oy Dp	1313 GTGCTGGGGATAAĞGTCAATGTTAGG-ACCAGACAGCAGATTGCCTGAAACTTCCAATTC 1371 1111111111111111111111111111111111
ACCACC	. Oy	1372 CCTTCTTGGACTT@TGTGTGTCCCCAAAGATGATGAATGAACTGGTAAGTGTACCT 1431 11
0010010	Qy	1432 TCCCTGACCTGAGAACCCTGCCTGCTCGGAAGTATTCAGGGGCAGAATTCTCTGTGA 1491 1
CCTGGT	Qy	1492 ACATGAAGAGAT-GAATCACACTGTCCTTAAGAAATTCCTGAAAGTCCAGGAACTTGAGC 1550
ACGGAGGCTGGGGGGAGTCCTGCGACCTGCTGTCTGCGACCCCCGGGCCTGGT 1249  TTGTCAGCCTGGGGCAGGCCCTGGCGCCATGGGCTGTGTCTCTTGGATGATGAGGATGA 538  TTGTCAGCCTGGGGCAGGCCCTGGCGCCATGGGGCTGTGTGTCTCTTGGATGATGAGGATGA 1100	oy da	1551 TITGTATTITCAGGATGCACATCTCTTAAGCACTCGCAAAACAGGAAGGCTCCACACCT 1610 
	Qy	1611 CTGGCAGGCCAGGGCTTTCTCTTCAGCATGAGAAAGACAAGGACAGCAGAGTACTCT 1670 11111111111111111111111111111111111
	Qy	1671 CTCTGGAGGACTAGĜCTAGCCTAGAATAAACACCCCAAA 1708

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Sequence 12, Application US/10010408
Publication No. US20020165185A1
GENERAL INFORMATION:
APPLICANT: John J. Castellot, Jr.
And USS0020165185Alel Heparin-Induced CCN-Like Molecules and Uses Therefor
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          969 AGGAGCCACAGCTCATGGAACAGTGCTTTCTAA 1001
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RADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Amy E. Mandragouras
REGISCHARITON UNDBER: 35,207
REFERENCE/DOCKET NUMBER: MBI-004
TELECOMMUNICATION: INFORMATION:
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FILING DATE: March 19, 1998
APPLICATION NUMBER: <UNKNOWN>
FILING DATE: <UNKNOWN>
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COUNTRY: USA
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                                                                                           Sequence 3, Application US/10010408
Publication No. US20020165185A1
GENERAL INFORMATION:
APPLICANT: John J. Castellot, Jr.
TITLE OF INVENTION: and US20020165185A1el Heparin-Induced CCN-Like Molecules
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                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
44.1%; Score 753; DB 15; I
100.0%; Pred. No. 3.1e-225;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFCATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/044,273
FILING DATE: MAPPLICATION NUMBER: <URNOWN-APPLICATION NUMBER: <UNKNOWN-EILING DATE: CURKNOWN-EILING DATE: <URKNOWN-
                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1..750
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617)742-4214 INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                         CITY: Boston
STATE: Massachusetts
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STRANDEDNESS: single
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                                                                                                                                                                                           NUMBER OF SEQUENCES: 13
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Best Local Similarity
Matches 753; Conserv
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                                                                                                                                                                                                                                                                                                                                       Length 1337;
                                                                                                                                                                                                                                                                                                                                       DB 11;
                                                                                                                                                                                                                                                                                                                                     Query Match 33.2%; Score 566.8; DB 11; Best Local Similarity 77.0%; Pred. No. 8.4e-167; Matches 728; Conservative 3; Mismatches 205;
               Human Secreted Proteins
                       FILE REFERENCE: PS7291
CURRENT APPLICATION NUMBER: US/09/915,582
CURRENT FILIG DATE: 2001-07-27
PRIOR APPLICATION NUMBER: PCT/US01/01431
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/231,968
PRIOR FILING DATE: 2000-09-12
PRIOR FILING DATE: 2000-09-12
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 97
SOFFWARE: PALCHIN Ver. 2.0
                                                                                                                                                                                                                                                                     ; NAME/KEY: SITE
; LOCATION: (1337)
; OTHER INFORMATION: n equals a,t,g, or
US-09-915-582-30
                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
 APPLICANT: Rosen
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                                                                                                                                                                                                    Length 681;
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                                                                                                                                                                                                 39.9%; Score 681; DB 15; I 100.0%; Pred. No. 1.1e-202; tive 0; Mismatches 0;
                                                                                                                                     LOCATION: 1.681
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-010-408-12
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TELEPHONE: (617)227-7400
TELEPAX: (617)42-4214
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                  LENGTH: 681 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                               Local Similarity
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Db   295   GGCAGGACCCGGTGGACCCTGTGCCTCTTGGCAGGACGACGCTGTGA 354     Oy   551   GGTGAATGGCGCAGGTACCTGGAGGACCTTTAAACCCAATTGCAGGTCTGTG	Db 595 TTCTGGCCTTGTCCTCTCCCTGGTGTCCCCAGAATGGAGCACGCCTG 654  Qy 851 GGGCCCTGCTCAACCACCTGTGGGCTAGGCACCCCAGAACCG 910	GENERAL INCOMBATION NO. US20030129689A1 GENERAL INCOMATION NO. US20030129689A1 APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maureen APPLICANT: Desmoyers, Luca APPLICANT: Desmoyers, Luca APPLICANT: Gerritsen, Mary E. APPLICANT: Gerritsen, Mary E. APPLICANT: Goddard, Audrey APPLICANT: Goddard, Audrey APPLICANT: Gerritsen, Mary E. APPLICANT: Gerritsen, Mary E. APPLICANT: Gerritsen, Mary E. APPLICANT: Sherwood, Steven APPLICANT: Sherwood, Steven APPLICANT: Maranabe, Colin K. APPLICANT: Watanabe, Colin K. APPLICANT: Ahang, Zemin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C151 CURRENT APPLICATION NUMBER: US/10/137, 866 CURRENT APPLICATION NUMBER: 60/056974 PRIOR APPLICATION NUMBER: 60/056974
Qy         856 CCTGCTCAACCACCTGTGGCCATGCCACCCGATGTCCAACCAGAACCGATTCT. 915           IIIIII   IIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 7  US-09-915-582-14  Sequence 14, Application US/09915582  Sequence 14, Application US/09915582  Sequence 14, Application US/09915582  Sequence 14, Application US/09915582  GENERAL INFORMATION:  APPLICANT: Rosen et al.  TILE OF INVENTION:  CURRENT APPLICATION NUMBER: US/09/915,582  CURRENT APPLICATION NUMBER: US/09/915,582  CURRENT APPLICATION NUMBER: US/09/915,582  PRIOR FILING DATE: 2001-01-17  PRIOR FILING DATE: 2001-01-17  PRIOR FILING DATE: 2000-01-31  PRIOR FILING DATE: 2000-02-04  PRIOR FILING DATE: 2000-02-04  PRIOR FILING DATE: 2000-02-04  SEQ ID NO: 14  LENGTH: 1352  TYPE: DNA  CORGANISM: Homo sapiens  US-09-915-582-14	Query Match         33.2%;         Score 566.6;         DB 11;         Length 1352;           Best Local Similarity 77.0%;         Pred. No. 9.7e-167;         Length 1352;           Matches 732;         Conservative 0;         Mismatches 209;         Indels 10;         Gaps 3;           Oy         191 Graccrccacacacacacacacacacacacacacacacac

R: 6 - 6 - 6 - 6 - 6 - 6 - 6 - 6 - 6 - 6	NUMBER: 60/059352 1997-09-19 1097-09-19 NUMBER: 60/05988 1997-09-24 NUMBER: 60/062260 1997-10-17 NUMBER: 60/06287 1997-10-17 NUMBER: 60/06287 1997-10-24 NUMBER: 60/063814 1997-10-24 NUMBER: 60/063816 1997-10-24 NUMBER: 60/063816 1997-10-24 NUMBER: 60/063816 1997-10-24 NUMBER: 60/063817 1997-10-34 NUMBER: 60/063327 1997-10-24 NUMBER: 60/063327 1997-10-24 NUMBER: 60/063327 1997-10-24 NUMBER: 60/063327 1997-10-24 NUMBER: 60/063329 1997-10-28 NUMBER: 60/063550 1997-10-28 NUMBER: 60/063551	1997-10-29  NUMBER: 60/063733  1997-10-29  NUMBER: 60/063738  NUMBER: 60/063738  1997-10-29  NUMBER: 60/064248  1997-11-07  NUMBER: 60/064809  1997-11-07  NUMBER: 60/065186  1997-11-12  NUMBER: 60/065186  1997-11-21  NUMBER: 60/065186  1997-11-21  NUMBER: 60/066518  1997-11-24  NUMBER: 60/066511  NUMBER: 60/066511  NUMBER: 60/066511  NUMBER: 60/066710  1997-11-24  NUMBER: 60/066710
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PRIOR APPLICATION NUMBER: 60/06994
PRIOR PILING DATE: 1997-12-11
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PRIOR PILING DATE: 1997-12-16
PRIOR PILING DATE: 1997-12-16
PRIOR PILING DATE: 1997-12-16
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PRIOR PILING DATE: 1998-02-09
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                        GCAGCCAGGAGCCACAGGCTCATGGAACAGTGCTTTCTA-AGGCCAACTGGGGATGCGGAT
                                                                                                                               ACAGGGCCTGCCATCCTCAGCAAATGACCCTAGGACCAGGCCCTGGACTGCTGGTAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R10318
CURRENT APPLICATION NUMBER: US/10/146,726
CURRENT FILING DATE: 2002-05-15
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Pred. No. 4e-165;
0; Mismatches 196; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prior Application removed – See File Wrapper or NUMBER OF SEQ ID NOS: 550 iEQ ID NO 319
                                                                                                                                                                                                                                                                        Sequence 319, Application US/10146726; Publication No. US20030129690A1; GENERAL INFORMATION:
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78.0%;
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Goddard, Audrey
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Filvaroff, Ellen
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Smith, Victoria
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Watanabe, Colin
Wood, William
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Best Local Similarity 78.0
Matches 701; Conservative
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US-10-146-726-319
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78.0%; Pred. No. 4e-165;
ive 0; Mismatches 196; Indels
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FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
                                                                                                                                        APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
                                                                                                                                                                                            APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
                                  APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
                                                            APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
                                                                                      APPLICATION NUMBER: 60/089907
                                                                                                                60/089947
                                                                                                                                                                                                                      APPLICATION NUMBER: 60/090538
FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26
                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091982
                        19/98-06-11
                                                                                                                              DATE: 1998-06-19
                                                                                                    1998-06-18
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Matches 701; Conservative
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                                                                                                    FILING DATE:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFRENCE: P33300R1C312
CURRENT APPLICATION NUMBER: US/10/146,727
CURRENT FILING DATE: 2002-05-15
CAGCCTGGGGCAGCCCTGGCGCCATGGGGCTGTGTCTTTGGATGAGGATGACGT
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Publication No. US20030129691A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Baker, Kevin P.
APPLICANT: Baresini, Maureen
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Goo, Wel-Qlang
APPLICANT: Goodward, Audrey
APPLICANT: Goddowski, Paul J.
APPLICANT: Ghodowski, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
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                                                                                                            TGCCCACAGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTGTAAAGTGTGTGCACGG
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                                                                        Length 1266,
                                                                                           Indels
 or Palm
                                                                         DB 14;
                                                                                         0; Mismatches 196;
                                                                         Score 561.4; DB Pred. No. 4e-165;

    See File Wrapper

                                                                         32.9%;
78.0%;
                                                                                 Best Local Similarity 78.0
Matches 701; Conservative
Prior Application removed
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 319
LENGTH: 1266
TYPE: DNA
                                               Sapien
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1022 ACAGGCCTGCCATCCTCAGCAAATGACCCTAGGACCAGGCCCTGGACTGCTGGTAGATG 1081
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                                                                                                       APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C397
CURRENT APPLICATION NUMBER: US/10/152,380
CURRENT FILING DATE: 2002-05-21
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                              783 CACCAACTITCIGCCCTIGICACTCCIGCTCTGCTGAIGCTCCTIGICCAAAIIGGAGC
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Pred. No. 4e-165;
); Mismatches 196; Indels 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 319, Application US/10152380
; Publication No. US20030129694A1
; GENERAL INFORMATION:
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78.0%;
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Stewart, Timothy A.
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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DeForge, Laura
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Watanabe, Colin K
Wood, William
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Filvaroff, Ellen
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Best Local Similarity 78.0°
Matches 701; Conservative
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; ORGANISM: Homo Sapien
US-10-152-380-319
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                                                                                                                                                                                                                                                                                                                  APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERBNCE: P3330R1G32
CURRENT APPLICATION NUMBER: US/10/146,788
CURRENT FILING DATE: 2002-05-15
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.9%; Score 561.4; DB 78.0%; Pred. No. 4e-165
                           Sequence 319, Application US/10146788 Publication No. US20030129693A1 GENERAL INFORMATION:
                                                                                                                  Desnoyers, Luc
Filvaroff, Ellen
Gao, Wel-Qiang
Gerritsen, Mary E.
Goddard, Andrey
Goddowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
                                                                  APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Godwaf, Pang
APPLICANT: Godwafd, Audrey
APPLICANT: Godwafd, Audrey
APPLICANT: Godwski, Paul J.
APPLICANT: Godwski, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo Sapien
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Matches 701; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 319
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                                                                                                                                                                               Length 1266;
                 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C412
CURRENT APPLICATION NUMBER: US/10/153,934
CURRENT APPLICATION NUMBER: US/202-05-22
Prior Application removed - See file Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 319
                                                                                                                                                                                Score 561.4; DB 14;
Pred. No. 4e-165;
                                                                                                                                                                                                     0; Mismatches 196;
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Watanabe,Colin
                                                                                                                                                                                                       Conservative
                                                                                                                                                 Sapien
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                                                                                                                          LENGTH: 1266
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Best Local Si
Matches 701;
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APPLICANT:
                                                                                                                                    TYPE: DNA ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddwark, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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R APPLICATION NUMBER: 60/063329

R FILING DATE: 1997-10-27

R APPLICATION NUMBER: 60/06350

R FILING DATE: 1997-10-28

R APPLICATION NUMBER: 60/063561

R APPLICATION NUMBER: 60/063704

R FILING DATE: 1997-10-29

R APPLICATION NUMBER: 60/063733

R FILING DATE: 1997-10-29

R APPLICATION NUMBER: 60/06373

R FILING DATE: 1997-10-29

R APPLICATION NUMBER: 60/063735
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REPLING DATE: 1997-11-03

REPLING DATE: 1997-11-03

REPLING DATE: 1997-11-07

REPLING DATE: 1997-11-12

REPLING DATE: 1997-11-12

REPLING DATE: 1997-11-12

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REPLING DATE: 1997-11-21

REPLING DATE: 1997-11-24

REPLING DATE: 1997-12-11

REPLING DATE: 1997-12-16

REPLING DATE: 1998-10-24

REPLING DATE: 1998-01-23

REPLING DATE: 1998-01-23

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REPLING DATE: 1998-02-04

REPLING DATE: 1998-02-04
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BR FILING DATE: 1998-03-12
BR FILING DATE: 1998-03-12
BR FILING DATE: 1998-03-20
BR FILING DATE: 1998-03-20
BR APPLICATION NUMBER: 60/079294
BR FILING DATE: 1998-03-25
BR FILING DATE: 1998-03-25
BR FILING DATE: 1998-03-31
BR FILING DATE: 1998-03-31
BR FILING DATE: 1998-03-31
BR FILING DATE: 1998-03-31
BR FILING DATE: 1998-04-09
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APPLICATION NUMBER: 60/081818
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082999
FILING DATE: 1998-04-24
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APPLICATION NUMBER: 60/063738
FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063755
FILING DATE: 1997-10-17
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1082 CT-CTTCTCCATGCTCTTGGCTGCAGTTAACTGTCCTGCTTGGATTCACTGTGTAGAGC 1139
                                                                                                            CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
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PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-08-26
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059117
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059184
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PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-17
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R FILING DATE: 1997-09-19
R FILING DATE: 1997-09-19
R APPLICATION NUMBER: 60/05988
R FILING DATE: 1997-09-24
R FILING DATE: 1997-09-24
R FILING DATE: 1997-10-17
R APPLICATION NUMBER: 60/062250
R FILING DATE: 1997-10-17
R APPLICATION NUMBER: 60/062285
R APPLICATION NUMBER: 60/062287
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R APPLICATION NUMBER: 60/062287
R FILING DATE: 1997-10-17
                                                                                                                                                                                                                                                                    Sequence 319, Application US/10028072 Publication No. US20030004311A1 GENERAL INFORMATION: APPLICANT: Baker, Kevin P.
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FILING DATE: 1997-10-24
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Stewart, Timothy A.
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E
Goddard, Audrey
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Watanabe, Colin K
Wood, William
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DeForge, Laura
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Gurney, Austin L.
Sherwood, Steven
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TITLE OF INVENTION:
FILE REFERENCE:
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US-10-028-072-319
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           303 TCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAG 362
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Publication No. US20030022239A1
GENERAL INFORMATION:
APPLICANT: Barer Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Godwaki, Paul J,
APPLICANT: Godwaki, Paul J,
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Pred. No. 4e-165;
0; Mismatches 196; Indels
PRIOR APPLICATION NUMBER: 60/08345
PRIOR FILING DATE: 1998-04-29
PRIOR PLEILOR DATE: 1998-04-29
PRIOR PLEILOR DATE: 1998-04-29
PRIOR PLICATION NUMBER: 60/084600
PRIOR PLICATION NUMBER: 60/084617
PRIOR PLICATION NUMBER: 60/084617
PRIOR PLICATION NUMBER: 60/084617
PRIOR PLICATION NUMBER: 60/085149
PRIOR PLICATION NUMBER: 60/085149
PRIOR PLICATION NUMBER: 60/085139
PRIOR PLICATION NUMBER: 60/085339
PRIOR PLICATION NUMBER: 60/08539
PRIOR PLICATION NUMBER: 60/08539
PRIOR PLICATION NUMBER: 60/08539
PRIOR PLICATION NUMBER: 60/08539
PRIOR PLICATION NUMBER: 60/08579
PRIOR PLICATION NUMBER: 60/086704
PRIOR PLICATION NUMBER: 60/08910
PRIOR PLICATION NUMBER: 60/08910
PRIOR PLICATION NUMBER: 60/08910
PRIOR PLICATION NUMBER: 60/089170
PRIOR PLICATION NUMBER: 60/090349
PRIOR PLICATION NUMBER: 60/0
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11 Similarity 78.0%;
701; Conservative
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         APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watenabe, Colin K
APPLICANT: Watenabe, Colin K
APPLICANT: Apong, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND ITTLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RLC17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
                                                                                                                                                                                                                 Length 1266;
                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                              Score 561.4; DB 15; Length
Pred. No. 4e-165;
0; Mismatches 196; Indels
                                                                                                                     Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
SEQ ID NO 319
LENGTH: 1266
                                                                                                                                                                                                              Query Match 32.9%;
Best Local Similarity 78.0%;
Matches 701; Conservative
Smith, Victoria
                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo Sapten
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B1826781 603077268
B1826781 60307263
B182562 603072631
BQ560868 H4067A01-
BG925960 AGENCOURT
BG922868 HAC57-1-D
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AA754979 vu55048.r
B0961357 AGENCOURT
BB849097 BB849097
BM75186 K-EST0028
AA717584 vt97c08.r
BE481184 vt97c08.r
BE481184 vt97c08.r
BR4899 pgm2n.pk0
AI225477 ue8Bb01.y
BC338695 602566932
B1823598 603040962
BC900069 HOAS1-1-A
BC900020 HOA48-1-G
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UI-R-CN1-cmq-k-07-0-UI.sl UI-R-CN1 Rattus norvegicus cDNA clone
UIR-CN1-cmq-k-07-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL55143 AL555143
BF49398 CM3 EN007
BB792544 BB722544
BB222795 BB222795
BB319151 BB319151
BB20676 BB319151
BB37499 BB374499
BF05642 7K20606
AL542806 AL542806
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
Oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
TTel: 319 335 8250
Fax: 319 335 9565
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches
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Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Minimum | Maximum |

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Alab_host="Weather Part73D-Peac (Pharmacia) with a modified notes" Vetcor: Part73D-Peac (Pharmacia) with a modified polylinker: Site_1: Not I: Site_2: Eoo Ri: The UT-R-CMI library is a subtracted library derived from the following pool of seven normalized rat libraries: normalized rat badder, normalized rat badder, normalized rat brown adipose, normalized rat cervix, normalized rat brown adipose, normalized rat cervix, normalized rat brown adipose, normalized rat cervix, normalized rat badder, normalized rat commission of the procedure described by Bonaldo, Lenno & Soares (Genome Research Genome 6: 791-806, 1996). For construction of the Procedure described by Bonaldo, Lenno & Soares (Genome Research Genome 6: 791-806, 1996). For construction of the Call library: plasmid DNA from the pool of normalized the CALL the WI library: plasmid DNA from the pool of normalized the CALL the used as a tracer in a subtractive hybridization with a cromate from amplified inserts from a planid DNA template preparation) comprising: a) a pool of about 29,000 clones from subtracted libraries CAO and CAL corresponding to plates R-5 was ware through R-CAO-BNC NATA through R-CAI-BNC NATA-BNC NA
tail. The sequence tag present in the cDNA between the NotI site and the Oilgo-dT track served to identify it as a clone from the normalized cervix library CDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) Seq primer: M13 Forward POLYA-YES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="UI-R-CN1-cmq-k-07-0-UI"
/clone_lib="UI-R-CN1"
                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Sprague-Dawley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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including CYO, C2O, DAO, DBO, DCO, DDO, and DEO corresponding to plates R-CYO-BXP through R-CYO-BXZ, R-CZD-BXZ-C, R-DAO-BXJ through R-CXD-BXI, R-DAO-BXJ through R-DAO-BXI, R-DAO-BXI through R-DAO-BXH, R-DBO-BZA through R-DAO-BZH, R-DBO-BZA, R-DOO-BZI through R-DAO-BZD, R-DEO-CAA, R-DBO-BZA, R-DEO-CAB through R-DBO-CAA, R-DBO-CBAC, and R-DEO-CAB through R-DBO-CAA, R-DBO-CBAC, and R-DEO-CAB through R-DBO-CAA, R-DBO-CBAC, and R-DEO-CAB through R-DBO-CAA.

R-DDO-CBB-C, and R-DEO-CAB through R-DBO-CAA.

The Gorresponding plates are R-CNO-BKH, R-CNO-BLD, R-CNO-BLG, R-CNO-BLP, R-CNO-BLP, R-CNO-BLP, R-CNO-BLP, R-CNO-BLP, R-CNO-BLP, R-CNO-BLP, R-CNO-BLC, R-CNO-BLP, R-CNO-BLP, R-CNO-BLP, R-CNO-BLP, R-CNO-BLP, R-CNO-BLP, R-CNO-BLC, R-CNO-BLP, R-CNO-BLC, R-CNO-BLP, R-CNO-BLC, R-CNO-BLP, R-CNO-BLC, R-CNO-
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0; Mismatches 6; Indels 0:
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1454 CCTGCTCGGGAAGTATFCAGGGGCAGAATTCTCTGTGAACATGAAGAGATGAATCACACT 1513

302 CTCAATGGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCCCCA	122 ATGCCGGTGGGAGTACCCCTGGTGCTGGGCTGTGGCTGCCGGGTATGTGCACG 422 GAGGCTGGGGAGCCTGCGACCACGCATGTCTGCGACCCCAGGCCTGGTTTG	Db   182 GCGCTGGGGAGCCCTGCGACCAACTCCACGTCGCACCCAGGGCCTGGTCTG 241	Qy         542 TAGCTGTGAGGTGAATGGCCGCAGGTACCTGGAGAGCCTTTAAACCCCAATTGCAG 601           Db	Qy         662 GCGCTGCCCACTGGGACTGCCCCAAGAAATACAGGTGCCAGGAAAGTGCTG         721           LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII         111111111111111111111111111111111111	OY 782 ACACCAACTTTCTGCCCTTGTCACTCTGCTGATGCTCTTGTCCAAATTGGAG 841	QY         902 CCAGAACCGATTCTGCCAACTGGAGATCCAACGCCGCTGTGTCTGCCCAGACCCTGCCT         961           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 3 BQ279131 LOCUS BQ279131 BQ279131 BQ279131 BQ279131 BQ279131 BQ279131 AGENCOURT 7046721 NIH_MGC_107 Homo sapiens CDNA clone IMAGE:5805819 S', mRNA sequence. ACCESSION BQ279131.1 GI:20489339 KEYWORDS EST. SOURCE human. ORGANISM HOMO sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	REFERENCE 1 (bases 1 to 979) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Contact: Robert Strausberg, Ph.D. Emall: Gapbs-r@mail.inh.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be
1614   1   1   1   1   1   1   1   1   1	1574 CICTTAAGCACTGGCAAAACAGGAAGGCTCCACACTCTGGCAGGGCCAGGGCCTTTCTCT	Qy 1634 TCAGCATGAGAAAGACAAGGACAGCAGAGTACTCTCTGGAGGACTAGTCTAGCCTA 1693		_	REFERENCE 1 (bases 1 to 1058)  AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.  TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  JOURNAL Unpublished (1999)  COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-rémail.nih.gov	Constituting the state of the s	/db_xref="taxon:9606" /clone=lib="IMAGE:5725937" /clone=lib="IMAGE:5725937" /lab_host="NHLMGC_125" /lab_host="DHLUB" /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: BCoRV (destroyed); Site_2: Not1; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size a library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics	### BASE COUNT   139 a   423 c   294 g   200 t   2 others    ORIGIN   29.98;   Score 511.2;   DB 14;   Length 1058;    Best Local Similarity   79.38;   Pred. No. 8.1e-128;   Matches 606;   Conservative   0;   Mismatches 158;   Indels   0;   Gaps   0;    Qy   242 CGGTGACATGAGGGCCACTGATCCATCTTCTGGCCACTTCCTTC

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/note—"Organ: pooled brain, lung, testis; Vector:

pCMV-SPORT6: Site_1: Noti; Site_2: EcoRV (destroyed); RNA
source annorymous pool of 6 male brains, age fange 21-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
elsertroyed upon cloning). Average insert size 18 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                    BI822142 886 bp mRNA linear EST 04-OCT-2001
603039845F1 NIH_MGC_115 Homo saplens CDNA clone IMAGE:5180650 5',
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673 CCAGCGCCGCCTGTGCCTGTCCAGGCCCTGCCACCCTCCAGGGGTCGCAGTCCACAAA 732
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Catarrhini; Hominidae; Homo.
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(bases 1 to 886)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) (npublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lettp://maqg.lih.gov
http://maqg.lih.gov
Plate: LLAMI1450 row: j column: 11
High quality sequence stop: 865.
Location/Qualifiers
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Pred. No. 2.5e-123;
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Pred. No. 2.8e-125;
0; Mismatches 147; Indels 0;
found through the I.M.A.G.E. Consortium/LLNL at:
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                       http://image.llnl.gov
Plate: LLCM2045 row: k column:
High quality sequence stop: 752.
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Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
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                                                                                                                                                                                                                                                                                                                                  Score 440.6; DB 13; Length
Pred. No. 1.2e-108;
Mismatches 165; Indels
                                /organism="Homo sapiens"
/db_xref="taxon:9606"
 Location/Qualifiers
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77.7%;
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Best Local Similarity 77.7
Matches 594; Conservative
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mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 916)
             TGTGATGACGGTGGCTTCACCTGCCGCTGTGCAGTGAGGATGTGCGGCTGCCCAGC
                                                                                                                                                                                                                                  TGTGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCAAGGACACCAACTTTCT
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                                                                               AATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAAACCCAAATTGCAGGGTCCTGTGCCGC
                                                                                                                AACGGCCGCCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCAGCATCCGCTGCCGC
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National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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High quality sequence stop: 778.
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Tissue Procurement: ATCC
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Eukaryota; Metazāa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 732)
SILHORO http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Lu pubblished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail: nih.gov
Tissue Procurement; Gilbert Smith, Ph.D.
Contact: Robert Strausberg, M.D.
Email: cgapbs-remail: nilbert Smith, Ph.D.
Contact: Robert Strausberg, N.D.
Email: cgapbs-remail: nilbert Smith, Ph.D.
Contact: Robert Strausberg, Consortium (LLNL)
DNA Sequencing by: Increased by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Lindon through the I.M.A.G.E. Consortium/LLNL at:
Lindon through the I.M.A.G.E. Consortium/LLNL at:
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/lab_host="lumor" lumo; Vector: pCWV-SPORT6; Site_l: Not!;
/lab_host="lumor" lumor lum
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                                                                                 110 CAGCTGTGAGGGGAACGGCCGCCTGTATCGGGAAGGGGAAGACCTTCCAGCCCCACTGCAG
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Location qualifiers
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/strain="@ZECH II"
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BF138093.1 GI:10977133
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/close="Organ: potB7; Site_1: 
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Everyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Everyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Everyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 750)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin information can be
found Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1929 row: k column: 19

High quality sequence stop: 714.

Location/Qualifiers
                                                                                                                                                                                                                     BMO43988 750 bp mRNA linear EST 07-NOV-2001 603620978F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5446794 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 TCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 CGGCTGGGGGGGGCCTGCGACTCCACGTCTGCGACGCCATGCCAGGCCTGGTCTG 249
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Pred. No. 1.6e-107;
0; Mismatches 146; Indels 5;
1. 750
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                    BM043988.1 GI:16773255
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79.0%;
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Best Local Similarity 79.0
Matches 569; Conservative
                                                                                                                                                                                                                                                                                                      mRNA sequence.
BM043988
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Homo sapiens CDNA clone IMAGE:5258159 5',
                       8;
                                                                                        TAAGGCCA-ACTGGGGATGCGGATACAGGGCCTGCCATCCTCAGCAAATGACCTTAGGAC 1057
                                                                                                                                                                                                                         AGGTGACCAGCTCCAGTTCTCTGG--TTCAGCCTGGAATTCTGGGTTCTCTGGCTCATT 1235
                                                                                                                                                                                                                                                                                                                                                         CCTGAAACTTCCAATTCCCTTCTTGGACTTCTGTATGCTTGTCCCCAAAGATGATGATG 1414
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                                                                                                                                                                                                                                                                                                              GGGCAAACCTGGCCACCGTGCTGGGGATAAGGTCAATGTTAGG-ACCAGACAGCAGATTG 1354
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) (Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                   121 CAGGCCCTGGACTGATAGATGCCCCTCTCCATGCTCTTGGCTGCAGATAACTGTCCT
                                                                                                                                                                             CCTCAAAACATCCCTGTACAAAAGGACAACCAAAAAGACCTTTAAACCTAGGCTATACT
                                                                                                                                                                                                                                                                                1534 AGTCCAGGAACTTGAGCTTTGTATTTTCAGGAATGCACATCTCTTAAGCACTCGCAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGCCCTGGACTGCTAGATGCTCTTCTCCCATGCTCTTGGCTGCAGTTAACTGTCCT
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                                            939 CTGTGTCTGCCCAGACCCTGCCTGCCAGGAGCCACAGCTCATGGAACAGTGCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                         479 ACCTTGTAAGTGTGCCTTTCCTGATCTGAGAACACCCTGCCGGCT-------
                        Gaps
  Length 792;
Score 432.4; DB 12;
Pred. No. 2e-106;
0; Mismatches 101;
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B1457141
B1457141.1 GI:15247797
 25.3%;
82.8%;
                       Conservative
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           al Similarity
596; Conserv
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 Query Match
Best Local Si
Matches 596)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:5258159"
/clone=lib="MIH_AGC_42"
/clone=lib="miH_AGC_44"
/clone=l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 CCTTGGACACCACCCCAGTGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465 AGCCAGGGCCTGGTTTGTCAGCCTGGGGCAGGCCCTGGCGGCATGGGGCTGTGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 AGCCA-GGCCTGGTCTGCCAGCCCGGGGCAGGACCCGGTGGACGGGGGGCCCTGTGCCTC
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                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM1869 row: g column: 24
High quality sequence stop: 651.
Location/Qualifiers
CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 430.2; DB 13; Length 651; Pred. No. 7.3e-106;
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Matches 518; Conserv
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654

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BO937887
AGENCOURT_8951807 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:6476852 5', mRNA sequence.
                                                                                                                                                                   1225 CCTGGCTCATTCCTCAAAACATCCCTGTACAAAAAGGACAACCAAAAAGACCTTTAAAAC 1284
       /clone_lib="NCI_GGAP_GC24"
/clone_lib="NCI_GGAP_GC24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 Kb. Constructed by Life
Technologies. Note: this is a NCI_GGAP Library."
                                                                                                                                                                                                                                                                                                                                                               1285 TAGGCTATACTGGGCAAACCTGGCCACCGTGGGGGATAAGGTCAATGTTAGG-ACCAG
                                                                                                                                                                                                                                                                                          540 GCAGCAGAT--GCTGAAACATCCAGGTCCCTTCTTGGACTTCTATGTGCTTGT-CCCACA
                                                                                                     1167 GTAGGCGGAGCAGGTGACCAGCTCCAGTTCTCTGG--TTCAGCCTGGAATTCTGGGTTCT
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ilarity 90.9%; Pred. No. 1.3e-104;
Conservative 0; Mismatches 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ937887
BQ937887.1 GI:22353365
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Best Local Simi
Matches 488;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
Plate: LLAM9276 row: h column: 13
High quality sequence stop: 613.
Location/Qualifiers
I. 966
/organism="Num musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="ImAGE:4021308"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-norgan: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo MT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                             966 bp mRNA linear EST 24-OCT-2000 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4021308 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      988 ACAGTGCTTTCTAAGGCCA-ACTGGGGATGCGGATACAGGGCCTGCCATCCTCAGCAAAT 1046
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                                                                                                                                                                                                                                                                                                           Mus musculus Sukaryotas, Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryotas; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 966)
11 (bases 1 to 966)
12 (http://mgc.ncl.nih.gov/.
Natlonal Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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86; Indels
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Pred. No. 1.4e-105;
0; Mismatches 86; Ii
                                                                                                                                                                                         mRNA sequence.
BF141695
BF141695.1 GI:10980735
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il Similarity 85.6%;
571; Conservative (
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house mouse.
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pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
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                                                                                                                                                         Query Match
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CDNA clone IMAGE:5753009
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                                                                                                                CCTGTCAG---CTTGTCCTAAAGTCTTAGCACTTGTGGTGGCTTGGGCTTCACACACTGT 176
                                                                                                                                                                                 CTTCTCTCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCA 356
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1006)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                        GCTG-GGCAGTGGCTTGGAATGGAGGTCTTTATTACTGGGAACTGAGGAGCTAAGAGGCT
                                                                            CAGACACCTTCGTGGTGGCCTCCACGGCCTCACCTTCAGGTTTGAAGCTGGCTCCACAAG
          GACGCTTCTGATCTCCAGAGGACCCTGGGGTGGGACAGGGGCCTTGGCAAGGCTGCAGCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM12788 row: b column: 18
High quality sequence stop: 593.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IAAGE:5753009"
/clone_lib="NHLMGC_115"
/lab_host="DH108"
/note="Organ: pooled brain, lung, testis; Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1006 bp mRNA AGENCOURT_6708025 NIH_MGC_115 Homo sapiens of mRNA sequence. BM921531 BM921531.1 GI:19371910
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Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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BQ073722 1073 bp mRNA linear EST 02-APR-2002 AGENCOURT_7046577 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:5806602
Source anonymous pool of 6 male brains, age range 23,27; I male lung, age 27; and 1 male testis, age 69. Library is oligo-dr primed and directionally cloned (Bcorw site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH MGC Library.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCTGCTCGACCACCCNTGTGGGCTGNGCATGGCCCACCCGGGTGTCCAAACCAGAACCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 CCTGCGACCACCTGCATGTCTGCGACCCCAGCCCAGGCCTGGTTTGTCAGCCTGGGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCCTGGCGGCCATGGGGCTGTGTCTCTTGGATGAGGATGACGGTAGCTGTGAGGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 421.2; DB 14;
Pred. No. 2.4e-103;
0; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A - - GGAGCCACAGCTCATGGAACAGTGCTTTCTAA
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661

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BMO46275 790 bp mRNA linear EST 07-NOV-2001 603626068F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5452480 5',
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lonpublished (1959)

Lontact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement. Corro/Orp

CDNA Library Argayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llni.gov

Plate: LLCM1944 Trow: h column: 17

High quality sequence stop: 780.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Euthegia; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to ½90)
                                                             816 GCTGATGCTCCTATGTCCAAATTGGAGCACAGCCTGGGGCCCCTGGTCAACCACCTGTGGG
                                                                                                                                                                                                                                                                                              696 AGAATACAGGTGCCAGGAAAGTGCTGCCCCGAGTGGGTATGTGACCAGGGAGTGACACCG
                                                                                                                                               GCGATCCAGCGGTCCACGCGCGAAGACACCAACTTTCTGCCCTTGTCACTCCTGCCTCT
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Pred. No. 9e-101;
0; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BM046275
BM046275.1 GI:16775542
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74 . 58 ;
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Best Local Similarity 74.5
Matches 562; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .790
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VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
BM046275
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/clone="Index:5806602"
/clone="Index:5806602"
/clone=lib="NIH_MGC_101"
/lissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: poTB7; Site_1: EcoRI; Site_2:
%hol; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/Xhol sites using the following 5' adaptor:
GGCACGAG(6). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             395
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

Nortional Institutes of Health, Mammalian Gene Collection (MGC)

L' Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: capabs-rémail.nih.gov

Tissue Procurement: Arayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLCM2047 row: k column: 19

High quality sequence stop: 517.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 TGCGTGCCGCTGTGCAGCGAGGATGTGCGGCTGCCCAGGTGGGACTGCCCCACCCCAGG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                             Euteleostomi;
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                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 417.8; DB 14; Length 1073;
Pred. No. 2.1e-102;
0; Mismatches 132; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 t
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                      BQ073722.1 GI:19902768
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ilarity 79.5%;
Conservative
mRNA sequence.
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                                                                                                                   human.
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Manal: capabs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian.Gene Collection (
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/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH\_MGC Library.

a 284 c 264 g 136 t lothers ė; 388 133 448 193 508 252 568 312 628 372 688 748 928 432 808 868 608 551 491 667 73 CCATCTTCTGGCCACTTCCTTCTCTCTCTCTCTAATGGTGTGTGCCCAGCTGTGCCG GGGGCCCTGTGCCTCTTGCCAGAGGACGACAGCAGCTGTGAGGTGAACGCCCGCTGTA - CCTGCCCCTGGTCCCCTGCCAGAATGGAGNCACGGC--TGGGACCCTGCTCGACCAC CTGTGGGCTGGGCATAGCCACCCGAGTGTCCAACCAGAACCGATTCTGCCAACTGGAGAT GACACCCTGTACCTGTCCTTGGACACCACCCCAGGGCCCACAGGGGGGTACCCCTGGTGCT GGATGGCTGTGCTGTGTAAAGTGTGTGCACGGAGGCTGGGGGGAGTCCTGCGACCACCT 449 GCATGTCTGCGACCCCAGGCCTGGTTTGTCAGCCTGGGGCAGGCCCTGGCGGCCA CCACGTCTGCGACGCCAGCCA-GGCCTGGTCTGCCAGCCCGGGGCAGGACCCGGTGGCCG 509 TGGGGCTGTGTGTCTCTTGGATGAGGATGACGGTAGCTGTGAGGTGAATGGCCGCAGGTA CCTGGATGGAGAGCCTTTAAAACCCAATTGCAGGGTCCTGTGCCGCTGTGATGACGGTGG CCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGCCCCGAGTGGGTATGTGACCAGGGAGT CCCCAGGAGGGTCGAGGTCCTGGGCAAGTGCTGCCTGAGTGGGTGTGCG-GCAAGGAGG GACACCGGCGATCCAGCGCTCCACGGCGCAAGGACACCAACTTTCTGCCCTTGTCACTCC TGCCTCTGCTGATGCTCCTTGTCCAAATTGGAGCACAGCCTGGGGGCCCCTGCTCAACCAC þe Gaps can 7; clone distribution information Length 800; DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information driving the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11420 row: g column: 18
High quality sequence stop: 788.
Location/Qualifiers
1. 800
/organism="Homo sapiens"
/db\_xref="taxon:9606"
/clone="INAGE:5169065"
/clone="INAGE:5169065"
/tissue\_type="medulia"
/tissue\_type="medulia"
/lab\_host="DH108" Indels DB 13; Score 410.2; DB 13; Pred. No. 2.2e-100; ); Mismatches 159;

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//organism="know sapiens"
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//clone="taxon:9606"
//clone="taxon:proper resistant"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
  CCAACGCCGCCTGTGTCTGCCCAGACCCTGCCTGGCAGCCAGGAGCCACAGCTCA - TGGA
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
plate: LLCM1833 row: m column: 18
High quality sequence start: 28
High quality sequence stop: 756.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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July 28, 2003, 15:59:01; Search time 486.369 Seconds (without alignments) 10471.464 Million cell updates/sec US-10-010-408-1\_COPY\_1534\_1708
175
1 AGTCCAGGAACTTGAGCTTT.......GCCTAGAATAAACACCCAAA 175 4109280 2054640 seqs, 14551402878 residues Total number of hits satisfying chosen parameters: OM nucleic - nucleic search, using sw model Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Title: Perfect score: Sequence: Scoring table: Searched: Run on:

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID	26895 AC126895	.8 AC095418 R	981 AF259981	24 AR210324	325 AR210325 Sequenc	AF100778 Mus mu	731698 Mouse	AL669906 Mus mus	AF126063 Mus mu	AC130013 Rattus	AP003608 Oryza	ACUZILIS HOMO	ACOQ4201 Ba++++	AC068103 Homo sa	АС096729 Ношо	AC122851 Mus mus	AC129096 Papio c	AC113225 Rattus	ACIIZIOS Rattus	AL59518	AL445199 Human D	AC090736	AC020603 Homo	AC109624 Mus	AL844489 Mus mus	ט מ	AC015689 Homo	AP003879 Oryza	AP004591	AC121976 Mus	AC122340 Mus mus	78 ACU48378 HOMO SB	AC128523 Rattu	7.1 ACLI4//1 HOWO	591003	70 AC122470 Mus mus	702_2 Continuat	26784 AC026784	3267 AP003267 Oryza s	81 AC0167
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## ALIGNMENTS

	137964 bp DNA linear HTG 24-JUL-2002	IN PROGRESS							Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Murinae;			, Allen,C.,	
	linear	Rattus norvegicus clone CH230-301E4, *** SEQUENCING IN PROGRESS							Vertebrata;	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,	
	bp DNA	-301E4, ***							Craniata;	Sciurognat			luola, B., Al	
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RESULT 1 AC126895	LOCUS	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM				REFERENCE	AUTHORS	

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Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bunke, S., Brieva, M., Brown, E., Brown, M., Bryant, N.C., Carron, T.Y., Char, G., Chen, G., Dayer, M.D., Dathorne, S.R., David, R., David, R., Daland, C.D., Daraper, H., Dugan, Rocha, S., Durbin, R., Delandy, K.R., Delang, M., Card, J., Poster, P., Frantz, P., Earnbart, C., Edgar, D., Edwards, C.C., Elbaj, C., Escotto, M., Ealls, T., Ferraguto, D., Edwards, C.C., Elbaj, C., Escotto, M., Gorrell, J. H., Gaevara, M., Gunarathe, P., Hanle, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hoggeon, M., Hogues, M., Holle, S., Joudah, S., Kanls, M., Hale, S., Joudah, S., Kanlson, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C., Liu, J., Liu, W., Loulseged, H., Locado, R.J., Lu, X., Lucler, A., Martinez, E., Karlsson, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C., Liu, J., Liu, W., Loulseged, H., Locado, R.J., Lu, X., Lucler, A., Martinez, E., Manesey, E., Martiney, E., Wartson, E., Martson, E., Martson, E., Martiney, E., Wartson, J., Newtson, J., Newtson, N., Noivedo, R., Payero, B., Peery, J., Perez, L., Rives, M., Noivedo, R., Pace, A., Payero, B., Peery, J., Perez, L., Rives, M., Rojas, A., Rojas, A., Rojas, A., Rojas, A., Tamerisa, A., Tamerisa, K., Taylor, P., Taylor, P., Taylor, P., Taylor, P., Taylor, P., Taylor, C., Taylor, T., Taylor, S., Wartek, A., Taylor, P., Vallalon, D., Vinson, D., Walls, W., Wull, Wull,
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NOTE: This is a 'working draft' sequence. It currently consists of 49 contigs. The true order of the pieces
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3 (bases 1 to 137964)
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Consensus quality: 89474 bases at least Q40
Consensus quality: 93422 bases at least Q30
Consensus quality: 96506 bases at least Q30
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record*will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F. Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Chen, R., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delagdo, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Dapper, H., Dugan-Rocha, S., Durbin, K.J., Falls, T., Ferraguto, D., Edwards, C., Elhaj, C., Escotter, P., Frantz, P., Garcia, A., Garner, T., Garza, N., Gill, R., Garcia, A., Garner, T., Garza, N., Gill, R., Garcia, A., Garner, T., Garza, N., Gill, R., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Harnandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Harrandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jackobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Klan, U., King, L., Korah, J., Kovar, C., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lucier, A., Lucier, R., Luna, R., Ma, J., Martinez, E., Massey, E., Mawhlhey, E., Martin, R., Martindale, A., Martinez, E., Massey, E., Marhlhey, E., Martin, R., Mayon, N., Newtson, N., Nguyen, N., Nickerson, E., Wickens, R., Pinius, E., Dul, L., Quiles, M., Ren, Y., Rives, M., Nolas, A., Rojubokan, I., Shoosheri, N., Shoon, Y., Shoon, Y., Shoon, Y., Shoon, Y., Shon, H., Shooker, M., Tamerisa, K., Tambrer, S., Warten, S., Stotte, M., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Shou, J., Shooker, M., Tang, C., Walliams, G., Walliamson, A., Walled, S., Warten, R., Walled, S., Walled
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Direct Submission
Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jul 10, 2002 this sequence version replaced gi:17941885.

Center: Baylor College of Medicine
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* (see http://www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* Consists of 1 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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Worley K.C.

Direct Submission

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza. Houston, TX 77030, USA

(bases 1 to 226303)
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 189550 bases at least Q40
Consensus quality: 190362 bases at least Q20
Consensus quality: 193076 bases at least Q20
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Web site: http://www.hgsc.bcm.tmc.edu/
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Rattus norvegicus clone CH230-7C10, *** SEQUENCING IN PROGRESS ***,
51 norordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
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contig of 3446 bp in 1
gap of unknown length
contig of 8021 bp in 1
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/db_xref="taxon:10116"
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Rattus norvegicus
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AF259981 1741 bp mRNA linear ROD 09-MAY-2000 Rattus norvegicus CCN family protein COP-1 (Cop-1) mRNA, complete
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1 (bases 1 to 1741)
2hang, H., Averboukh, L., Zhu, W., Zhang, H., Jo, H., Dempsey, P.J.,
Coffey, R.J., Pardee, A. B. and Liang, P.
Identification of rCop-1, a new member of the CCN protein family,
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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8: gap of unknown length

9: contig of 10422 bp in length

9: gap of unknown length

2: contig of 10782 bp in length

2: gap of unknown length

2: contig of 18295 bp in length

7: gap of unknown length

7: gap of unknown length

7: gap of unknown length

8: contig of 18595 bp in length
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/db_xref="taxon:10116"
/clones="CH230-7C10"
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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contig of 1867 b
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contig of 1197 b
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5117 others

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AF100778
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Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.
WISP Polypeptides and nucleic acids encoding same
Patent: US 6387657-A 17 14-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                             Liang, P.
Direct Submission
Submitted (24-APR-2000) Cell Biology, Vanderbilt-Ingram Cancer Schritted (24-APR-2000) Cell Biology, Vanderbilt-Ingram Cancer Center, 649 MRB II, Nashville, TN 37232, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGTCCAGGAACTTGAGCTTTGTATTTTCAGGAATGCACATCTCTTAAGCACTCGCAAAAC
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as a negative regulator for cell transformation
Mol. Cell. Biol. 18 (10), 6131-6141 (1998)
98414629
                                                                                                                                                                                                                                                               /product="CCN family protein COP-1"
/protein_id="AAF69011.1"
/db_xref="G1:7739781"
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
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Pred. No. 7e-34;
0; Mismatches 23;
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Pred. No. 8.8e-45;
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                                                                                                                                           /organism="Rattus norvegicus"
/db_xref="taxon:10116"
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/gene="Cop-1"
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ilarity 97.1%;
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Best Local Similarity 86.3%;
Matches 151; Conservative
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1 AGTCCAGGAACTTGAGCTTTGTATTTTCAGGAATGCACATCTCTTAAGCACTCGCAAAAC 60

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AF100778 17-DEC-1998
Mus musculus connective tissue growth factor related protein WISP-2
PAT 20-JUN-2002
                                                                                          (bases 1 to 1734)

Botstein, D.A., Cohen, R.L., Goddard, A.D., Gurney, A.L., Hillan, K.J.,
Barrence, D.A., Levine, A.J., Pennica, D., Roy, M. Ann. and Wood, W.I.
WISP Polypeptides and nucleic acids encoding same
Patent: US 6387657-A 18 14-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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Nus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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1 (bases 1 to 1734)

Pennica, D., Swanson, T.A., Welsh, J.W., Roy, M.A., Lawrence, D.A., Lee, J., Bush, J., Taneyhill, L.A., Deuel, B., Lew, M., Watanabe, C., Cohen, R.L., Melhem, M.F., Finley, G.G., Quirke, P., Goddard, A.D., Hillan, K.J., Gurney, A.L., Botstein, D. and Levine, A.J. D., WISP genes are members of the connective tissue growth factor family that are up-regulated in wnt-1-transformed cells and aberrantly expressed in human colon tumors

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Pred. No. 7e-34;
0; Mismatches 23; Indels 1;
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AF100778.1 GI:4028578
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Best Local Similarity 86.3%;
Matches 151; Conservative
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chemistry or covered by high quality data (1.e., phred quality) an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr;, TREMBL; WP:, WORMPEP: Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-161B3 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. PCTOR: pbAce36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17748 AGTCCAGGAACTTGACCTTTGTATTTGTAAAATACACATCTCTTAAATGCTCACAAAGC 17807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus chromosome 2 clone RP23-217C2, *** SEQUENCING IN ALGESS ***, 21 unordered pieces.
         regions were either double-stranded or sequenced with an alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus sims, S. i to 216757)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (23-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 15A, UK. E-mail enquiries:
humquery@sanger.ac_uk Clone requests: clonerequest@sanger.ac_uk
On Jul 25, 2002 this sequence version replaced g1:18181793.
Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGTCCAGGAACTTĞAGCTTTGTATTTTCAGGAATGCACATCTCTTAAGCACTCGCAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GACAGCAGAGTACTÖTCCTCTGGAGGACTAGTCTAGCCTAGAATAAACACCCAAA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 61072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator Big Dye; 100% of reads
CONSENSE quality: 211865 bases at least 040
Consensus quality: 213403 bases at least 030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 72.1%; Score 126.2; DB 10;
Best Local Similarity 86.3%; Pred. No. 1.3e-33;
Matches 151; Conservatiÿe 0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-23"
15405 a 15368 c 15033 g 15266 t
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. 61072
7. organism="Mus musculus"
/db_xrsf="taxon:10090"
/chromosome="2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASEI; HTGS_CANCELLED.
Mus musculus.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP23-161B3"
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SOURCE
ORGANISM
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AL669906
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hunguery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
nMay 25, 2002 this sequence version replaced g1:21213601.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-wronp.it.mcop.it.it.alsplcilsmvysqlcpapcacpwpppocppgvp
LVLDGCGCCRYCARRIGESCDHLHVCDPSQGLVCQPGAGPSGRGAVCLFEEDDGSCEV
LWLDGCGCCRYCARRIGESCDHLHVCDPSQGLVCQPGAGPSGRGAVCLFEEDDGSCEV
WRONDAWDPANDPSSAQGHQLSALVTPASADGPCPNWSTAWGPCSTTCGLGIATRVS
NQNRFCQLEIQRRLCLSRPCLASRSHGSWNSAF"
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Pennica,D.
Direct Submission
Submitted (23-02T-1998) Molecular Oncology, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             /product="connective tissue growth factor related protein
WISP-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL731698 61072 bp DNA linear ROD 24-MAY-2003
Mouse DNA sequence from clone RP23-161B3 on chromosome 2, complete
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTCAGCATGAGAAAGACAAGG
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                                                                                                                                                                                         /db_xref="taxon:10090"
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/fissue_type="mammary"
/note="transformed by Wnt-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 t
                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAC96320.1"
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Eukaryota; Metazoa; Chordata; C1
Mammalla; Eutheria; Rodentia; S2
1 (bases 1 to 61072)
Wallis,J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GI:4028579"
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                                                                                                                                                                                                                                                                                                                                                             257. .1012
/gene="Wisp2"
/codon_start=1
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257. .1012
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AUTHORS
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AL731698
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Consensus quality: 214139 bases at least Q20
Insert size: 214757; sum-of-contigs
Insert size: 234243; 1.8% error; agarose-fp
Quality coverage: 6.29x in Q20 bases; sum-of-contigs Quality
coverage: 5.90x in Q20 bases; agarose-fp
                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87500 98601: control of 100 bp

98602 98701: gap of 100 bp

98702 105522: control of 6821 bp in length

105623 105622: gap of 100 bp

105623 119773: control of 14151 bp in length
                                                                                                                                                                                                                                                                                                                                   4001 100: gap of 100 bp in length
4101 15267: contig of 11167 bp in length
15268 15367: gap of 100 bp
15368 34970: contig of 19603 bp in length
34971 35070: qap of 19603 bp in length
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ap of 100 bp
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51673 169686: contig of 18014 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71: gap of 100 bp
46360: contig of 6589 bp in length
60: gap of 100 bp
49809: contig of 3349 bp in length
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34653 141202: conilg of 6550 bp in length
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141303 145808: contig of 4506 bp in length
445809 145908: gap of 100 bp
145909 151572: contig of 5664 bp in length
                                                                                                                                                                                                                                                                                                                              4000: contig of 4000 bp in length
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/note="assembly_fragment:00814
fragment_chain:1"
15368. .34970
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fragment_chain:1"
35071. 39671
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/db_xref="taxon:10090"
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35071 39671: conti
39672 39771: gap of
39772 46360: conti
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41203 141302; gap of
41303 145808; conti
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169687 169786; gap of
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87500 98601: cont
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46361
46461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 126.2; DB 2; Length 216757;
Pred. No. 1.7e-33;
0; Mismatches 23; Indels 1; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector_side:right"
56425 a 51573 c 51904 g 54852 t 2003 others
                                                                                 46461 ...49809
fnote-assembly_fragment:03410
fragment_chain:2"
49910 ...54509
fnote-assembly_fragment:00811
fragment_chain:2"
54610 ...65989
fnote-assembly_fragment:02217
fragment_chain:2"
66090 ...84635
fnote-assembly_fragment:03529
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fnote-assembly_fragment:01019
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fragment_chain:5"
151673. 116968
/note="assembly_fragment:02207
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169787. 200095
/note="assembly_fragment:02849
fragment_chain:6"
200196. 213877
/note="assembly_fragment:01052
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213978. 216757
   Jy/72. 46360
/note="assembly_fragment:01438
fragment_chain:1"
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fragment_chain:4"
134653. 141202
/note="assembly_fragment:01951
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141303. .145808
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98702. 105525
/note="assembly_fragment:02829
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/note="assembly_fragment:01476
|fragment_chain:4"
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fragment_chain:5"
145909. .151572
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'note="assembly_fragment:03544
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86.3%;
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Best Local Similarity 86.39
Matches 151; Conservative
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                                     אוזאם 1739 bp mRNA linear ROD 12-OCT-1999
Mus musculus connective tissue growth factor-like protein precursor
(Ctgfl) mRNA, complete cds.
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NGRRYLDGEFFRNGRVLCRCDDGGFTCLPLCSEDYRLPSWDCPRPRIJQVBGRCCPE
WVCDQAVWQPAIQPSSAQGHQLSALVTPASADGPCPNWSTAMGPCSTTCGLGIATRVS
NGNRFCQLEIQRRLCLSRPCLASSRGSWNSAF"
480 c 489 g 395 t
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Identification and cloning of a connective tissue growth
factor-like cDNA from human osteoblasts encoding a novel regulator
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (04-FEB-1999) Bone & Cartilage Biology, UW 2109,
SmithKline Beecham, 709 Swedeland Rd., King of Prussia, PA 19406,
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"connective tissue growth factor-like protein precursor"
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Kumar,S., Hand,A.T., Connor,J.R., Dodds,R.A., Ryan,P.J.,
Trill,J.J., Fisher,S.M., Nuttall,M.E., Lipshutz,D.B., Zou,C.
Hwang,S.M., Votta,B.J., James,I.E., Rieman,D.J., Gowen,M. an
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Pred. No. 3.7e-32;
0; Mismatches 26; Indels 1;
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J. Biol. Chem. 274 (24), 17123-17131 (1999)
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/db_xref="G1:4337060"
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/db_xref-"taxon:10090"
/tissue_type-"lung"
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84.6%;
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Kumar, S. and Zou, C.
Direct Submission
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Best Local Similarity 84.6'
Matches 148; Conservative
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Ratus,
Rattus norvegicus clone CH230-19J17, *** SEQUENCING IN PROGRESS ***, 66 unordered pieces.
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Submitted (08-AGC-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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HTG; HTGS_PHASE1.
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Best Local Similarity 61.7
Matches 58; Conservative
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                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft" sequence. It currently consists of 66 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
      Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 136047 bases at least 040
Consensus quality: 146914 bases at least 020
Consensus quality: 153752 bases at least 020
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unknown length
of 1054 bp in length
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Oncolous Sapiens, Clone KF11-330L21

Unpublished

2 (bases 1 to 143565)

Barren, B. Lifton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choepel, T., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Dewarellano, K., Dewar, K., Domino, M., Ferrestor, J.,
Ferrelra, P., Fitzhugh, M., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Gäant, G., Hagos, B., Haeford, A., Horton, L.,
Howland, J.C., gohnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
McHeeters, R., Meldrim, J., Memeus, L., Morrow, J., Naylor, J.,
Norman, C.H., OgConnor, T., O'Donnell, P., Olivar, T.M., Peterson, K.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramalan, A., Talamas, J., Tasfaye, S., Theodore, J.,
Zinmer, A. and Zody, M.
Direct Submission
AL Submission
Al repeats were identified using Repeatmasker:
Sult, A. R., & Green, P. (1996-1997)
http://ftp.genome.Center
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ....... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This record contains 160 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L5859
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910 1721: contig of 812 bp in length
1722 1821: gap of 100 bp
1822 2585: contig of 764 bp in length
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                                                                                       Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-336L21
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Web site: http://www-seq.wi.mit.edu
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ORGANISM
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AUTHORS
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JOURNAL
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
clone:9007012.

Lubulished Only in Database (2001)

2 (bases 1 to 112855)

Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission

Submitted (10-MAY-2001) Takuji Sasaki, National Institute of
Submitted (10-MAY-2001) Takuji Sasaki, National Institute of
Agroblological Resources, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of I contigss
are presented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the Submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group) chromosome 6 clone P0007G12, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideee; Oryzeae; Oryza.
                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:P0007G12.
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54 9853: gap of 100 bp 10645: contig of 792 bp in length 16 10745: gap of 100 bp 11537: contig of 792 bp in length 18 11637: gap of 100 bp 12431: contig of 794 bp in length 18 12531: gap of 100 bp 100 bp 13392: contig of 771 bp in length 13 13402: gap of 100 bp 100 bp
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18690: contig of 784 bp in length
90: gap of 100 bp
19604: contig of 814 bp in length
04: gap of 100 bp
20542: contig of 838 bp in length
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16002: contig of 806 bp in length
16102: qap of 100 bp
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AL6/1848 190964 bp DNA linear ROD 09-JUL-2002 Mouse DNA sequence from clone RP23-110K5 on chromosome X, complete sequence.
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Pred. No..0.96;
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11 5470; cantig of 818 bp in 11 5450; cantig of 818 bp in 11 55560; gap of 100 bp 11 55660; gap of 100 bp 11 5564; gap of 100 bp 11 57470; gap of 100 bp 11 57470; gap of 100 bp 11 57470; gap of 100 bp 11 55844; cantig of 806 bp in 15844; cantig of 806 bp in 158844; gap of 100 bp in 18884; gap of 100 bp in 18884; gap of 100 bp in 1888 bp in 188
            5 43064: gap of 100 bp 4 3883: contig of 819 bp in 4 49893: gap of 100 bp 4 44875: contig of 792 bp in 4 4875: gap of 100 bp 6 45675: contig of 800 bp in 4565: gap of 100 bp 6 4565: contig of 787 bp in 46662: gap of 100 bp 3 46662: gap of 100 bp in 47457: contig of 795 bp in 47457: contig o
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52844: contig of 815 bp
144: gap of 100 bp
53752: contig of 808 bp
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                                                                                                                                                                                                                                                                                                                                                                        Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation any not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSRROT; Tr:, TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54490 CACAATCCTAACCATCTCCCACCTGGGCATCTCTCCAAGTCTCTGCTAGGCTAGGTGTT 54431
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 190964)
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                                                                                       Submitted (09-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Jul 10, 2002 this sequence version replaced gi:21655363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-110K5 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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MARZYD DW. Addmas.C., McHo-Cdoulab B. All-camer, R. Malten C., Marzyd DW. Addmas.C., McHo-Cdoulab B. All-camer, R. Malten C., Marzens S. Barton, J. Brown, H. Brown, H. Brytch, R. C., Barton, J. Barton, J. Brown, H. Brown, H. Brytch, R. C., Carron, H. Brytch, R. C., Carron, F. Barton, J. Brown, H. Brytch, R. C., Carron, F. Carron, R. Carron, H. Brytch, R. C., Carron, F. Carron, R. Carron, H. Brytch, R. C., Carron, R. Carron, H. Brytch, R. C., Carron, R. Carron, R. Carron, H. Brytch, R. C., Carron, R. Marson, R. Wellige, R. Werther, R. Marson, R. Wellige, R. Werther, R. Wellige, R. C. Carron, R. Mellige, R. C. Carron, R. Mellige, R. Carron, R. Mellige, R. Carron, R. Mellige, R. C. Carron, R. Carron
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Homo sapiens chromosome 4 clone RP11-18114 map 4, WORKING DRAFT SEQUENCE, 38 unordered pieces. AC068103 AC068103 AC068103 HTG. PHSE1: HTGS_PRAFT. Homo sapiens. HTGS_DRAFT. Homo sapiens. HTGS_DRAFT.
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1 (bases 1 to 144233)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 4, clone RP11-18114
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
          NOTE: This is a "working draft' sequence. It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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36923: contig of 2698 bp in length
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61528: contig of 5273 bp in length
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8798: gap of 100 bp
116661: contig of 7863 bp in length
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18769: contig of 1963 bp
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            Anderson, S., Baldwin, T., Bastien, V., Bedar, F., Anderson, S., Baldwin, J., Bastien, V., Bedar, F., Boguslavkiy, L., Boukhgalter, B., Chopepl. V., Colangelo, M., Collins, S., Campopiano, A., Castle, A., Chopepl. V., Colangelo, M., Collins, S., Colampolano, A., Cooke, P., Dekellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyas, S., Glode, S., Goyette, M., Garlam, L., Grant, G., Hados, B., Haaford, A., Horton, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., Minova, T., O'Donnell, P., O'Nell, D., Ollvar, T.M., Ollvar, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Severy, P., Spencer, B., Vasillev, H., Vlei, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Tirrell, A., Travers, M., Trigillo, J., Young, G., Zainoun, J., And Zoody, M., And Zoody, M., Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 14, 2000 this sequence version replaced g1:7658404. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
  Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality coverage: 3.1 in Q20 bases; agarose-fp Quality coverage: 3.5 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smit, A.F.A. & Green, F. (1990-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chemistry: Dye-terminator Big bye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 125189 bases at least Q40 Consensus quality: 133535 bases at least Q30 Consensus quality: 137574 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: L7833
Center clone name: 181_1_4
Center clone name: 181_1_151_5
Sequencing vector: M13; M77815; 100% of reads
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3822: cor
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3923 5190; co
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AUTHORS
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COMMENT

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ö Query Match 19.7%; Score 34.4; DB 2; Length 144233; Best Local Similarity 54.8%; Pred. No. 1.3; Matches 68; Conservative 0; Mismatches 56; Indels 0; Gaps

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72514 AACACAACTAATAAACTCAGGGACTTAGTGCTCCACTCTGTGGGAACAAATTGACCACTG 72455 69 TCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTCAGCATGAGAAAGACAAGGGACAGCAG 128 a õ

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Search completed: July 29, 2003, 00:48:37 Job time: 491.369 secs

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Probe

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Title: Perfect score:

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Searched:

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Database

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Heparin-induced CCN-like protein; HICP; cell-associated activity; ss; cardiovascular disorder; aberrant cell proliferation; fibrotic disorder.
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AAS72577
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99WO-US05999.
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Mouse WISP-2 prote
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8504.365 Million cell updates/sec
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preater than or equal to the score of the result being printed,
derived by analysis of the total score distribution.
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                 GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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and is derived
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Human CDNA encodin Human ORFX ORF2471 DNA encoding novel Human ORF1909 CDNA

Drosophila melanog

Drosophila melanog Human EST-derived DNA encoding novel DNA encoding novel

Nucleic acid sequences encoding rat heparin-induced CCN-like protein, used in methods to identify modulators or in diagnostic applications

Human polynucleoti Novel human polynu

Pred. No.

Score

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                                            Agents that stimulate or inhibit HICP protein activity or expression. Attisense HICP nucleic acid molecules and HICP antibodies, can be used to modulate cell-associated activity. HICP modulators can be used to treat disorders characterized by aberrant HICP protein activity or expression. Probes capable of hybridizing to HICP protein activity or expression. HICP can be used to detect HICP activity in a biological sample. HICP can be used to treat disorders, such as a cardiovascular or fibrotic disorder, characterized by aberrant cell proliferation.
                                                                                                                                                                                                                                                                                                        1594 AGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTCAGCATGAGAAAGACAAGG 1653
                                    This cDNA encodes a rat heparin-induced CCN-like protein (HICP) protein
                                                                                                                                                                                                                                   1 AGTCCAGGAACTTGAGCTTTGTATTTTCAGGAATGCACATCTCTTAAGCACTCGCAAAAC
                                                                                                                                                                                                                                                                                 61 AGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTCAGCATGAGAAAGACAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour; connective tissue growth factor; cancer; metalanoma; arteriosoflerosis; leukaemia; lymphoid malignancy; haematopoiesis-related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion; kidney disorder; bone-related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation; bern; testicular-related disorder; anglogenesis; immunological disorder; ss.
                                                                                                                                                                                                                                                                                                                                              1654 GACAGCAGAGTACTCTCTCTGGAGGACTAGTCTAGCCTAGAATAAACACCCAAA 1708
                                                                                                                                                                                                                                                                                                                                121 GACAGCAGAGTACTCTCTCTGGAGGACTAGTCTAGCCTAGAATAAACACCCAAA 175
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                                                                                                                                                                                    Length 1708;
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Wood WI;
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                                                                                                                                                            Sequence 1708 BP; 362 A; 486 C; 478 G; 382 T; 0 other;
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                                                                                                                                                                                  100.0%; Score 175; DB 20;
100.0%; Pred. No. 1.4e-50;
ive 0; Mismatches 0;
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Pennica D,
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98US-0073612
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Levine AJ,
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           2; Fig 1; 108pp;
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P-PSDB; AAY17651.
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Lawrence DA,
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                                                                                                                                                                                                                                                                                                        셤
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products from the present invention can be used to treat WISP related disorders such as breast, ovarian, and colon cancer or melanoma. The products can be used to treat diseases e.g. benign and malignant tumours.

Consider the diseases e.g. benign and malignant tumours.

I eukaemia and lymphold malignancies, neuronal, glial, astroaytal, hypothalamic and other glandular, macrophagal, epithelial, stroaytal, alsorders, skin disorders, haematopolesis related disorders, tissue-growth disorders, bone-related disorders in the product stroams such as burns, incisions, and other wounds, connective tissue disorders, catabolic states, tefticular-related disorders, and inflammatory, catabolic states, tefticular-related disorders, and inflammatory products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transgenic or knock-out animals.
death in WISP-1, 2 or 3 overexpressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat; OST; osteoregenegative; parathyroid hormone; tiblae; osteopathic; gene therapy; parathygoid hormone receptor ligand; bone disorder; bone formation disorder; bone resorption disorder; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGCTTTGTATTTCAGGAATGCACATCTCTTAAGCACTCGCAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
nesulves where induced secreted polypeptides, hovel WiSP polypeptides, designated WiSP-1, WiS ogy to connective tissue growth factor (CTGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20; Length 1734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1734 BP; 355 A; 491 C; 495 G; 393 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 126.2; DB 2
Pred. No. 1.4e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
The present invention describes Wnt-1 WISP-1, 2 and 3. The novel WISP polype and WISP-3 have homology to connective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat OST23 gene fragment SEQ ID NO:23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteopenia; osteopetr@sis; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                        individuals with neoplastic cell
can be used in the production of
Antibodies can be used to induce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.1%;
86.3%;
tve (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL59575 standard; DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1536 AGTCCAGGAACTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 151; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGTCCAGGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Horesovsky GJ, Noel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) GLAXO GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-401989/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200224943-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus sp.
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The present invention describes a method (M1) for identifying parathyroid hormone receptor ligands (I) and osteoregenerative agents by contacting a test cell population (P) comprising cells expression nucleic acid sequences (S) of 0571-47 and 48, with a test agent, measuring nucleic acid sequence expression, comparing it with reference CP and identifying the ligand and agent by the difference in expression levels. Also described is a method (M2) for treating a bone disorder in a subject by administering to the subject an agent that modulates the expression or activity of (S). (I) have osteopathic activities, and can be used to modulate the expression of 057 1-48, and can also be used in gene activity of (S). (I) have osteopathic activities, and can be used to modulate the expression of of 1-48, and can also be used in gene considered in a sessing the osteoregenerative agents. OST gene sequence can be used for assessing the osteoregenerative activity of a test agent in a subject, and for diagnosing or determining the susceptibility to bone disorder and assessing efficacy of a treatment of a bone disorder. In a subject, human or rodent. (M2) is useful for treating a bone disorder. Osteoporosis, osteopenia and osteopetrosis). OST polypeptides are useful as immunogens to raise anti-OST antibodies (II). Parathyroid hormone receptor disorder man assembled to a set of the contact of of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTCAGCATGAGAAAGACAAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 AGTCCAGGAACTTGAGCTTTGTATTTTCAGGAATGCACATCTTTAAGCACTCGCAAAAC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
Identifying parathyroid hormone receptor ligands and osteoregenerative agents involves detecting the expression of nucleic acids which are regulated by parathyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AGTCCAGGAACTTGAGCTTTGTATTTCAGGAATGCACATCTCTTAAGCACTCGCAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders. The present sequence represents an OST23 gene fragment isolated from rat tibiae, from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcript detection oligonucleotide SEQ ID NO:2937.
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e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 439 BP; 128 A; 108 C; 99 G; 104 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 71.9%; Score 125.8; DB 24; Best Local Similarity 96.8%; Pred. No. 1.1e-33; Matches 150; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  405 GGACCAGCAGAGTACTTTTCCTCTGGAGGACTAGT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 G--ACAGCAGAGTAC-TCTCCTCTGGAGGACTAGT 152
                                                                                                         Claim 45; Page 22; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN30189 standard; DNA; 65 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUL-2001; 2001WO-IB01903.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200210449-A2.
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ABN30189
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(COMP-) COMPUGEN INC.

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The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcription units that populate a genome. The library comprises cranscription units that populate a genome. The library comprises caveral oligonucleotides, each capable of hybridising selectively to a several oligonucleotides, each capable of hybridising selectively to a consecret of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants of the oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or acceptation of transcriptomes and splice variants of human or animal cranscriptomes. The libraries may also be used as specialised mini cranscriptomes. The libraries may also be used as specialised mini clibraries to detect transcripts of a sub-transcriptome under a categorie of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological confit expressed in specific tissue under a specific pathological confit to a particular disorder. ANNA7253 to ANNE9589 represent

C condition: to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a patricular disorder. ANNA7253 to ANNE9589 represent

C condition but was obtained in electronic form part of the printed of a patient of the printed of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TTCAGGAATGCACATCTCTAAAGCACTCGCAAAACAGGAAGGCTCCACACCTCTAAACAGC 60
                                                                                                                      New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 TICAGGAATGCACATCTCTTAAGCACTCGCAAAACAGGAAGGCTCCACACCTCTGGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human haematological malignancy-related antigen coding sequence #359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytostatic; vascular; gene therapy; vaccine; lymphoma; haematological malignancy; antigen; chronic lymphocytic leukaemia; follicular lymphoma; Hodgkin's lymphoma; ss.
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Pred. No. 4.4e-10;
0; Mismatches 5; Indels
                          Faigler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 65 BP; 21 A; 20 C; 13 G; 11 T; 0 other;
                          Mintz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                  Example 1; SEQ ID 2937; 47pp; English.
                          Mintz E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK54634 standard; cDNA; 463 BP.
                                                                                                                                                                                                developmental-specific genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.6%;
92.3%;
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Best Local Similarity 92.33
Matches 60; Conservative
                          Wasserman A,
                                                                    WPI; 2002-257383/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 CCAGG 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200164886-A2.
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                          Shoshan A,
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qq
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84 GGCCAGGGCCTTTQTCTTCAGCATGAGAAAGACAAGGGACAGCAGAGTACTCTCCTCTGG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16175 ABL1051), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). This sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster expressed polynucleotide SEQ ID NO 29240.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.4%; Score 30.4; DB 23; Length 2155; 59.1%; Pred. No. 3.5; tive 0; Mismatches 36; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 29243; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 AGGACTAGTCTAGCĞTAGAATAAACACC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        925 GGACTCAGTTTGC@GCTGTTAAACTCC 898
                                                                                                                                                                                                        Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL11586 standard; cDNA; 14091
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                                                         23-MAR-2001; 2001WO-US09231.
                                                                                               23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 59.1
es 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
                                                                                                                                                                                                        Adams M,
                                                                                                                                                                                                                                              WPI; 2001-656860/75.
                                                                                                                                                               (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                                                                interactions
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                   27-SEP-2001.
                                                                                                                                                                                                    Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL11586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to compositions and methods for the detection, diagnosis and therapy of haematological malignancies. The present sequence is the coding sequence of a human haematological malignancy related antigen. The methods of the present invention comprise detecting the presence of haematological malignancy related antigen(s) in a sample obtained from the patient (an increased level of the polypeptide, compared to an unaffected individual, is indicative of an increased risk). Haematological malignancies which can be treated using the present invention are chronic lymphocytic leukaemia, lymphoma, follikular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTCAGCATGAGAAAGACAAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09
                                                                                                                                                                                                                                                                                                                                                                                                     Compositions and methods for the detection of hematological malignancies, e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and Hodgkin's and T/B cell non-Hodgkin's lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGTCCAGGAACTTGAGCTTTGTATTTTCAGGAATGCACATCTCTTAAGCACTCGCAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster expressed polynucleotide SEQ ID NO 29243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 17.6%; Score 30.8; DB 22; Length 463; I Similarity 53.3%; Pred. No. 1.3; 65; Conservative 0; Mismatches 57; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 463 BP; 104 A; 117 C; 88 G; 146 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 31; Page 426; 1252pp; English.
                                                                                                                                                                                                                                                                                                                             Mannion J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL11587 standard; cDNA; 2155 BP.
                                                                    28-APR-2000; 20000S-0200303.
28-APR-2000; 20000S-0200779.
01-MAY-2000; 20000S-0200999.
04-MAY-2000; 20000S-0202084.
22-MAY-2000; 20000S-0202011.
14-JUL-2000; 20000S-0218950.
03-AUG-2000; 2000US-0222903.
                                                       2000US-0200545
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                                      2000US-0190479
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                                                                                                                                                                                                                                                                                                                             Algate PA,
                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-514842/56
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Matches 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GA 122
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                                  17-MAR-2000;
27-APR-2000;
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                                                                                                                                                                                                                                                                                                                           Gaiger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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diagnosing and treating e.g. leukaemia, inflammation and immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Garcia V, Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s,
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Reinhard C, Randazzo F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-091805/10.
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                                  Claim 1; SEQ ID
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                                                                                                                                                                 inflammation
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            disorders
                                                                                                                                                                                                                                                                                                                              69
                                                                                                                                                                                                                                                                                                                                                    188
                                                                                                                                                                                                                                                                                                                                                                                                                               AAF64359;
                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         breast
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Matches
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                                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                               solated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL/16/ABL/30311), expressed DNA sequences (ABL/16/175) and the encoded proteins
                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                 17.4%; Score 30.4; DB 23; Length 14091; 59.1%; Pred. No. 7.6; 1ive 0; Mismatches 36; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing
                                                                                                        Claim 1; SEQ ID NO 29240; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                             Sequence 14091 BP; 3932 A; 3192 C; 3264 G; 3703 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                             8227 GGACTCAGTTTGCCGCTGTTAAACTCC 8200
                                                                                                                                                                                                                                                                                                                                                                       144 AGGACTAGTCTAGCCTAGAATAAACACC 171
           Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO 12021.
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           PWD,
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2000US-0577409.
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Best Local Similarity 59.11
Matches 52; Conservative
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                                                               New isolated nucleic
          Adams M,
                              WPI; 2001-656860/75
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P-PSDB; AA012030.
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                                           P-PSDB; ABB67483
                                                                                      interactions -
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18-MAY-2000;
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          Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT,
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                                                                    The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                    production of other cytokines in other cell populations. The polynocleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodilatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kassam A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AACTTGAGCTTTGTATTTTCAGGAATGCACATCTCTTAAGCACTCGCAAAACAGGAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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meon G, Drmanac R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; gene therapy; colon cancer; prostate cancer; cancer; lung cancer; cancer detection; ss.
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Kennedy GC, Pot D, Lamson G, Drman
Dickson M, Labat I, Leshkowitiz D;
LW, Strache-Crain B;
NO 12021; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 330 BP; 106 A; 91 C; 70 G; 63 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGCTGCGATGGGGAGCACAGGGTCTTTCAGCTC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 57.4%; Pred. No. 2.2; hes 54; Conservative 0; Mismatches
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99US-0142311.
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ABA52750;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 CTTAAGCACTCGCAAAACAGGAAGGCTCCACACCTCTGGCAGGCCCAGGGCCTTTCTCTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.1%; Score 30; DB 22; Length 422; 61.5%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1018; 327pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30; Indels
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    Claim 9; Page 561; 1046pp; English.
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2000US-0234687.
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2000US-0608408
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04-OCT-2000;
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30-JUN-2000;
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\overset{\mathsf{A}}{\times}\overset{\mathsf{C}}{\times}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\overset{\mathsf{C}}{\vee}\ove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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for encode proteins. They are useful for assessing the toxicity of chemical expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater characters for probes for measuring gene expression, with far less bias than expressed sequence for measuring gene expression, with far less bias than expressed sequence and microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 CTTAAGCACTCGCAAAACAGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTC 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.1%; Score 30; DB 22; Length 483; Ilarity 61.5%; Pred. No. 2.6; Conservative 0; Mismatches 30; Indels
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2000US-0608408.
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Best Local Similarity
Local 48; Conserve
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monitoring and prognosing diseases of the human heart and vascular system
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                                                                                                                                                                                                                   43 CTTAAGCACTCGCAAAACAGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTC 102
                                                                                                                                                                                                                                  The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe #1000 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; gene expression; heart; microarray; vascular system; probe;
cardiovascular disease; hypertension; cardiac arrhythmia;
congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in
                                                                                                                                                                                             ;
0
                                                                                                                                                                   Length 483;
                                                                                                                                                                              Pred. No. 2.6;
0; Mismatches 30; Indels
                                                                                                                                          Sequence 483 BP; 94 A; 136 C; 146 G; 107 T; 0 other;
                                                                                                                                                                   DB 22;
                                                                                                                                                                Query Match 17.1%; Score 30; Best Local Similarity 61.5%; Pred. No. 3 Matches 48; Conservative 0; Mismatch
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                                                                                                                                                                                                                                                                                     299 GTCAGGGGAAAGTCCAGG 316
                                                                                                                                                                                                                                                                                                                                                              ABA22534 standard; DNA; 483 BP
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2000US-0608408.
2000US-0632366.
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2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                  probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                     43 CTTAAGCACTCGCAAAACAGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTC
                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                         Score 30; DB 22; Length 483;
Pred. No. 2.6;
                                                                                                                                                                                                                                                                               30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human brain expressed single exon probe SEQ ID NO: 996.
                                                                                                                                                                     Sequence 483 BP; 94 A; 136 C; 146 G; 107 T; 0 other;
                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
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61.5%;
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2000GB-0024263.
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                                                                                                                                                                                                                                                                                  48; Conservative
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Best Local Similarity
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04-OCT-2000;
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21-SEP-2000;
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BP.

DNA; 483

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AAI11091 standard;
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AAI11091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 CTTAAGCACTCGCAAAACAGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTTC 102
                                                 43 CTTAAGCACTCGCAAAACAGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTC 102
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                             Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                         Human bone marrow expressed single exon probe SEQ ID NO: 1019.
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Score 30; DB 22; Length 483; Pred. No. 2.6;
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                  30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        analyzing gene expression in human bone marrow
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                   0; Mismatches
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299 GTCAGGGGAAAGTCCAGG 316
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17.18;
61.58;
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2000US-0608408.
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                  Conservative
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                                                                                                                                              AAK26462 standard;
        Local Similarity
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30-JUN-2000;
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Query Match
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                        Probe #1024 for gene expression analysis in human cervical cell sample.
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                                                                                                                    human; microadray; gene expression; cervical epithelial cell;
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2000US-0632366.
2000US-0234687.
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04-OCT-2000; 2000GB-0024263.
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Matches 48; Conservative∻
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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12-OCT-2001
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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on:

July 28, 2003, 15:55:06; Search time 9.52094 Seconds

(without alignments)
5636.882 Million cell updates/sec

Title:

US-10-010-408-1_COPY_1534_1708

Perfect score:

1 AGTCCAGGAACTTGAGCTTT........GCCTAGAATAAACACCCAAA 175

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched:
441362 seqs, 153338381 residues
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Total number of hits satisfying chosen parameters:

Database : Issued\_Patents\_NA:\*

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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
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5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
6: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## APPII APPIII APPIII APPIII APPIII APPIII APPIII APPIII Sequence 17, Appl Appl Description Sequence 1 Sequence 1 Sequence 3 Sequence 7 Sequence 7 Sequence 1 Sequence 3 Sequence 5 Sequence 7 Sequence Seq Sequence Seq Seguence 3-08-724-394A-21 3-08-724-394A-22 3-08-791-849A-14 US-09-182-145-17 US-08-652-265-1 US-08-652-265-5 US-08-652-265-5 US-08-652-265-5 US-08-834-497A-1 US-08-834-497A-1 US-08-834-497A-3 US-08-834-497A-3 US-08-834-497A-3 US-08-503-444A-1 US-09-503-444A-3 US-09-503-444A-3 US-09-503-444A-3 US-09-724-394A-21 US-08-724-394A-21 US-08-724-394A-21 US-08-724-394A-21 US-08-724-394A-21 US-08-724-394A-21 US-08-734-38-43 US-08-734-38-43 US-08-631-328-43 US-08-631-328-43 US-08-631-328-43 US-08-631-328-43 US-08-631-328-43 US-08-631-328-43 .08-724-394A-20 ·08-438-753B-43 ·08-443-883A-43 -08-455-524B-43 US-08-438-753B-11 SUMMARIES В Length 10825 12146 246240 246240 246240 13011 Query 7777777777777 Result υ

RESULT

Appl Appl Appl Appl Appl Appl Appli		i,	60 1595	120
11, Appl 11, Appl 11, Appl 11, Appl 22, Appl 22, Appl 7, Appl	SAME	Gaps	AGTCCAGGAACTTGAGCTTTGTCAGGAATGCACATCTCTTAAGCACTCGCAAAAC	AGGAAGGCTCCACACCTCTGGCAGGCCCTTTCTCTTCAGCATGAGAAGACAAGG
		34;	CTCGC	AAAGA       AGAGA 
sednence sed	ENCODING	h 17 s	AAGCA     AAATG	ATGAGATGAGATGAGA
	ACIDS 1	Length Indels	CTCTT	AGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTCAGCATGAGAAAGA
		3.4; 12; 23;	ACATO	CTCTI         CTCTI       TCTG
13A-11 18-11 14B-11 17-11 17-11 17-11 11B-11 18-7 18	MENTS AND NUCLEIC 145B 704 612 695	, DE .6e-3 .es	AATAC	CCTTI CCTTI CCTTI ICTAG
43 - 44 - 44 - 44 - 44 - 44 - 44 - 44 -	ALIGNMENT 45B 10DES AND 7182,145B 7063,704 7073,612	ore 126.2; DB ed. No. 1.6e-32 Mismatches 2	TCAGG   GTAAA	CAGGG CAGGG CAGGG ACTAG
US-08-443-883A-11 US-08-631-328-11 US-08-455-554B-11 US-08-045-467-11 US-09-188-930-22 US-09-188-930-22 US-08-698-551-7 US-08-698-551-7 US-08-693-311A-7 US-08-833-901B-7 US-08-833-901B-7 US-08-833-901B-7 US-08-833-012A-7 US-08-839-013A-7 US-08-839-013A-7 US-08-185-256C-7 PCT-US92-11196-5 US-08-185-256C-7 US-08-185-256C-7	ALIG 145B 9/182 0/063 0/081	UH	TATT       TATT	CAGGC         CAGGC  GAGG
11 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5-17 (Application US/09182 6387657 CORMATION: Botstein, David A. COhen, Robert Goddard, Audrey Gurney, Austin L. Hillan, Kenneth J. Lawrence, David A. Invention, Margaret Ann Wood, William I. Invention: WISP POLYPEP RENCE: Pl176R2 PPLICATION NUMBER: US/0 ILING DATE: 1998-10-29 PPLICATION NUMBER: US 6 ILING DATE: 1998-04-14 SEQ ID NOS: 156	0	CTTTG	rcreg IIIII ICTCF
588 588 588 588 10023 10023 10023 10023 10023	n US/ irey irey irey in L in L in L in L in L in L in L in L	72.1 86.3	rTGAG          TGAC	ACACCT
	llication 157 110N: 110N	ty erval	GAAC	CTCC  - - - - -
155.00 15	pplic 7657, 7657, ATION ATION ADA TIDA, WITON WI	ch 72.1%; l Similarity 86.3%; 151; Conservative	TCCAG        TCCAG	GAAGG - 111 G-AGG CAGCA -111 CAGTA
5.5.5.5.5.5.5.5.6.6.6.6.6.6.6.6.6.6.6.6	45-17 17, App 17, App 18, App 18, Bots 11: Gode 11: Gode 11: Gode 11: Gurn 11: Levi 11: Levi 11: Levi 11: Wood 11: Wood 11: Wood 11: Wood 11: Wood 11: Wood 11: Wood 11: Wood 11: Wood 11: Wood 12: Wood 13: Wood 14: Wood 15: Wood 16: Wood 17: Wood	ch 1 Sim 151;	1 AG    36 AG	61 AG     96 AA   21 GA   65 AA
<b>ด็ดีดีดีดีดีดีดีดีดีดีดีดีดีดีดีดีดีดีด</b>	RESULT 1 US-09-182-145-17 Sequence 17, Application US/09182145B Patent No. 6387657 GENERAL INFORMATION: APPLICANT: Botstein, David A. APPLICANT: Gonen, Robert APPLICANT: Goney, Audrey APPLICANT: Griney, Austin L. APPLICANT: Hillan, Kenneth J. APPLICANT: Hillan, Kenneth J. APPLICANT: Hillan, Kenneth J. APPLICANT: Lavrence, David A. APPLICANT: Pennica, Dane APPLICANT: Ponnica, Diane APPLICANT: Ponnica, Diane APPLICANT: Ponnica, Diane APPLICANT: Ponnica, David A. APPLICANT: Nood, William I. FILLE REPERENCE: Pl176R2 CURRENT APPLICATION NUMBER: US 60/063,70 EARLIER APPLICATION NUMBER: US 60/073,61 EARLIER FILING DATE: 1998-10-29 EARLIER FILING DATE: 1998-04-14 NUMBER OF SEQ ID NOS: 156 SEQ ID NO 17 LENGTH: 1734 TYPE: DNA ORGANISM: MUS MUSCULUS US-09-182-145-17	ήü	15:	159
00000000000000000000000000000000000000	SULT 1 - 09-182- Sequence Sequence Septing APPLICE CURRENT CUR	Query Ma Best Loc Matches		
000000000000	80		QY Dp	OY OY Ob
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NAME/KEY: CDS
LOCATION: join(361,.436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: join(361,.436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: 6400..3153, 7107..7147)
OTHER INFORMATION: '/product="Hereditary Hemochromatosis of There Information: december of the Theory of Theory of Theory of The Theory of The Theory of The Theory of The Theory of Theory of Theory of Theory of Theory of The
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NAME/KEY:

NAME/KEY:

LOCATION:

JOOGHEN 11NFORMATION:

OTHER INFORMATION:

OTHER INFORMATION:

OTHER INFORMATION:

OTHER INFORMATION:

Gequence surrounding variant for 24d2(C)

OTHER INFORMATION:

Allele (SEQ ID NO:41)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aphenotype- "normal or wild-type (unaffected)"
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/iabel= 2447
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      Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                        17957-000500
                                                            UMBER US/08/652,265
23-MAY-1996
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LOCATION: replace(3872, "c")
OTHER INFORMATION: (phenotype-
OTHER INFORMATION: (unaffected
OTHER INFORMATION: /label= 244
FEATURE:
                                                                                                                     CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: SMILL, WIlliam M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1795
TELECHONE: (415) 576-0200
TELECHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISHICS:
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OTHER INFORMATION: /phenotype
OTHER INFORMATION: (unaffect
OTHER INFORMATION: /jabel- 24
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OTHER INFORMATION: /phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 65.1%;
Matches 41; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                          LEGICH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 5507..602
CUTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
                                                               APPLICATION NUMBER
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                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ROY, Margaret Ann APPLICANT: ROY, Margaret Ann APPLICANT: Wood, William I. TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER PPLICATION NUMBER: US 60/063,704
EARLIER PLILING DATE: 1999-10-29
EARLIER PLILING DATE: 1999-02-04
EARLIER FILING DATE: 1998-04-14
EARLIER FILING DATE: US 60/081,695
EARLIER FILING DATE: 1998-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GACAGCAGAGTACTCCTCTGGAGGACTAGTCTAGCCTAGAATAAACACCCAAA 175
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APPLICANT: Gnirke, Andreas
APPLICANT: Gnirke, Andreas
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
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Two Embarcadero Center, Eighth Floor
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Pred. No. 1.6e-32;
0; Mismatches 23
                            Sequence 18, Application US/09182145B Patent No. 6387657 GENERAL INFORMATION:
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BDIUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6025130
GENERAL INFORMATION:
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                                                                                                                  APPLICANT: Botstein, David A. APPLICANT: Cohen, Robert APPLICANT: Goddard, Audrey APPLICANT: Gurney, Austin L. APPLICANT: Hillan, Kenneth J. APPLICANT: Levine, Arnold A. APPLICANT: Levine, Arnold J. APPLICANT: Pennica, Diane
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86.3%;
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Matches 151; Conservative
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US-09-182-145-18/c
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LENGTH: 1734
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STATE:
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2609 AGGCCAAGGAGAGAGAGATTCTGAGGAGTTCAAGACCAGCCTGGGCAACACAGCA 2668
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                                                                                                                  FEATURE:
NAME/KEY: allele
LOCATION: replace(5834, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 24d1
US-08-652-265-3
                           LOCATION: 5507..6023
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Reder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORECTEN THE COMPUTATION OF STREMS FOR SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                             Query Match 15.9%; Score 27.8; DB 3; Best Local Similarity 65.1%; Pred. No. 11; Matches 41; Conservative 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CTTY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08652265 Patent No. 6025130
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NAME: Smith, william M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1795:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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APPLICANT: Thomas,
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US-08-652-265-5
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2609 AGGCCAAGGAGAGAGAGATCCTGAGCTCAGGAGTTCAAGACCAGCCTGGGCAACACAGCA 2668
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LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Hereditary Hemochromatosis (HH) gene 24dl allele"
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OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(C) allele (SEQ ID NO:41)" FERIURE:
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OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: 24d1 allele cDNA (SEQ ID NO:10)"
                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/652,265 FILING DATE: 23-MAY-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE DOCKET NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 3:
EROUTH: 10825 base pairs
TENGTH: 10825 base pairs
TENGTH: 10825 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                        Sequence 3, Application US/08652265 Patent No. 6025130
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OTHER INFORMATION:
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2669 AAA 2671
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NAME/KEY:
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/label- 24dl
                           ATTORREY AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 17957
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid;
STRANDEDNESS: single
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: -
LOCATION: 5507..6023
OTHER INFORMATION: /k
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US-08-652-265-7
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                CLASSIFICATION:
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2669 AAA 2671
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NAME/KEY:
LOCATION:
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US-08-834-497A-1
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COTHER INFORMATION: /Phenotype= "Hereditary Hemochromatosis
COTHER INFORMATION: /label= 24d2
US-08-652-265-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 10825;
                                                                         OTHER INFORMATION: mutation" OTHER INFORMATION: /note= "Hereditary Hemochromatosis (HH) OTHER INFORMATION: gene 24d2 allele" FRATURE:
LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /Product= "Hereditary Hemochromatosis OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 5507..6023
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(G) allele (SEQ ID NO:20)"
                                                                                                                                                                                          LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: 24d2 allele cDNA (SEQ ID NO:11)"
                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirk, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Refaitary Hemochromatosis Gene
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 15.9%; Score 27.8; Di
Best Local Similarity 65.1%; Pred. No. 11;
Matches 41; Conservative 0; Mismatches
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23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08652265
Patent No. 6025130
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: -
LOCATION: 55
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                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
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113 AGACAAGGGACAGCAGAGTACTCTCTCTGGAGGACTAGTCTAGCCTAGAATAAACACCC 172
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                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: join(361,436,3762.4025,4235..4510,5606..5881,LOCATION: join(361,436,7107..7147)
LOCATION: GO40..6153,7107..7147)
COTHER INFORMATION: /Product="Hereditary Hemochromatosis OTHER INFORMATION: /OTHER INFORMATION: /Once="Hereditary Hemochromatosis OTHER INFORMATION: Gene containing a combination of both OTHER INFORMATION: 2401 and 2402 alleles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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LOCATION: replace(3872, "g")
COTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION: /pabel= 24d2
FEATURE: Allele
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OTHER INFORMATION: /ghenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 10825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Prote-"start and stop positions for OTHER INFORMATION: CDNA containing a combination of both OTHER INFORMATION: 2401 and 2402 alleles OTHER INFORMATION: $560 ID No:12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY:
LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anote- "start and stop positions for
genomic sequence surrounding variant
for 24d1(A) allele (SEQ ID NO:21)"
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17957-000500
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SSEE: Pennie & Edmonds LLP: 1155 Avenue of the Americas New York
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                                                                                                                                                                                                                                                                          LOCATION: replace(3872, "c")
OTHER INFORMATION: /phenotype
OTHER INFORMATION: (unaffecte
OTHER INFORMATION: /label= 24
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APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drayna, Dennis T.
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Best Local Similarity 65.1º
Matches 41; Conservative
                                                                                                            NAME/KEY: -
LOCATION: 5507..6023
      OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: allele
LOCATION: replace
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                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
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US-08-834-497A-3
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Hereditary Hemochromatosis (HH) gene
allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)

OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) allele OTHER INFORMATION: CDNA (SEQ ID NO:9)"
                                                                                                                                                                                                                     HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
CLASSIFICATION NUMBER: US 08/632,673
FILING DATE: 23-MAY-1996
CLASSIFICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: 10-APR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: O4-APR-1996
CLASSIFICATION NUMBER: 28,462
REFIRENCE/DOCKET NUMBER: 28,462
REFIRENCE/DOCKET NUMBER: 28,462
REFIRENCE/DOCKET NUMBER: 8907-0056-9
RECISTRATION NUMBER: 28,462
REFIRENCE/DOCKET NUMBER: 8907-0056-9
TELEPHONE: 650-493-4935
FILEPHONE: 650-493-4935
FILEPHONE: 650-493-4935
FILERS: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
Sequence 1, Application US/08834497A
Patent No. 6140305
                                                           APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY INUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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nucleic acid
SDNESS: single
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LOCATION: 3852..3891
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OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY:
LOCATION: 140.7319
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LOCATION: join
LOCATION: 6040
                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EATURE:
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113 AGACAAGGGACAGCAGAGTACTCCTCGGAGGACTAGTCTAGCCTAGAATAAACACC 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
/note= "start and stop positions for normal or wild-type (unaffected) genomic sequence surrounding variant for 24d2(C) allele (SEQ ID NO:41)"
                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /note- "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d1(G) OTHER INFORMATION: allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 10825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Feder, John N.
APPLICANT: GALIKE, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
CORRESPONDENCE: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /phenotype= "normal or wild-type (unaffected)" /label= 24d2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: replace(3878, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 2447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /phenotype= "normal or wild-type (unaffected)" /label= 24d1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.9%; Score 27.8; D 65.1%; Pred. No. 11; ive 0; Mismatches
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NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /product- "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS NUMBER OF SEQUENCES: 76 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mote- "Hereditary Hemochromatosis (HH)
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OTHER INFORMA
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ZIP: 10036-2811
COMPUTRY: USA
ZIP: 10036-2811
COMPUTRY: BEDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows Version 2.0b
CURRENT APPLICATION DĀTA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: U4-APP.1997
CLASSIFICATION: 514
PROR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 104-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMAȚION:
RECISTRATION NUMBER: B.462
RECISTRATION NUMBER: B.463
FILERAX: 660-493-5556
TELECOMMUNICATION INFORMATION:
TELEPAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
FEGUENCE CLARRACTERISTICS:
FERCHT : 10825 base palis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1155 Avenue of the Americas
                                                                                                                                           Sequence 5, Application US/08834497A
Patent No. 6140305
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Feder, John N.
APPLICANT: Gairke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchinash, Zenta
APPLICANT: Tsuchinash, Zenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                               US-08-834-4,97A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 AGACAAGGGACAGCAGAGTACTCTCCTCTGGAGGACTAGTCTAGCCTAGAATAAACACCC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: join(361...436, 3762...4025, 4235...4510, 5606..5881, LOCATION: 6040..6153, 7107...7147)
OTHER INFORMATION: /product- "Hereditary Hemochromatosis OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.9%; Score 27.8; DB 3; Length 10825; 65.1%; Pred. No. 11;
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OTHER INFORMATION: /Phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Hereditary Hemochromatosis (HH) gene 24d1 allele"
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OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: 24d1 allele cDNA (SEQ ID NO:10)"
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                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 10-APR-1996
CLASSIFICATION NUMBER: US 08/632,673
FILING DATE: 10-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: POLSSENT INFORMATION:
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-556
TELEFAX: 650-493-556
TELEFAX: 650-493-556
TELEFAX: 650-493-556
TELEFAX: 610-493-556
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23 MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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STRANDEDNESS: single
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LOCATION: 5507..6023
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OTHER INFORMATION:
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|2669 AAA 2671
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LOCATION:
LOCATION:
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2669 AAA 2671
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                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                         15.9%; Score 27.8; DB 3; Length 10825;
65.1%; Pred. No. 11;
11ve 0; Mismatches 22; Indels 0;
                                                                                                                                                                                                                                                                       /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
                                  /note= "start and stop positions for genomic sequence surrounding variant for 24d2(G) allele (SEQ ID NO:42)"
                                                                                                                                                    OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(G) allele (SEQ ID NO:20)" FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZOWING COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastERD for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: OF APRIL 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
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PRIOR APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08834497A
Patent No. 6140305
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TILE OF INVENTION: HEREDITARY HEWO
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                  /label- 24d2
                                                                                                                                                                                                                                                    LOCATION: replace(3872, "g")
OTHER INFORMATION: /phenotype
OTHER INFORMATION:
OTHER INFORMATION: /label- 24
                                                                                                                                                                                                                                                                                                                                                                                                                41; Conservative
                                                                                                                     5507..6023
                3852..3891
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APPLICATION NUMBER:
                                                     OTHER INFORMATION:
OTHER INFORMATION:
                  LOCATION: 3852..38 OTHER INFORMATION:
                                                                                                                                                                                                                                      NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
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                                                                                            FEATURE:
NAME/KEY:
NAME/KEY:
                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                  US-08-834-497A-5
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113 AGACAAGGGACAGCAGAGTACTCTCTCGGAGGACTAGTCTAGCCTAGAATAAACACCC 172
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OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: and 24d2 mutations"

OTHER INFORMATION: /note= "Hereditary Hemochromatosis OTHER INFORMATION: /note= "Hereditary Hemochromatosis (HH) OTHER INFORMATION: /pone containing a combination of both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: replace(3872, "g")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
/Jabel= 24d2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 10825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Hereditary Hemochromatosis (HH)
gene containing a combination of both
24dl and 24d2 alleles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "start and stop positions for CDNA containing a combination of both 24d1 and 24d2 alleles (SEQ ID NO:12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: -
NAME/KEY: -
LOCATION: 3852..3891
COTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 5507..6023
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
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               CLASSIFICATION: 514
ATTORNEY/AGENT INCORMATION:
NAME: POISSANL, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-5556
TELEFAX: 650-493-5556
INFOREMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.9%; Score 27.8; D
65.1%; Pred. No. 11;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                   LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.9
Best Local Similarity 65.1
Matches 41; Conservative
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OTHER INFORMATION: CD
OTHER INFORMATION: CD
OTHER INFORMATION: 24
OTHER INFORMATION: 34
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FEATURE:
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LOCATION: join
LOCATION: 6040
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2609 AGGCCAAGGAGAGAGATTCTGAGGAGTTCAAGACCAGCCTGGGCAACACAGGA 2668
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                                                                                                              NAME/KEY: -
LOCATION: 5507..6023

LOCATION: 5507..6023

OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: sequence surrounding variant for 24d1(G) OTHER INFORMATION: allele (SEQ ID NO:20)"

FEATURE: NAME/KEY: allele (JoCATION: /phenotype= "normal or wild-type OTHER INFORMATION: /phenotype= "normal or wild-type OTHER INFORMATION: /label= 24d2

FEATURE: NAME/KEY: allele LOCATION: /phenotype= "normal or wild-type OTHER INFORMATION: /label= 24d2

FEATURE: NAME/KEY: allele LOCATION: /phenotype= "normal or wild-type outer INFORMATION: /phenotype= "normal or wil
normal or wild-type (unaffected) genomic sequence surrounding variant for 24d2(C) allele (SEQ ID NO:41)"
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APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Breder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TILEONT: Wolff, Roger K.
TILEONT: Wolff, Roger K.
CORRESPONDENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /phenotype= "normal or wild-type (unaffected)" /label= 24d7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /phenotype= "normal or wild-type OTHER INFORMATION: «(unaffected)"
OTHER INFORMATION: %label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.9%; Score 27.8; DB 4; Best Local Similarity 65.1%; Pred. No. 11; Matches 41; Conservative 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/503,444A FILING DATE: 14-Feb-2000 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Widdows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Pennie & Edmonds LLP
1155 Avenue of the Amer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09503444A Patent No. 6228594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: (unaffected OTHER INFORMATION: /label= 24 FRATURE: allele INCATION: replace(5834, "g")
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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CITY: New York
STATE: New York
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US-09-503-444A-3
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Hereditary Hemochromatosis (HH) gene
allele"
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OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: /note= "No. 6228594mal or wild-type (unafOTHER INFORMATION: Hereditary Hemochromatosis (HH) gene OTHER INFORMATION: allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "start and stop positions for
normal or wild type (unaffected) allele
CDNA (SEQ ID NO:9)"
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LOCATION: 3852..3891
OTHER INFORMATION: /note- "start and stop positions for
                                                                                                          GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8907-0088-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
FILING DATE: 34-May-1996
FILING DATE: 16-Apr-1996
FILING DATE: 16-Apr-1996
FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: POISSARIC, BLIAN M.
REGISTRATION NUMBER: 28,462
                                                       Sequence 1, Application US/09503444A Patent No. 6228594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 20.402
REFERENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nuclei
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                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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NAME/KEY: - 140..7319
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OTHER INFORMATION: ,
OTHER INFORMATION: 1
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: New York
RY: USA
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2609 AGGCCAAGGAGAGAGAGATCCTGAGCTCAGGAGTTCAAGACCAGCCTGGGCAACACAGCA 2668
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OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: untation)

OTHER INFORMATION: /nutation | CTHER INFORMATION | CTHER INFORMATION | CTHER INFORMATION | CTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: replace(5834, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /note- "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 2442(C) allele (SEQ ID NO:41)" FBATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
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                                APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
RIGH APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATORNEY/AGENT INFORMATION:
NAME: POISSANT, BITAN M.
REGISTRATION NUMBER: 28,462
TELECOMMUNICATION INFORMATION:
TELECHENS: 212-990-9090
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TELEX: 66141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
PRIOR APPLICATION DATA:
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2669 AAA 2671
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
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US-09-503-444A-5
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LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutation"
/note= "Hereditary Hemochromatosis (HH)
gene 24d2 allele"
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OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)" FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: 24d2 allele cDNA (SEQ ID NO:11)"
                                                                                                                                                                                                                NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dare 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0088-999
                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,4444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATION NUMBER: 04-Apr-1996
Sequence 5, Application US/09503444A
Patent No. 6228594
                                                                                                                           APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                               Thomas, Winston J. Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 10825 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO:
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LOCATION: 140..7319
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          New York
: New York
RY: USA
                                                     GENERAL INFORMATION:
APPLICANT: Thomas,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
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                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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STATE:
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INFORMATION FOR SEQ ID NO: 7:
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                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                          NAME/KEY: allele
LOCATION: replace(3872, "g")
CTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d2
                                                                                                                                                                                                                                                                                        15.9%; Score 27.8; DB 4; Length 10825;
65.1%; Pred. No. 11;
tive 0; Mismatches 22; Indels 0;
                                   OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(G) allele (SEQ ID NO:20)" FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Gnirke, Andreas
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Hought, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
CORRESPONDENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28.462
REFERENCE/FOCKET NUMBER: 8907-0088-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTONREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/0950344AA Patent No. 6228994 GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                               Best Local Similarity 65.19
Matches 41; Conservative
              5507..6023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
New York
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2669 AAA 2671
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                                                                                                                                                                                                                                                US-09-503-444A-5
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                                                                                                                                                                                                                                                                                ..436, 3762..4025, 4235..4510, 5606..5881,
53, 7107..7147)
/product- "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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OTHER INFORMATION: Aphenotype= "Hereditary Hemochromatosis
OTHER INFORMATION: Aphenotype= "Abreme" Aphenotype | Aphenot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 10825;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "Hereditary Hemochromatosis (HH) gene containing a combination of both 24d1 and 24d2 alleles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note- "start and stop positions for CDNA containing a combination of both 241 and 2462 alleles (SEQ ID NO:12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 5507..6023
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27, Application US/09277457
Patent No. 6355425
GENERAL INFORMATION:
APPLICANT: Rothenberg, Barry E.
APPLICANT: Sawada-Hiral, Ritsuko
APPLICANT: Barton, James G.
TITLE OF INVENTION: MUTHINGNS ASSOCIATED WITH IRON DISORDERS
FILE REFERENCE: 10653/002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                         and 24d2 mutations"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Aphenotype OTHER THROUGH
                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                          LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /P'
OTHER TABLET
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5507..6023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION: 140.7319
COTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
NAME/KEY: allele
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OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                       LOCATION: join(361, LOCATION: 6040..61
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US-09-503-444A-7
                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION OTHER INFORMATION
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2669 AAA 2671
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                                                                                                                                                                                                                                                         NAME/KEY:
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Sequence 189371, Sequence 3892, Sequence 18932, Sequence 6, App11 Sequence 12168, A Sequence 174961, Sequence 174961, Sequence 12167, A Sequence 12167, A Sequence 12167, A Sequence 21981, A Sequence 21981, A Sequence 2788, A Sequence 2788, A Sequence 2766, Ap Sequence 2766, Ap

Sequence 25, Appl Sequence 27, Appl Sequence 13, Appl Sequence 1, Appli Sequence 2, Appli Sequence 2916, A Sequence 2916, A Sequence 2816, A Sequence 28016, Appli

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database

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Sequence I, Application US/10010408
Publication No. US20020165185A1
GENERAL INFORMATION:
APPLICANT: John J. Castellot, Jr.
And Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
15 US-10-027-632-281405
15 US-10-027-632-189371
15 US-10-027-632-189372
11 US-09-960-352-3899
10 US-09-897-214-6
11 US-09-960-352-12168
11 US-09-960-352-12168
11 US-09-960-352-12167
12 US-10-027-632-12182
15 US-10-027-632-12182
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15 US-10-027-632-2182
15 US-10-027-632-2184
17 US-09-764-891-9766
18 US-10-027-632-296356
19 US-09-764-891-9766
11 US-09-886-055-134
11 US-09-886-055-134
                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-880-107-3327
US-10-301-844-1
US-09-918-995-29616
US-09-918-995-29616
US-09-918-995-9209
US-09-918-995-9209
US-10-027-632-284014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFICATION: «Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/04,273
FILING DATE: March 19, 1998
APPLICATION NUMBER: «Unknown>
FILING DATE: «Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Any E. Mandragouras
REGISTRATION NUMBER: 36.207
REFERENCE/DOCKET NUMBER: MBI-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                     25701
25758
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235033
237326
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     US-10-010-408-1
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Sequence 18, Appl
Sequence 12045, A
Sequence 359, Appl
Sequence 359, Appl
Sequence 4928, Appl
Sequence 4928, Appl
Sequence 4928, Appl
Sequence 1000, Appl
Sequence 17772, A
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Sequence 205550,
Sequence 110489,
Sequence 222, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 222, App
Sequence 20, Appl
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8368.853 Million cell updates/sec
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                                                                                                                                                                                                                                                 1 AGTCCAGGAACTTGAGCTTT......GCCTAGAATAAACACCCAAA 175
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                                                                                                                                  July 28, 2003, 15:36:41; Search time 43.1391 Seconds
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" (gn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
" (gn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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" (gn2_6/ptodata/2/pubpna/DSO6_NEW_PUB.seq:*
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" (gn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                    2879534
                       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-027-632-110489
US-09-560-863-222
US-09-771-208-20
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US-10-027-632-12045
US-09-796-692-359
US-09-796-692-4928
US-10-040-862-359
US-09-864-761-1000
US-09-864-761-17772
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175
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Maximum Match 100%
Listing first 45 summaries
                                                                                               OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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28.8 28.8

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126.2 126.2 125.8

Result Š. 31.2 30.8 30.8 30.8

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APPLICANT:
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APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: Plinks
CURRENT APPLICATION NUMBER: US/10/112,267
CURRENT FILING DATE: 2002-03-27
CURRENT FILING DATE: EARLIER FILING DATE: 1998-10-29
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-0-29
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
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                                                                                                                                                                                                                                                                                                                                                                                                                               61 AGGAAGCCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTCAGCATGAGAAAGACAAGG
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es 23; Indels
                                                                                                                                                                                                                                                Query Match 100.0%; Score 175; DB 15;
Best Local Similarity 100.0%; Pred. No. 7.2e-53;
Matches 175; Conservative 0; Mismatches 0;
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Pred. No. 3.1e-
0; Mismatches
                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-010-408-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/10112267 Publication No. US20030068678A1 GENERAL INFORMATION:
LENGTH: 1708 base pairs
                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                          .1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 72.1%;
Best Local Similarity 86.3%;
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Botstein, David A.
                                              TOPOLOGY: 11near MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cohen, Robert
Goddard, Audrey
                                                                                                                                  NAME/KEY: CDS
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                                                                                                                                                            LOCATION:
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61 AGGAAGGCTCCAÇACCTCTGGCAGGCCAGGCCTTTCTCTTCAGCATGAGAAAGACAAGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGTCCAGGAACTŴGAGCTTTGTATTTTCAGGAATGCACATCTCTTAAGCACTCGCAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURENT APPLICATION NUMBER: US/10/112,267
CURENT APPLICATION NUMBER: US/02-03-27
PRIOR APPLICATION NUMBER: 2002-03-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
PRIOR FILING DATE: BARLIER FILING DATE: 1998-10-29
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
NUMBER: OF SEQ ID NOS: 156
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Pred. No. 3.1e
0; Mismatches
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APPLICANT: No. US20030091973A11 II,
APPLICANT: Raha, Debasiĝh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23, Application US/09956522A Publication No. US20030091973A1 GENERAL INFORMATION:
                                                                                                                                                                      Sequence 18, Application US/10112267 Publication No. US20030068678A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              Cohen, Robert
Goddard, Audrey
Gurney, Austin L.
Hillan, Kemeth J.
Lawrence, David A.
Levine, Arnold J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 72.1%;
Best Local Similarity 66.3%;
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pennica, Digne
APPLICANT: ROy, Margaret Ann
APPLICANT: Wood, Willigm I.
TITLE OF INVENTION: WISP POLYP
FILE REFERENCE: P1176R2
                                                                                                                                                                                                                                                       APPLICANT: Botstein, Dayld A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mus musculus US-10-112-267-18
                                                                                                                                                    US-10-112-267-18/c
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285 AGTCCAGGAACTTGAGCTTTGTATTTTCAGGAATGCACATCTCTTAAGCACTCGCAAAAC 344
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                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                DB 12; Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 707;
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2.6e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        405 GGACCAGCAGAGTACTTTCCTCTGGAGGACTAGT 439
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                                                                                                                                            Score 125.8; I
Pred. No. 2.6e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-07-20
PRIOR PLING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR PELING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12045
LENGTH: 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/156,358
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Best Local Similarity 54.3%;
Matches 63; Conservative (
                                                                                                                                            Query Match 71.9%;
Best Local Similarity 96.8%;
Matches 150; Conservative
                                                                                ; ORGANISM: Rattus norvegicus US-09-956-622A-23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 439
TYPE: DNA
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US-10-027-632-12045
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ORGANISM:
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Sequence 359, Application US/09796692 Publication No. US20020198362A1

RESULT 6 US-09-796-692-359

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APPLICANT: MAINLON, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
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APPLICANT: Algate, Paul A.
APPLICANT: Annion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
FILE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
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53.3%; Pred. No. 0.57;
tive 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                         CURRENT FILING DATE: 2001-03-01, PRIOR APPLICATION NUMBER: 60/186,126
PRIOR PELIKON DATE: 2000-03-01
PRIOR PELIKON DATE: 2000-03-01
PRIOR PELIKON DATE: 2000-03-17
PRIOR PELIKON DATE: 2000-04-29
PRIOR PELIKON DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200, 303
PRIOR PELIKON DATE: 2000-04-28
PRIOR PELIKON DATE: 2000-04-28
PRIOR PELIKON DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR PELIKON NUMBER: 60/202, 084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/202, 084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/202, 903
PRIOR PELING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/223, 903
PRIOR APPLICATION NUMBER: 60/223, 416
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Publication No. US20020198362A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/223,378 PRIOR FILING DATE: 2000-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: n = A,T,C or G
US-09-796-692-359
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Best Local Similarity 53.3%
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APPLICANT: Adjace, Paul A.

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APPLICANT: Refere Marc

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther

TITLE OF INVENTION: NUMBER: US 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR PELICATION NUMBER: US 60/200,303

PRIOR PELICATION NUMBER: US 60/200,303

PRIOR APPLICATION NUMBER: US 60/200,709

PRIOR APPLICATION NUMBER: US 60/200,709

PRIOR APPLICATION NUMBER: US 60/200,909

PRIOR PELING DATE: 2000-03-01

PRIOR PELING 
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0.57;
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Best Local Similarity 53.3%; Pred. No. 0.57
Matches 65; Conservative 0; Mismatches
                                                                                                                                                                                                 Sequence 359, Application US/10040862
Publication No. US20030078396A1
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; LCCATION: (1)...(463)
; OTHER INFORMATION: n = A,T,C or G
US-10-040-862-359
                                                                                                                                                                                                                                    Publication No. US20030078396,
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
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       385 AA 386
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                                                                                                                      RESULT 8
US-10-040-862-359
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                                   PRIOR FILING DATE: 2001-03-01
PRIOR PELING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR PRIOR APPLICATION NUMBER: 60/200, 999
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR PRIOR DATE: 2000-05-01
PRIOR PRIOR APPLICATION NUMBER: 60/202, 084
PRIOR PRIOR DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-02
PRIOR PRIOR PAPLICATION NUMBER: 60/218, 950
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR PRIOR FILING DATE: 2000-08-03
PRIOR P
CURRENT APPLICATION NUMBER: US/09/796,693
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LOCATION: (108)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (110)
OTHER INFORMATION: n=A,T,C or G
LOCATION: (420)
OTHER INFORMATION: n=A,T,C or G
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US-09-796-692-4928
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LOCATION: (47)
OTHER INFORMATION: n=A,T,C or
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OTHER INFORMATION: n=A,T,C or
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Best Local Similarity 53.3%;
Matches 65; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Harzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTCAGCATGAGAAAGACAAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 TTGAATGAGTTAATCAAATTCCAGGCCATCGTCCACGCCACCAACAGTCAAAGGCCAAGG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||| ||||| ||| || || || || || || ||| ||| ||| ||| || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || 
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                                                                                                                                                                                                                                                                                                 Length 463;
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                             Score 30.8; DB 15;
Pred. No. 0.57;
0; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PILLING DATE: 2000-02-04
PRIOR PLILING DATE: 2000-02-04
PRIOR PLILING DATE: 2000-02-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLILING DATE: 2000-08-03
PRIOR PLILING DATE: 2000-06-03
PRIOR PLILING DATE: 2000-09-04
PRIOR PILING DATE: 2000-10-04
PRIOR PLILING DATE: 2000-10-04
PRIOR PLILING DATE: 2000-10-04
PRIOR PLILING DATE: 2000-10-04
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-864-761-1000
; Sequence 1000, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
                                   FEATURE:
NAME/KEY: unsure
LOCATION: (448)
OTHER INFORMATION: n=A,T,C or G
OTHER INFORMATION: n=A, T, C or G
                                                                                                                                                                                                                                                                                                 17.6%;
53.3%;
                                                                                                                                                                                                                                                                                                                            Best Local Similarity 53.38
Matches 65; Conservative
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                                                                                                                                                                                                                          APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Corriva Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
GURRENT APPLICATION NUMBER: US/10/040,862
CURRENT APPLICATION NUMBER: US/60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NA REFLICATION NUMBER: US 60/200, 203

NA APPLICATION NUMBER: US 60/200, 779

NA FILING DATE: 2000-04-28

NA FILING DATE: 2000-05-01

NA PRICATION NUMBER: US 60/202, 084

NA PRICATION NUMBER: US 60/202, 084

NA PRICATION NUMBER: US 60/202, 084

NA PRILING DATE: 2000-05-04

NA PRILING DATE: 2000-05-05

NA PRILING DATE: 2000-05-20

NA PRILING DATE: 2000-05-20

NA PRILING DATE: 2000-05-20
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-07-14
PELICATION NUMBER: US 60/222,903
FILING DATE: 2000-08-03
APPLICATION NUMBER: US 60/223,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
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LOCATION: (110)
OTHER INFORMATION: n=A,T,C or G
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LOCATION: (108)
OTHER INFORMATION: n-A,T,C or
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NAME/KEY: unsure
LOCATION: (47)
OTHER INFORMATION: n=A,T,C
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LOCATION: (45)
OTHER INFORMATION:
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LOCATION: (43)
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SEQ ID NO 4928
LENGTH: 463
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APPLICANT: Ma, Younhong
APPLICANT: Lih, Chih-Jian
APPLICANT: Chen, Fan
APPLICANT: Chen, Fan
APPLICANT: Chen, Yil-Der I.
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF INSULIN RESISTANCE AND RELATED CONDITIONS
FILE REFERENCE: 421452000300
CURRENT APPLICATION NUMBER: US/10/161,803
CURRENT FILING DATE: 2002-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 CTTAAGCACTCGCAAAACAGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N: EXPRESSED IN LUNG, SIGNAL = 2.2

N: EXPRESSED IN LUNG, SIGNAL = 2.2

N: EXPRESSED IN HEARIN, SIGNAL = 3.8

N: EXPRESSED IN HEARIN, SIGNAL = 2.2

N: EXPRESSED IN PLACENTA, SIGNAL = 1.2

N: EXPRESSED IN BT474, SIGNAL = 4.9

N: EXPRESSED IN HELA, SIGNAL = 1.6

N: EXPRESSED IN HELA, SIGNAL = 2.6

N: EXPRESSED IN HIT: 0.000+00
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                                                                 PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
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SOFTWARE: FastSEQ for Windows Version 4.0
       PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/295,264
PRIOR FILING DATE: 2001-06-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 AGCATGAGAAAGACAAGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Homo sapiens
US-10-161-803-23
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 17772
LENGTH: 1096
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APPLICANT: Rank, David R.

APPLICANT: Hancal, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION UNDER: US 60/180,312

PRIOR FILING DATE: 2000-06-03

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-09-03

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 CIGCGGTAGGCAGAAGACTGGAATCGGTGGCACCTCTGCGGGGCGAGGCCCTTCCTCTTG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 10; Length 483;
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BONE MARROW, SIGNAL = 1.
HELA, SIGNAL = 2.6
                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN BADILT LIVER, SIGNAL

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.8

OTHER INFORMATION: EXPRESSED IN PEART, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN BOTA SIGNAL = 4.9

OTHER INFORMATION: EXPRESSED IN BOTA MARROW, SIGNAL

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
                                                              NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 1000
LENGTH: 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
PRIOR APPLICATION NUMBER: US 09/774,203 PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17772, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 AGCATGAGAAAGACAAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 GTCAGGGGAAAGTCCAGG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
17.1%;
Best Local Similarity 61.5%;
Matches 48; Conservative
                                                                                                                                                                                                                   TYPE: DNA . ORGANISM: HOMO sapiens
                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: E. OTHER INFORMATION: E.
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FILING DATE: 2000-07-12
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Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Human
US-10-027-632-110489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-560-863-222/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Fa
                                                                                                                                                                                                                                                                                                                                LENGTH: 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                              54 GCAAAACAGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTCAGCATGAGAAA 113
                                                                                                       47 AGCACTCGCAAAACAGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTCAGCA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 TGAGAAAGACAAGGGACAGCAGAGTACTCTCCTCTGGAGGACTAGTCTAGCCTAGAATAA 166
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                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 110489, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David.G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
    Length 1753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 624;
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    DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 15;
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Score 29.4; DI
Pred. No. 2.9;
0; Mismatches
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Pred. No. 2.8;
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,318
PRIOR APPLICATION NUMBER: US 60/185,318
                                                                                                                                                              114 GACAAGGACAGCAGAGTACTCTCCTC 140
                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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PRIOR APPLICATION NUMBER: US 60/218,006
                                                                                                                                                                                                                                                                                                     Sequence 205550, Application US/10027632 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.6%;
52.0%;
Query Match
Best Local Similarity 58.6%;
Matches 51; Conservative
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Best Local Similarity 52.09
Matches 65; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nehls, Michael C.
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020110809Alel Human Polynucleotides and the TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: LEX-0018-USA
CURRENT APPLICATION NUMBER: US/09/560,863
FRIOR APPLICATION NUMBER: US 60/132,408
PRIOR FILING DATE: 1999-04-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR PILICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SEQ ID NOS: 325720
SEQ ID NO 110489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1008
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: n = A,T,C or G
US-09-560-863-222
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63.8%;
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Best Local Similarity 62.5%;
Matches 45; Conservative
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168 GGACTGCAG 176
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Search completed: July 28, 2003, 21:31:58 Job time: 47.1391 secs

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BE077992 228201 MA
BB75647 BB775647
BB7712425 MI-P-A3-a
AV751782 AV751782
AZ574816 333PVB05
AZ574816 333PVB05
AL301654 Tetraodon
AL246194 Tetraodon
AL246194 Tetraodon
B175728 603030731
B0278875 AGBNOURT
AM694655 NF078F055
AL379783 MLBB47D11
AM694655 NF078F055
AL379783 MLBB47D11
AV063522 AV065322
BF549593 UI-R-C2-m
AQ120776 HE-3970_B
BA256378 518732 MA
BL256378 518732 MA
BL256378 518732 MA
BL256378 SOJNBD009
BQ12076 HE-3566_B
AZ127785 OSJNBD009
BQ210400 UI-R-DX1-ASTA178
AZ127785 OSJNBD009
BQ210400 UI-R-DX1-ASTA178
AZ127785 OSJNBD009
BQ218534 AGENCOURT
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                                                                                                                         BE515213 BB515213
BB792544 BB792544
BB58051 BB58051
BF138093 601785003
AZ574808 332PvH07
BI147316 602913743
AQ345221 RPC111-13
BB701454 BB701454
AL800293 AL800293
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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Fax: 319 335 9565
Email: msoarese@lue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand CDNA and therefore this may represent a bonafide poly A
                                                    BB518921
BB213539
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to
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Program for Rat Gene Discovery and Mapping
University of Iowa
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BB772425
AV75174825
AZ574814
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CNSO31XH
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FEATURES SOURCE

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and the oligo-dr track sereed to identify it as a clone from the commalized cervix librery CDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.trespen.com)

Loortion/Conference of the committee o
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including CYO, C2O, DAO, DBO, DCO, DDO, and DEO
corresponding to plates R-CYO-BXP through R-CYO-BXZ,
R-C2D-BXA through R-C2D-BXI, R-CZD-BXZ-C, R-DAO-BXI,
through R-DAO-BYP, R-DAO-BXI through R-DAO-BXI,
through R-DAO-BYP, R-DAO-BXI through R-DCO-BXO, R-DEO-CAY
through R-DEO-CAB, R-DDO-ZXI through R-DEO-CAA,
R-DDD-CBB-C, and R-DEO-CAB through R-DEO-CAA.
R-DDD-CBB-C, and R-DEO-CAB through R-DEO-CAA.
The corresponding plates are R-CNO-BKB-CAA.
The corresponding plates are R-CNO-BKM, R-CNO-BLC,
R-CNO-BLG, R-CNO-BLP through R-CNO-BLT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Organ: uterus; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pregnant mouse uterus, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB367824 RIKEN full-length enriched, 16 days embryo head Mus
musculus cDNA clone C130039K03 3' similar to AF126063 Mus musculus
connective tissue growth factor-like protein precursor (Ctgf1) mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGTCCAGGAACTTGAGCTTTGTATTTTCAGGAATGCACATCTCTTTAAGCACTCGCAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 418;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 72.1%; Score 126.2; DB 9; Best Local Similarity 86.3%; Pred. No. 2.9e-32; Matches 151; Conservative . 0; Mismatches 23;
                                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="imaGE:1498133"
/clone_lib="soares_NMPu"
/sex="female"
                                                                                                                Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                            High quality sequence stop: 403.
Location/Qualifiers
                                                                                                                                                                       MGI:935757
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                            /dev_stage="adult"
/lab_host="DH10B"
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                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                 1. .418
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Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayshizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
System. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTS (Konno,H., et al.)
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                                                                                                                          Unpublished (2000)
Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokobama Institute
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Please visit our web site (http://genome.rtc.riken.go.jp) for
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Pred. No. 8.5e-32;
0; Mismatches 24; Indels
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Fri Aug

249 AACAGTAGAGTACCCTCCTGGAGGACTGGCCCGGTCTGGAATAAACACCCCAAA 303

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Division of Experimental Animal Research in Riken

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BB374499 RIKEN full-length enriched, 16 days embryo head Musmusculus cDNA clone C130075616 3' similar to AF126063 Mus musculus connective tissue growth factor-like protein precursor (Ctgfl) mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Yoshihide Hayashizaki
                                                                                                                                    BB374499.1 GI:9086993
                                                                                                  , mRNA sequence.
BB374499
                                                                                                                                                                     house mouse.
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house mouse.
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les 149; Conserv
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                                                    DREALL: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Muramatsu,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,
Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carnindi,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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further details.
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/dev_stage="16 days embryo"
/lab_host="DH10B"
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1. .315
/organism="Mus musculus"
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/clone="C130075G16"
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EMARGAGES (Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 307)

1 (bases 1 to 307)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fükuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hara, C., Hayatsu, N., Hirozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kadota, M., Kadota, K., Kadota, S., Kurinara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Salto, H., Sakai, C., Sato, K., Shibata, Y., Shigemoto, X., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Yano, R., Yano, R., Yano, R., Yano, H., Okota, T., Yoshida, K., Yoshik, M., Muramatsu, M., and Hayashizaki, Y.
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
.N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
rhermostabilization and thermoactivation of thermolabile enzymes by
                                                                                                    prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-grapper. Second strand cDNA was prepared with the primer adapter of sequence [5' and adapter of sequence [5' and adapter of sequence [7' as a closed into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9922
contibuted to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGACTCTTTTTTTTTTTTTTVN 3'], cDNA was
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Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation carninci,P. and Hayashizaki,Y.
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/lab_host="Hi0B"
/lab_host="Hi0B"
/note="Site_1: Sall; Site_2: BamHI; cDNA library was propered and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKBN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5"
GAGAGAGAAGAGCTCTTTTTTTTTTTTTVN 3'], cDNA was
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RIKEN full-length enriched, adult male aorta
                                                                                                                                                                 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 AACAGTAGATACCTTCCTGGAGGACTGGCCCGTTCTGGAATAAACACCCAAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 307;
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Pred. No. 3.7e-30;
0; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="aorta and vein"
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/clone="A530061F23"
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84.0%;
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1 (Dases 1 to 337)

2 (Nono, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci

2 (Nono, H., Alzawa, K., Eshika, Y., Ishikawa, J., Ishikawa, T., Carninci

3 (P., Endo, T., Fukuda, S., Fukunishi, Y., Ishikawa, J., Ishikawa, T., Kadota, K., Kagawa, I., Kaj.C., Kawai, J., Kikuchi, N., Izawa, M., Kadota, K., Kagawa, I., Kaj.C., Kayai, J., Kikuchi, N., Kayoswa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Sughara, Y., Sughara, Y., Sughara, Y., Sughara, Y., Suzuki, H., Tagawa, A., Takhashi, F., Tominaga, N., Toya, Y., Suzuki, H., Yanoda, Y., Watanabe, S., Yamanura, T., Yamanaka, I., Yano, R., Yano, R., Yasunishi, A., Yokota, T., Yamanura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yamanura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yamanura, T., Yano, J., Yokota, T., Yokohida, K., Yoshida, K., Yoshiki, A., Yokohama, Institute

Nikima, Matsuki, M., Matsuki, M., Matsuki, M., Muranatsu, M., Muranatsu, M., Muranatsu, M., Muranatsu, M., Muranatsu, M., Muranatsu, M., Jana, J., T.-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216

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Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
System. Genome Res. 9 (5), 463-470 (1999)
Carningi,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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Pred. No. 4e-30;
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/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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/db_xref="taxon:10090"
/clone="B230378P10"
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                                                                                                                                                                                                                    /note-"Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
   /clone_lib="RIKEN full-length enriched, adult male aorta
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/lab_host="DH10B"
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Contact: Yoshihide Hayashizaki
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishilyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
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Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Y. and Hayashizaki,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y., Osawa,Y., Muramatsu,M., Okazaki
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB222795 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A330079119 3' similar to AF126063 Mus musculus connective tissue growth factor-like protein precursor (Ctgfl) mRNA 'mRNA sequence.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
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High-effictency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                              1 AGTCCAGGAACTTGAGCTTTGTATTTCAGGAATGCACATCTCTTAAGCACTCGCAAAAC
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Please visit our web site (http://genome.rtc.riken.go.jp) for
   Gaps
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   27; Indels
   Mismatches
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/db_xref="taxon:10090"
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Mammalia; Euthería;
   147; Conservative
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TITLE JOURNAL COMMENT

KEYWORDS SOURCE ORGANISM

ACCESSION VERSION

REFERENCE AUTHORS

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                                                                                                                                                Email: genome-resegsc riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
.N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                         Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-ho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGACTCTTTTTTTTTTTTTVN 3'], cDNA was
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/dev_stage="adult"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: Sall: Site_2: BamHI; cDNA library was
/note="site_1: Sall: Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
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  Laboratory for Genome Exploration Research Group, RIKEN Genomic
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Pred. No. 5.6e-28;
0; Mismatches 31,
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/clone="B230309009"
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al Similarity 81.7%;
143; Conservative
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RESULT 9 BB518921

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Louden, Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, F., Konno, H., Alzawa, K., Akahira, S., Rkinnishi, Y., Hara, A., Hayatsu, N., Hivozane, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hort, F., Ishi, Y., Kai, J., Kikuchi, N., Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N., Matayama, T., Miki, K., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Matayama, T., Miki, K., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saitch, H., Sauchi, H., Sauchi, H., Suzuki, H., Taqawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Takahashi, F., Tominaga, N., Toya, T., Yano, R., Yasunishi, A., Yokta, T., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

N., Muramatsu, M. and Hayashizaki, Y.

Inpublished (2000)

Contact: Voshihade Hayashizaki
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Figure 1. No National Sci. 1. S. 
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BB518921 RIKEN full-length enriched, 16 days neonate heart wus musculus cDNA clone D83003xK05 3' similar to AF126063 Mus musculus connective tissue growth factor-like protein precursor (Ctgfl) mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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heart"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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/lab_host="DH10B"
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1. (Dates 1 to 218)

Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hivozane, T., Horl, F., Ishli, Y., Hara, A., Hayatsu, N., Ishkawa, T., Itch, M., Isawa, M., Kadota, K., Kagawa, J., Ishikawa, T., Itch, M., Isawa, M., Kadota, K., Kadota, T., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuno, Y., Makim, Oda, H., Oka, H., Oka, K., Shipata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Subaki, H., Susuki, H., Susuki, H., Susuki, H., Susuki, H., Susuki, H., Susuki, H., Yanamaka, T., Yamamura, T., Yamamaka, T., Yawamaka, T., Yawa, Yamamaka, Yamamaka, T., Yamamaka, T., Yamamaka, Yamam
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URL:http://genome.gsc.riken.go.jp,
carninci.p., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad.Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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133 AGTCCAGGAACTTGACCTTTGTATTTGTATAAATACACTTTTTTAAATGCTCACAAAGC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTCAGCATGAGAAAGACAAGG 120
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 218)
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                                                                                                                                                                                                                                                                 Length 316;
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                                                                                                                                                                                                                                                        Score 113.4; DB 10;
Pred. No. 6e-28;
0; Mismatches 31; 1
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                                                                                                                                                                                                                                                   Query Match 64.8%;
Best Local Similarity 81.7%;
Matches 143; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bunanalia; Buthegla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to [289)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Eukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Horli, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Kiyosawa, H., Kodi, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kodima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Mitsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata
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Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

Localion/Qualifiers

Localions musculus musculus model in the conference of 
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Pred. No. 6e-27;
....matches 33; Indels
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URL:http://genome-gac.riken.go.jp,
URL:http://genome-gac.riken.go.jp,
Carninoi,P., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
.N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S. A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Y. and Hayashizaki,Y., Ozawa,Y., Muramatsu,M., Okazaki
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Schences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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/dev_stage="adult"
/lab_host="bH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"/db_xref="taxon:10090"
                                                                                                                                                                                                 Contact: Yoshihide Hayashizaki
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Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishi, Y., Hara, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, K., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saitch, H., Sata, C., Sato, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Watanishi, A., Taqawa, A., Takahashi, F., Tominaga, N., Toya, T., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshino, RIKEM Mouse ESTS (Konno, H., et al.)
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p. Nibhiyama.yr. Westover,A., Itoh,M., Nagaoka,S., Sasaki
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                 BB515213 RIKEN full-length enriched, 16 days neonate heart Mus musculus CDNA clone DB30007F15 3' similar to AF126063 Mus musculus connective tissue growth factor-like protein precursor (Ctgf1) mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
1-7-22 Suebhiro-ho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases, 1 to 290)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RIKEN full-length enriched, 16 days neonate
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/dev_stage="16 days neonate"
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/db_xref="taxon:10090"
/clone="D830007F15"
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                                                                                                                                                                                                                                                                                                                                                                    , mRNA sequence.
BB515213
BB515213.1 GI:9566671
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GAGAGAGAGCGCCCCAACTCGACTTTTTTTTTTTTVN 3'], CDNA was prepared by using trehalose thermo-activated reverse transcriptuse and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTATTATATTATATATCCCCCCCCCCC 3']. CDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Rawal, J., Kolima, Y., Konda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, H., Tagawa, Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
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BB792544 RIKEN full-length enriched, kidney CCL-142 RAG cDNA Mus
musculus cDNA clone G430141015 3', mRNA sequence.
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URL:http://genome.goc.riken.go.jp/
Carnindi.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
A., Konno,H., Okazaki,Y., Hayatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper selected cDNns to
prepare full-length cDNA libraries for rapid discovery of new
peneare full-length cDNA libraries for rapid discovery of new
agenes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watchiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-81: 81-45-503-922
Fax: 81-45-503-9216
Bmail: genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer \{5^{\prime}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Division of Experimental Animal Research in Riken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 AACAGTAGAGTACCCTCCTGGAGGACTGGCCCTTCTGGAATAAACACCCAAA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 290;
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Pred. No. 7.2e-27;
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80.6%;
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/tissue_type="kidney"
/cell_line="CCL-142 RAG"
/note="pooled cell lines; (cell_line=CRL-1751 WEHI 164),
(cell_line=CRL-216 JC), (cell_line=RCB-0035 WEHI-3),
(cell_line=RCB-0464 Meth-A), (cell_line=RCB-0545 OHTA),
(cell_line=RCB-0559 K-1. FI), (cell_line=RCB-1283 B16
melanoma), (cell_type=Leydig cells, cell_line=CRL-1702 WEHI 231),
(cell_type=Nullipotent stem cell, cell_line=CRL-2076 WEHI 231),
(cell_type=Nullipotent stem cell, cell_line=CRL-2070 WE),
(tissue_type=blander, cell_line=RCB-0544 MBT-2),
(tissue_type=bone marrow, cell_type=strome cell,
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cell_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,
cell_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,
cell_type=B cells, cell_line=CRL-1669 BCLI clone 13.20-3B3)
), (strain=C3H, tissue_type=brain, cell_line=CRL-1443)
        sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fekfaishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full.length cDNA encyclopedia: ideal-time sequence clustering for construction of a nonredundant cDNA ibrary. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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1. 369

Aorganism="Mus musculus"

Adb_tataon:10090"

/clone="G430141015"

/clone="HENEW full-length enriched, kidney CCL-142 RAG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 324)
Konno, H., Aizawa K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fuguda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
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RIKEN integrated sequence analysis (RISA) system -- 384 - format
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6e-25;
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Pred. No. 6e-25
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Best Local Similarity 85,88;
Matches 151; Conservative
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 792 bp mRNA linear EST 24-OCT-2000 601785003F1 NCI\_CGAP\_Lu30 Mus musculus cDNA clone IMAGE:4012801 5', BF138093

BF138093.1 GI:10977133

house mouse. Mus musculus

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Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Kiyosawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, M., Mianura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Sughera, Y., Sughera, Y., Sulgemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watanabe, S., Yamamura, T., Yamanata, M., Muramatsu, M. and Hayashizaki, Y. Yamanura, T., Yamanaka, I., Yano, R. Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Gontact: Yoshihide Hayashizaki, Y. Upublished (2000)

N. Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p. Nishiyama.y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
.V., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
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transcriptuse and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5
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/dev_stage="2 days pregnant adult"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="E330032A10"
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1. 792

/ Organism="Mus musculus"
/ Strain="ECECH II"
/ Ab_xref="taxon:10090"
/ Clone="INAGE:4012801"
/ Clone="INAGE:4012801"
/ Clone=Lib="NCI_CGAP_LU30"
/ Lissue_type="tunor, metastatic to mammary"
/ Lab_nost="DH10B"
/ Note="Organ: lung; Vector: pCWV-SPORT6; Site_1: NotI;
/ Note="Organ: lung; Vector: pCWV-SPORT6; Site_1: NotI;
/ Site_2: SalI; transgenic model WNT-1, expression driven by
/ MMTV-LTR enhancer: Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

33 a 204 c 205 g 190 t
                                                                                                                                                                                               Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Inoyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov/f column: 02
Plate: LLAM9254 row: f column: 02
High quality sequence stop: 705.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 792)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Best Local Similarity 81.7%; Pred. No. 2.8e-14;
Matches 98; Conservative 0; Mismatches 21;
                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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Job time : 316.515 secs
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(without alignments)
10471.464 Million cell updates/sec US-10-010-408-1\_COPY\_1\_635 635 1 GAGGTTCTGATCTCCAGAG......GTGATGACGGTGGCTTCACC 635 July 28, 2003, 15:59:01; Search time 1764.82 Seconds OM nucleic - nucleic search, using sw model Title: Perfect score: Sequence: Run on:

IDENTITY\_NUC Gapor 10.0 Gapor 10.0 Scoring table:

4109280 Total number of hits satisfying chosen parameters:

2054640 seqs, 14551402878 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl: \* Database :

90-rac:\* 90-ph:\* 90-pr:\* 90-ro:\* 90-sts:\* 90-sy:\* gb\_vi:\* em\_ba:\* em\_fun:\* em\_hum: \* em\_pat:\* gb\_ba:\* gb\_htg:\* gb\_in:\* gb\_om:\* gb\_ov:\* gb\_pat:\* em\_in:\* em\_or:\* em\_mu:\* em\_ov:\* em\_om: em\_ph:

em\_htg\_hum:\* em\_htg\_inv:\* em\_htg\_other:\* em\_htgo\_hum:\* em\_htg\_mus:\* em\_htg\_pln:\* em\_htg\_mam:\* em\_htg\_vrt:\* em\_htq\_rod:\* em\_ro:\* em\_sts:\* em\_pl:\* em\_un:\*

Pred. No. is the number of results predicted by chance to have a

em\_htgo\_mus:\*
em\_htgo\_other:\*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		AF259981 Rattus no	AR210324 Sequence		æ	3 Mus	Seque	AX464186 Sequence		Seque	_				Sedue		Rattus		Rattus	AL731698 Mouse DNA	AL669906 Mus muscu	ALISSISZ HUMAN DNA	TOAA96 Chicken CEE	AB015877 Rattus no	E13814 cDNA encodi	Ношо	AF003594 Homo sapi	Ношо		AA334333 Sequence HA2015 Homo santen		Homo sapie	Ношо	BC009199 Homo sapi	Y11307 H.sapiens C	AF228049 Rattus no		AX206704 Sequence	AX206702 Sequence	$\mathbf{z}$	1167	H	5239	m
SUMMARIES ID		AF259981	AR210324	AR210325	AF100778		AX076919	AX464186	AF083500	AR210322	AR210323	AF074604	AF100780	BC017782	AR210338	AR210337	AC126895	AC095418	AC126895	AL731698	AL669906	ALL39332	CHKOFF	AB015877		AF031385	AF003594	BC001271	AX336386	HSIT62015	HSGIGIPET	HSCYR61M	BC016952	BC009199	HSCYR61	AF228049	AF320592	AX206704	AX206702	MUSCYR61A	NVI271167	HSNOVH	AX035239	AX342093
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% Query Match		91.6	82.1	82.1	82.1	Ξ.	43.0	43.0	Ξ.	<u>-</u>	43.0	43.0	43.0	0	۲.	7	6.	σ,	33.9	31.4	31.4	20.07	14.0	14.3	S	ı,	13.5	w.	ر ب		. יר	'n	S.	5	3.5	4.	3.3	3.2	3.2	?	3.0	٥.	3.0	٥.
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AF259981 1741 bp mRNA linear ROD 09-MAY-2000 Rattus norvegicus CCN family protein COP-1 (Cop-1) mRNA, complete Rattus norvegicus. Rattus norvegicus. Eukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 1741) Zhang,R., Averboukh,L., Zhu,W., Zhang,H., Jo,H., Dempsey,P.J., AF259981 AF259981.1 GI:7739780 RESULT 1 AF259981 LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS ACCESSION

ALIGNMENTS

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/product="CCM family protein COP-1"
/protein_id="AAF69011.1"
/d=xref="C1:7739781"
/translation="MRGSPLIRLANSFLCLLSMVCAQLCRTPCTCPWTPPOCPQGVP
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NGRRVLDGETERPNCRVLCRCDDGGFTCLPKCSEDYTLPSWNCPRPRRIQVPGKCCPE
WRCDGGVTPAIORSAAQGHQLSALVTPASADAPWPNWSTAWGPCSTTCGLGIATRVSN
OMFRCQLETRRCLERPRCLARRSHSSWNSAF"
491 c 480 g 384 t
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           family
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                                                                                          Vanderbilt-Ingram Cancer
12, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACCTTCGTGGTGGCCTCCACGGCCTCACGTTTGAAGCTGGCTCCACAAGGGAC
                                                                                                                                                                                                                                                                                                                                             Gaps
           CCN protein
                                                                                                                                                                                                                                                                                                                         DB 10; Length 1741
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Coffey,R.J., Pardee,A.B. and Liang,P.
Identification of rCop-1, a new member of the CC
as a negative regulator for cell transformation
Mol. Cell. Biol. 18 (10), 6131-6141 (1998)
98414629
                                                                                                                                                                                                                                                                                                                         Score 581.4; DB 10;
Pred. No. 1.4e-129;
0; Mismatches 11;
                                                                             Direct Submission
Submitted (24-APR-2000) Cell Biology, Van
Center, 649 MRB II, Nashville, TN 37232,
                                                                                                                             /organism="Rattus norvegicus"
/db_xref="taxon:10116"
1. .1741
                                                                                                                                                                      262. .1014
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/note="secreted protein"
/codon_start=1
                                                                                                              Location/Qualifiers
                                                                                                                                                            /gene="Cop-1"
262. .1014
                                                                                                                                                                                                                                                                                                                        Match 91.6%;
Local Similarity 97.8%;
les 621; Conservative
                                                       2 (bases 1 to 1741)
Liang, P.
                                                  9742130
2 (base
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Best Local Si
Matches 621
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                                                         REFERENCE
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TITLE
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                                                                                                                                                                                         Unclassified, (1734)

1 (bases 1 to 1734)

Botstein,D.A. Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J., Botstein,D.A. Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I. WISP polypeptides and nucleic acids encoding same Patent: US 6387657-A 17.14-MAY-2002;

Localion/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         72
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Pred. No. 3.8e-115;
0; Mismatches 41;
                                                                                                                 DNA
                                GGGTCCTGTGCGCTGTGATGACGGTGGCTTCACC
                                                                                                                 1734 bp
US 6387657.
                                                                                                                                                                                                                                                                                                     393
                                                                                                                                                                                                                                                                                       /organism="unknown"
491 c 495 g
                                                                                                                            patent
                                                                                                                                                GI 21512525
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92.0%;
1ve 0
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/translation="megnplitalselcilsmvysolcpapcacpwppocppgvp
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MVCDQAVMQPAIQPSSAQGHQLSALVTPASADGPCPNWSTAWGPCSTTCGLGIATRVS
NQNRFCQLEIQRRCLSRPCLASRSHGSWNSAF"
491 c 495 g 393 t
                                                               AF100778 17-DEC-1998
Mus musculus connective tissue growth factor related protein WISP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-OCT-1998) Molecular Oncology, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA Location/Qualifiers
                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to I734)
Pennica, D., Swanson, T.A., Welsh, J.W., Roy, M.A., Lawrence, D.A., Lee, J., Brush, J., Taneyhill, L.A., Deuel, B., Lew, M., Watanabe, C., Cohen, R.L., Melhem, M.F., Finley, G.G., Quirke, P., Goddard, A.D., Hillan, K.J., Gurney, A.L., Botstein, D. and Levine, A.J.
WISP genes are members of the connective tissue growth factor family that are up-regulated in wnt-1-transformed cells and aberrantly expressed in human colon tumors
Proc. Natl. Acad. Sci. U.S.A. 95 (25), 14717-14722 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="connective tissue growth factor related protein WISP-2"
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Pred. No. 3.8e-115;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="transformed by Wnt-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAC96320.1"
/db_xref="G1:4028579"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .1734
/organism="Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/cell_line="C57MG"
/cell_type="epithelial"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="mammary
                                                                                               (Wisp2) mRNA, complete cds.
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257. 1012
/gene="Wisp2"
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Best Local Similarity 92.0
Matches 586; Conservative
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JOURNAL
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Botstein, D. A., Cohen, R. L., Goddard, A. D., Gurney, A. L., Hillan, K. J.,
Bartene, D. A., Levine, A. J., Pennica, D., Roy, M. Ann. and Wood, W. I.
WISP polypeptides and nucleic acids encoding same
Patent: US 6387657-A 18 14 MAY-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 TGTCAG --- CTTGTCCTAAAGTCTTAGCACTTGTGGGGGCTTGGGGCTTCACACACTGTCA 178
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Pred. No. 3.8e-115;
0; Mismatches 41;
DNA
                                                                                                           1734 bp
US 6387657.
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                                                                                                                                                                                                                                                                                                                                           /organism="unknown"
495 c 491 g
                                                                                                                        Sequence 18 from patent AR210325
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al Similarity 92.0%;
586; Conservative
                                                                                                                                                                                                                    Unclassified
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Best Local S:
Matches 586
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and thrombospondin type I (TSP1) domains; member of the CCN (CTGE/CYF61/Nov) family; lacks the fourth carboxy-terminal (CT) domain present in other members of the CCN family.  // Codon_start=1 // product="connective tissue growth factor-like protein precursor" // protein_id="AAD18058.1" // Ab_xref="GI:437060" // translation="MRGMPLIHLLAISFLCILSMVYSOLCPAPCACPWTPPQCPPGVP LVLDGGGCCRVARRIGESCHLHVCDPSOGLVCOPGAGPSGRGAVCLFEEDDGSCEV NGRRYLDGGTFCLPLCSEDVRLPSWDCPRPRRIQVPGRCCPE WVCDQAVWQPAIQPSSAQGHQLSALVTPASADGPCPNWSTAWGPCSTTCGLGIATRVS BASE COUNT 375 a 480 c 489 g 395 t ORIGIN	Query Match         80.9%;         Score 513.6;         DB 10;         Length 1739;           Best Local Similarity         91.5%;         Pred. No. 2.9e-113;         Aatches 580;         Conservative         0;         Mismatches 44;         Indels 10;         Gaps 3;           Qy         6         TTCTGATCTCCAGAGGACCCTGGGGACAGGGCCTTGGCAAGGCTGCAGCCGCTG-64         64         Indels 10;         Indels 10;	Qy         65 GGCAGTGGCTTGGAATGGAGGTCTTTATTACTGGGAACTGAGGAGCTCCTGT 124	Oy 182 ACCTTCGTGGTGGCCTCCACGCCTCACCTTCAGGTTTGAAGCTGCTCCACAAGGGACA 241	Oy   302 CTCAATGGTGTGCCCAGGTGTGCCGGACACCCTGTAGGACACCCCCA 361   111111111111111111111111111111111	422 GAGGCTGGGGGAGTCCTGCACCTGCATCTGGGACCCCAGCCAG	535 GAGCTGTGAGGCCGCAGGTACCTGGATGGGGAGACCTTTAAACCCAATTGCAG 602 GGTCCTGTGCCGCTGTGATGACGGTGCCTTCACC 635 11	RESULT 6 AX076919 LOCUS AX076919 LOCUS DEFINITION Sequence 31 from Patent W00105836. ACCESSION AX076919 VERSION KEYWORDS AX076919.1 GI:13121575
ACACGGTGACATGGTGGCCTCCTCGGCCTCAGGTTTGAAGCTGGCTCCACAAGGG	SATGA SATGA SATGA AATTG	CAGGGTCTGTGCCGCTGTGATGACGGTGGCTTCACC 635	AF126063 ON Mus musculus connective tissue growth factor-like protein precursor (Ctgfl) mRNA, complete cds. N AF126063 AF126063. GI:4337059 Mus musculus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 1739) S Kumar, S., Hand, A.T., Connor, J.R., Dodds, R.A., Ryan, P.J., Hand, A.T., Connor, J.R., Lipshutz, D.B., Zou, C., Hand, S.M., Votta, B.J., James, I.E., Rieman, D.J., Gowen, M. and Lee, J.C.	Identification and cloning of a connective tissue growth factor-like CDNA from human osteoblasts encoding a novel regulator of osteoblast functions 97 Biol. Chem. 274 (24), 17123-17131 (1999) 9287915 9287915 9287915 9287915 9287915 9387916 9388067 9388918 9388916 9388916 9388916 9388916 938916 9	9	/gene-"Ctgfl" 242997 /gene-"Ctgfl" /gene-"Ctgfl" /note-"Similar to the Mus musculus WISP-2 protein encoded by the sequence presented in GenBank Accession Number AR100778; putative growth factor; CTGF-L; contains IGF binding (IGFBD), Von Willebrand Factor type C (VWC) repeat
4 6 4 6 4 6 4 6 6 6 6 6 6 6 6 6 6 6 6 6	3 & 8 & 6	Qy Db RESULT 5	ACT SOURCE SOURC		TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOUFCE qene	COS

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1283 bp mRNA linear PRI 04-NOV-1998
Homo sapiens connective tissue growth factor-like protein
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                                                                                                                                                                                                              64 TCAAAGGTGCGTACCCAGCTGTGCCCGACACCATGTACCTGCCCCTGGCCACCTCCCCGA 123
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Submitted (11-AUG-1998) Bone & Cartilage Biology, UW 2109,
SmithKline Beecham, 709 Swedeland Road, King of Prussia, PA 19406,
USA
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Kumar, S., Hand, A.T., Connor, J.C., Dodds, R.A., Ryan, P.J., Rrill, J.G., Fisher, S.M., Slemmon, J.Y., Lipshutz, D.B., Bartholomew, V., James, I.E., Rieman, D.J., Gowen, M. and Lee, J.C. Identification and cloning of CTGF-L from human osteoblasts, a lovel cysteine rich protein containing an IGF binding domain 2 (bases 1 to 1283)
                                                                                                                                                                                                                                                                             184 CGGCTGGGGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGGCCAGGCCTGGTTGC
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9. .761
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Pred. No. 2.5e-55;
0; Mismatches 75
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/chromosome="20"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1266)
Botstein,D., Goddard,A., Gurney,A.L., Hillan,K.J., Roy,M.A. and Wood,W.I.
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Goo, W.Q., Gerritsen, M. E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.L. and Zhang, Z.
                                                                                                             methods for the treatment of tumors
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                         Polypeptidic compositions and method
Patent: WO 0105836-A 31 25-JAN-2001;
Genentech, Inc. (US)
Location/Qualifiers
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Sequence 319 from Patent WO0140466.
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    TCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAG
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11 Similarity 80,9%;
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NGRINERARGEPCOPOLHYCDASQGINCQPCAGPGGRGALCLLAEDDSSCEV

NGRINERARGEPCOPOLHYCDASGENCYPLCSEDVRLPSWDCPHPRRVEVLGKCCPE

WCGGGGGGLGTQPLPAGGPGGLYSSLPPGVPCPEWSTAWGPCSTTCGLGMATRYSN

QNRRFCRLETQRRLCSRRCPPGRGRSPONSAF"

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1 (bases 1 to 1293)

Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.
MISP polypeptides and nucleic acids encoding same
Patent: US 6387657-A 13 14-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                               302
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Pred. No. 2.5e-55;
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Pred. No. 2.5e-55;
); Mismatches 75; Indels
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the fourth carboxy-terminal domain members of the CCN family"
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/product="connective tissue
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US 6387657.
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425 c 393 q
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AR210322
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Homo sapiens connective tissue growth factor related protein WISP-2 (WISP2) mRNA, complete cds.
AF100780.
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Submitted (23-OCT-1998) Molecular Oncology, Genentech, Inc., 1 DNA
Way, South San Francisco, CA 94080, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="connective tissue growth factor related protein WISP-2"
121 TGCCCGCTGGGAGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGCCGGGTATGTGCACGG 180
                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.

Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.

To 1427)

Pennica,D., Swanson,T.A., Welsh,J.W., Roy,M.A., Lawrence,D.A.,
Lie,J., Brush,J., Taneyhill,L.A., Deuel,B., Lew,M., Watanabe,C.,

Cohen,R.L., Melhem,M.F., Finley,G.G., Quirke,P., Goddard,A.D.,

Hillan,K.J., Gurney,A.L., Botstein,D. and Levine,A.J.

MISP genes are members of the connective tissue growth factor
family that are up-regulated in wnt-1-transformed cells and
aberrantly expressed in human colon tumors

Proc. Natl. Acad. Sci. U.S.A. 95 (25), 14717-14722 (1998)
                              CAGCCTGGGGCAGGCCCTGGCGGCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGGT
                                                                                                                                                                        AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAACCCAATTGCAGG
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/organism="Homo sapiens"
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/chromosome="20"
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/tissue_type="lung"
/dev_stage="fetus"
1. .1427
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/gene="WISP2"
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Pennica, D.
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/db_xref="d1:3128192"

/tanslation="MRGTPKTHILLAFSLLCLLSKVRTQLCPTPCTCPWPPPRCPLGVP

LVLDGGGGCRVCARKLGEPCDOLHVCDASQGIVCQPGAGPGGRGALCLLAEDDSSCEV

NGRLYREGETFQPHCSIRCRCEDGGFTCVPLCSEDVRLPSWDCPHPRRVEVLGKCCPE

WRRYGGGGGTGTQPLPAQGPGPSGLVSSLPPGVPCPEWSTAWGPCSTTGGLGMATRVSN

QNRRCPRLETQRRLCERRCPPSRGRSPQNSAF"

1 others
                                                                                                                                                                                               AF074604 1309 bp mRNA linear PRI 18-JUL-1998 Homo sapiens connective tissue growth factor-related protein precursor (CT58) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="contains three of four modules found in growth regulators related to connective tissue growth factor as described in FEBS Letters 327:125-130,1993; identified in yeast two-hybrid screen using the epithelial muchi
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/product="connective tissue growth factor-related protein
precursor"
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Wowles, J. and Gendler, S.

Direct Submission 1998) Biochemistry and Molecular Biology, Mayo Submitted (25-JUN-1998) Biochemistry and Molecular Biology, Mayo Clinic Scottsdale, 13400 E. Shea Blvd., Scottsdale, AZ 85259, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1309)
Rowles,J. and Gendler,S.
CT58, a new member of the connective tissue growth factor family, interacts with the breast cancer associated mucin MUC1
                AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAAACCCAATTGCAGG
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Pred. No. 2.5e-55;
); Mismatches 75;
                                                                               0; Mismatches
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/db_xref="taxon:9606"
/cell_line="HeLa"
1. .1309
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1. .1309
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80.9%;
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Best Local Similarity 80.9
Matches 318; Conservative
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AF074604
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Local

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/prodúct="NWT1 inducible signaling pathway protein 2"
/prodúct="NWT1 inducible signaling pathway protein 2"
/protéin_id="AAH17782.1"
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WVCGGGGGCIGTOPLPAGCPQFSGLVSSLPPGVPCPEWSTAWGPCSTTCGLGMATRVSN
QNRRCREDGRACLSRCPPGSRGRSPONSAF"

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Botstein, D.A., Cohen, R.L., Goddard, A.D., Gurney, A.L., Hillan, K.J.,
Lawrence, D.A., Levine, A.J., Pennica, D., Roy, M. Ann. and Wood, W.I.
WISP polypeptides and nucleic acids encoding same
Patent: US 6387657-A 9 14-MAY-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 TGCCCGCTGGGAĞTACCCCTGGTGCTGGATGGCTGTGGCTGCTGCCGGGTATGTGCACGG 338
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Best Local Similarity 00.9%; Pred. No. 2.5e-55;
Matches 318; Conservative 0; Mismatches 75;
                   /clone="MGC:22271 IMAGE:4691574"
/tissue_trpe="Lung"
/clone_llb="NIH_MGC_77"
/lab_host="DH10B"
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Sequence 39 from patent US 6387657.
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                                                                                                         /note="Vector: pDNR-LIB"
165. .917
    'db_xref="taxon:9606"
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297 c 280 g
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 1450)
Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs.refmail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
NA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (03-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Homo sapiens, WNT1 inducible signaling pathway protein 2, clone
MGC:22271 IWAGE:4691574, mRNA, complete cds.
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                                                               TGCCCACAGGGGGTACCCCTGGTGCTGGTGGCTGTGGCTGTGTAAAGTGTGTGCACGG
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                      Indels
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Contact: MGC help desk
Pred. No. 2.5e-55;
); Mismatches 75;
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/db_xref="LocusID:8839"
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80.08;
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DEFINITION RESULT 13 BC017782

ACCESSION. VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL

REMARK

COMMENT

REFERENCE AUTHORS

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Gaps ;

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Botstein.D.A., Cohen.R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.
WISP polypeptides and nucleic acids encoding same
Patent: US 6387657-A 38 14-MAY 2002;
Location/Qualifiers
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Pred. No. 1.7e-52;
0; Mismatches 71;
     DB 6;
  Score 271.4; DB 6;
Pred. No. 6.5e-55;
0; Mismatches 76;
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es 317; Conserv
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                                  Agents that stimulate or inhibit HICP protein activity or expression.

antisense HICP nucleic acid molecules and HICP antibodies, can be used to
modulate cell-associated activity. HICP modulators can be used to
disorders characterized by aberrant HICP protein activity or expression.

Probes capable of hybridizing to HICP mRNA or antibodies specific for
HICP can be used to detect HICP activity in a biological sample. HICP
can be used to treat disorders, such as a cardiovascular or fibrotic
disorder, characterized by aberrant cell proliferation.
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                            CDNA encodes a rat heparin-induced CCN-like protein (HICP) protein.
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                                                                                                                                             100.0%; Score 635; DB 20; 100.0%; Pred. No. 1.9e-170;
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         1; 108pp; English.
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The present invention describes Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-3 have homology to connective tissue growth factor (CTGF).

Products from the present invention can be used to treat WISP-related disorders such as breast ovarian, and colon cancer or melanoma. The products can be used to treat arteriosclerosis. The products can also be used to treat other disease e.g. benign and malignant tumours, lenkaemia and lymphoid malignancies, neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, and blastocoelic disorders, amentopoiesis-related disorders, tissue-growth disorders, bone-related disorders such as osteoporosis, trauma such as burns, incisions, and other wounds, connective tissue disorders, catabolic states, testicular-related disorders, and inflammatory, angiogenic and immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The products can be used to transgenic or knock-out animals.
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Pred. No. 3.8e-138;
0; Mismatches 41;
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Pennica D,
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97US-0083704.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cohen RL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
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586; Conserv
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29-OCT-1997;
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Lawrence DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-FEB-1998;
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or

308

368 120 120 180 488 240 240 548 300 608

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e used to treat disorders, such as a cardiovascular characterized by aberrant cell proliferation. The
                                                                                                                                                                                                                                                                                                    GTGTGTGCCCAGCTGTGCCGGACACCCTGTACTGTCCTTGGACACCACCCCAGTGCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                     WNT-1 induced secreted protein; WISP-1; WISP-3; CTGF; tumour; connective tissue growth factor; cancer; melanoma; arteriosclerosis; leukaemia; lymphoid malignancy; haematopoiesis-related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion; kidney disorder; bone related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation; testicular-related disorder; anglogenesis; immunological disorder; ss.
                                                                                                                                                                                                                      CAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTAAAGTGTGTGCACGGAGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGGAGTCCTGCGACCTGCATGTCTGCGACCCCAGCCAGGCCTGGTTTGTCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGGCCAGGGCCTGGTTTGTCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGCAGGCCCTGGCGGCCATGGGGGCTGTGTGTCTCTTGGATGAGGATGACGGTAGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGTGAATGGCCGCAGGTACCTGGATGGAGACCTTTAAAACCCAATTGCAGGGTCCTG
      used to detect HICP activity in a biological
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse WISP-2 protein complementary nucleotide sequence SEQ ID NO:18.
                                                                                                                                                                                 ó
                                                                                                                                       Length 753;
                                                             sequence of rat HICP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillan K;
                                                                                                                                                                                 Indels
                                                                                                    Sequence 753 BP; 132 A; 235 C; 230 G; 156 T; 0 other;
                                                                                                                                       Score 387; DB 20; I
Pred. No. 4.6e-100;
O; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       635
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                                                             present sequence represents the coding
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                                                                                                                                              100.08; Pre-
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AAX76489/C

XX
AC AAX76489;
XX
AC AAX76489;
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DT 06-AUG-1999 (first entry)
XX
MOUSE WISP-2 protein complemen
XX
KW connective tissue growth factor
KW tissue-growth disorder; skin d
XX tidnes: lymphoid malignancy
KW tissue-growth disorder; skin d
XW connective tissue growth factor
XW tissue-growth disorder; skin d
XW toonnective tissue disorder; ca
XW woo9921998-A1.
XX
MUS SP.
XX
M
                                                                                                                                         60.9%;
    specific for HICP can be
sample. HICP can be used
fibrotic disorder, charac
                                                                                                                                                                                 Conservative
                                                                                                                                                          Best Local Similarity
Matches 387; Conserv
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                                                                                                                                     TCTCTCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACC 358
                                                                                                                                                                                                                                                                                                                                         protein. Agents that stimulate or inhibit HICP protein activity or expression, antisense HICP nucleic acid molecules and HICP antibodies, can be used to modulate cell-associated activity. HICP modulators can be used to treat disorders characterized by aberrant HICP protein activity or expression. Probes capable of hybridizing to HICP mRNA or antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heparin-induced CCN-like protein; HICP; cell-associated activity; ss; cardiovascular disorder; aberrant cell proliferation; fibrotic disorder
CCAGTGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGGCTGCTGTAAAGTGTGTGC
                                                                                                                                                                                                                                                                                                                                                                              TTGTCAGCCTGGGGCAGGCCCTGGGGGCCTGTGTGTCTCTTGGATGAGGATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGGTCCTGTGCCGCTGTGATGACGGTGGCTTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-562060/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409947556-A2
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318 CAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAGTGCCCACAGGGGGGTA 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAGCTGTGCCGGACACCTGTACCTGCCTTGGACACCACCCCAGTGCCCACAGGGGGTA 60
                   Reparin-induced CCN-11ke protein; HICP; cell-associated activity; ss;
cardiovascular disorder; aberrant cell prollferation; fibrotic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  438 TGCGACCACCTGCATGTCTGCGACCCCAGCCAGGCCTGGTTTGTCAGCCTGGGCAGGC
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                                                                                                                                                                                                                                                                                                                                   Nucleic acid sequences encoding rat heparin-induced CCN-like protein, used in methods to idéntify modulators or in diagnostic applications
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.1%; Score 318; DB 20; Length 681;
100.0%; Pred. No. 1.9e-80;
1ve 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 681 BP; 121 A; 211 C; 215 G; 134 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2; 10gpp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX16595 standard; cDNA; 1522 BP
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Best Local Similarity 100.0
Matches 318; Conservative
                                                                                                                                                                                                                          (TUFT ) TUFTS COLLEGE.
                                                                                                                                                                                                                                                                                     WPI; 1999-562060/47.
                                                                                                                                                                                                                                                                                                      P-PSDB; AAY27440
                                                                                                W09947556-A2.
                                                                                                                                                                                                                                                         Castellot JJ;
                                                                                                                                                             18-MAR-1999;
                                                                                                                                                                                           19-MAR-1998;
                                                                                                                              23-SEP-1999
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                                                                                                                   The present invention describes Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-1, abave homology to connective tissue growth factor (CTGF).

Products from the present invention can be used to treat WISP-related disorders such as breast, ovarian, and colon cancer or melanoma. The products can be used to treat arteriosclerosis. The products can also be used to treat other diseases e.g. benign and malignant tumours, leakwamia and lymphoid malignancies, neuronal, gilal, astrocytal, hypothalamic and other glandular, macrophagal; epithelial, stromal, and blastocoelic disorders, desmoplasia, fibrotic lesions, kidney disorders, and other wounds, connective tissue disorders, catabolic states, testicular related disorders, and inflammatory, angiogenic and immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The products can be used to induce death in WISP-1, 2 or 3 overexpressing
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                                                              New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
   Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 753 BP; 159 A; 229 C; 238 G; 127 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 347; DB 20;
Pred. No. 1.1e-88;
0; Mismatches 25;
   Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat HICP mature polypeptide coding sequence.
                                                                                             Disclosure; Page 179-180; 284pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 54.6%;
Best Local Similarity 93.5%;
Matches 362; Conservative
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   Levine AJ,
                               WPI; 1999-337420/28
 Lawrence DA,
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The invention provides novel human secreted proteins and polynucleotides encoding them. The secreted proteins can be expressed by standard recombinant methodology. The secreted proteins and polynucleotides are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can also be used in diagnosing a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neopleams of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DR, Olsen HS;
Fiscella M;
CCAGGGCCTGGTTTGTCAGCCTGGGGCCAGGCCCTGGCGGCCATGGGGGCTGTGTCTCTT
                                                                                                                                                                                                                                          114 CCGGGTATGTGCACGCCGCTGGGGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used to preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                       587 TAAACCCAATTGCAGGGTCCTGTGCCGCTGTGATGACGGTGGCTTCACC 635
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Shi Y, Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein encoding cDNA (clone Id HBODE48).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 427-428; 482pp; English.
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Duan DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            opthalmalogical; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH46952 standard; cDNA; 1337
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04-FEB-2000; 2000US-0180628.
12-SEP-2000; 2000US-0231968.
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Moore PA, Wei P, Ebner R,
Ni J, Ruben SM, Barash SC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes human growth factor-like protein (HGFLP) which has homology to connective tissue growth factor (CTGF) and fisp-12, which are members of the platelet-derived growth factor (PDGF) superfamily of growth factors. Antisense oligonucleotides and HGFLP antagonists can be used to treat or prevent cancer, and connective tissue disorders including ankylosing spondylitis, atherosclerosis, bupuytren's contracture, eosinophilic fasciltis, Felty syndrome, Goodpasture's disease, Hunter syndrome, Hunler syndrome, kelolds, Marfan syndrome, nodular fasciltis, scleroderma, systemic lupus erythematosus, nodosa, rheumatogia arthritis, scleroderma, systemic lupus erythematosus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGGACACCACCCCAGTGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGCTG 406
                                                                                                                                              connective tissue growth factor; platelet-derived growth factor; keloid; connective tissue disorder; cancer; ankylosing spondylitis; scleroderma; atherosclerosis; Dupuytren's contracture; eosinophilic fascitis; Felty syndrome; Goodpasture's disease; Hunter syndrome; Hurler syndrome; Marfan syndrome; nodular fascitis; osteogenesis imperfecta; restenosis; rheumatoid arthritis; systemic lupus erythematosus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and restenosis following angioplasty. HGFLP antibodies and polynucleotides can also be used in diagnostic assays for conditions or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTCCACAAGGGACACGGTGACATGAGGGGCAGCCCACTGATCCATCTTCTGGCCACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDGF family;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide encoding growth factor-like protein - useful for preventing and treating connective tissue disorders and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
8
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llarity 79.1%; Pred. No. 6.2e-75;
Conservative 0; Mismatches 90; Indels 8
                                                                                                                                fisp-12; CTGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1522 BP; 279 A; 496 C; 459 G; 288 T; 0 other;
                                                                                 Human growth factor-like protein encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases characterised by GRFLP expression
                                                                                                                            growth factor-like protein; HGFLP;
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
256..1008
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                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-080954/07.
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les 371; Conserv
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                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9858063-A1
                                        29-APR-1999
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AAX16595;
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Matches
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e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present sequence represents a human secreted protein encoding cDNA.
nervous system disorders e.g.
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                                                                                                                                                                                                                                              GCAGCCCACTGATCCATCTTCTGGCCACTTCCTTCTTGCCTTCTCTCAATGGTGTGTG
                                                                                                                                                                                                                                                                                                                                            CCCAGCTGTGCCGGACACCCTGTACCTTGGACACCACCCCAGTGCCCACAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                   294 GACCCGGTGGMCGGGGGCCCTGTGCCTCTTGGCAGAGGACGACAGCAGCTGTGAGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGCCGCAGGTACCTGGATGGAGACCTTTAAACCCAATTGCAGGGTCCTGTGCCGCT
                                                                                                                                                                                                                                 196 CTCCACGCCTCACCTTCAGGTTTGAAGCTGGCTCCACAAGGGACACGGTGACAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGCGACCACCTGCATGTCTGCGACCCCAGGGCCTGGTTTGTCAGCCTGGGGCAG
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                                                                                                                                                                                                        Gaps
                                                                                                                                                                          Score 278.4; DB 22; Length 1337; Pred. No. 4.3e-69;
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6
                                                                                                                                                                                                       84; Indels
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                                                                                                                                                Sequence 1337 BP; 257 A; 427 C; 396 G; 252 T; 5 other;
                                                                                                                                                                                                     3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         635
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                                                                                                                                                                          43.8%;
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                                                                                                                                                                                                     345; Conservative
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                                                                                                                                                                                         Similarity
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The invention provides novel human secreted proteins and polynucleotides encoding them. The secreted proteins can be expressed by standard encoding them. The secreted proteins and polynucleotides are ecombinant methodology. The secreted proteins and polynucleotides are used to prevent, treat or ameliorate a medical condition in e.g. humans, also be used in diagnostic a condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme treated include autoimmune diseases e.g. radioimmunoassays or liver, treated include autoimmune diseases e.g. rhoproproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infections raused by bacteria, viruses and fungi and cused to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumbur, to maintain organs before transplantation, concupanting cell culture of primary tissues, to regenerate tissues and in the present of increase or decrease storage capabilities. The present concupant decrease storage capabilities. The present concupant decrease to decrease storage capabilities.
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                                                                                     Olsen HS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGTGCCCAGCTGTGCCGGACACCCTGTACCTTGCACACCACCACCAGTGCCCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 GGGAGTACCCCTGGTGCTGGATGGCTGTGGCTGCCGGGTATGTGCACGGCGGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 GTGGCCTCCACGCCTCACCTTCAGGTTTGAAGCTGGCTCCACAAGGGACACGGTGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 GAGGGGCAGCCCÁCTGATCCATCTTCTGGCCACTTCCTTCCTCTGCCTTCTCTAATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGCTAAAGTGTGTGCACGGAGGCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                     DR, Olsen
Fiscella M;
                                                                                                                                                                                                                            treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 1352;
                                                                                                                                                                                                          encoding human secreted
                                                                                     CE, Soppet
Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1352 BP; 268 A; 431 C; 399 G; 254 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88;
                                                                                     Birse CE
Shi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.8%; Score 278.2; DB 2
78.4%; Pred. No. 4.9e-69;
1ve 0; Mismatches 88
                                                                                     Baker KP,
Duan DR,
                                                                                                                                                                                                          isolated nucleic acid molecules
                                                                                                                                                                                                                                                               Claim 1; Page 415; 482pp; English.
                                                 (HUMA-) HUMAN GENOME (SCI INC.
04-FEB-2000; 2000US-0180628.
12-SEP-2000; 2000US-0231968.
                                                                                                    PA, Wei P, Ebner R,
Ruben SM, Barash SC,
                                                                                     Rosen CA, Komatsoulis GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 78.4 Matches 349; Conservative
                                                                                                                                                       WPI; 2001-476220/51
                                                                                                                                                                                                                            used to preventing,
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                                                                                                                        Ni J,
                                                                                                      Moore
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Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate, cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                          244 CAGCCCGGGGCCAGGACCCGGTGGCCGGGGGCCCTGTGCCTCTTGGCAGAGGACGACAGC 303
                                                                                                                                                                                                   CAGCCTGGGGCAGGCCCTGGCGCCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGGT
                TGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTAAAGTGTGTGCCACGG
                                                                                                                                                                                      543 AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGCCTTTAAACCCAATTGCAGG
                                                                       Human cDNA sequence encoding for PRO261 polypeptide.
                                                                                                                                                                                                                                                            603 GTCCTGTGCCGCTGTGATGACGGTGGCTTCACC
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                                                                                                                                                                                                                                                                                                                                             AAS21403 standard; cDNA; 1266 BP
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99WO-US28551.
99WO-US28564.
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20-DEC-1999;
20-DEC-1999;
30-DEC-1999;
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18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
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11-FEB-2000;
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01-MAR-2000;
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02-JUN-2000;
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                                                                                                                                                                                                                                                                                                                  RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a human PRO261 nucleotide sequence. PRO261 is a growth factor. The invention relates to isolated antibodies which bind to a polypeptide. The "PRO" polypeptides are encoded by genes which are over expressed in the genome of tumour cells. Vectors and host cells comprising the nucleic acid encoding the antibodies are used in the production of the antibodies. The antibodies and nucleic acids encoding them are used for diagnosing a tumour in a mammal. The antibodies are used for inhibiting the growth of tumour cells and identifying compounds that inhibit a biological or immunological activity of and/or expression of a PRO187, PRO533, PRO214, PRO211, PRO230, PRO261, PRO246 or PRO317 polypeptide. The antibody can be used in antibody dependent enzyme mediated prodrug therapy (ABPET) by conjugating the antibody to a prodrug-activating enzyme which converts a prodrug to an anti-cencer drug. The antibodies can be fluorescently labelled and monitored by light increased the antibodies can be fluorescently labelled and monitored by light increased the antibodies can be fluorescently labelled and monitored by light increased.
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                                                                                                                                                                                                            Antibody; PRO187; PRO513; PRO214; PRO240; PRO211; PRO250; PRO261; PRO246; PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; human; cell growth; proliferation; growth factor; ADEPT; antibody dependent enzyme mediated prodrug therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 TCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated antibodies which bind to specific polypeptides used for diagnosis and treatment of neoplastic cell growth and proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Botstein D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 273; DB 21; Length 1266;
Pred. No. 1.4e-67;
0; Mismatches 75; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1266 BP; 216 A; 418 C; 390 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy MA,
611 CCGCTGTGATGACGGTGGCTTCACC 635
                 Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 7; Fig 13; 200pp; English
                                                                                                                                                                                   Human PRO261 nucleotide sequence.
                                                                                                 AAA30048 standard; cDNA; 1266 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.9%;
Matches 318; Conservative
                                                                                                                                                                                                                                                                                                                                                                        99WO-US20594
                                                                                                                                                                                                                                                                                                                                                                                                    98US-0099803
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                                                                                                                                                       09-AUG-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-271386/23.
P-PSDB; AAY88573.
                                                                                                                                                                                                                                                                                                               WO200015666-A2.
                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                        08-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-1998;
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                                                                                                                            AAA30048;
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Fri Aug

AAF60368 standard; cDNA; 1266

AAF60368

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AAS21244-AAS21518 encode for novel human secretory and transmembrane
PRO polypeptides. The PRO polypeptides are useful to detect other
PRO polypeptides, to link bloactive molecules to cells expressing
PRO polypeptides, to modulate biological activities of cells expressing
PRO polypeptides, and to detect the presence of mammalian lung, colon,
breast, prostate, rectal, cervical or liver tumours by comparing PRO
polypeptide expression in a cell sample to that in a control sample.
Some of the 275 sequences are also useful to stimulate the release of
tumour necrosis factor-alpha (TNF-alpha) from human blood, the
proliferation or differentiation of chondrocytes, the proliferation or
gene expression in pericyte cells, the release of proteoglycans from
cartilage, the proliferation of inner ear utricular supporting cells or
of T-lymphocytes, the release of a cytokine from peripheral blood
monocytes (PBMCs), or the proliferation of endothelial cells. Some of
the PRO polypeptides may modulate glucose or free fatty acid uptake by
skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
to factor VIIA. The PRO Polypeptides can be used in assays to identify
molecules involved in binding interactions. The polynucleotides encoding
PRO polypeptides can be used to generate probes, antisense RNA/NNA,
transgenic or knock out animals and can be used in gene therapy.
                                                      Gao W;
                                                                                                                                                                                                                                    Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
                                                Beresini M, Deforge L, Desnoyers L, Filvaroff E, G
4E, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Fig 319; 813pp; English.
(GETH ) GENENTECH INC.
                                                                                                         Stewart TA,
                                                                                                                                                        WPI; 2001-408281/43.
                                                                                                                                                                                P-PSDB; AAU12331
                                                                            Gerritsen ME,
Smith V, Stewa
                                                Baker KP,
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Sequence 1266 BP; 216 A; 418 C; 390 G; 242 T; 0 other;

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243
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                                                                                                                                                                                                               542
                                                                                              64 TCAAAGGTGCGTACCCAGCTGTGCCCGACCATGTACCTGCCCCCTGGCCCACCTCCCCGA 123
                                                                                                                            422
                                                                                                                                      AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGCCTTTAAACCCAATTGCAGG 602
                                                                                                                                                                                                                                                                   63
                                                                                                                                                                               303 TCAATGGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAG
                                                              363 TGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTAAAGTGTGTGCACGG
                                                                                                                                                                   CAGCCTGGGGCAGGCCCTGGCGGCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGGT
                       Gaps
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  Length 1266;
                     75; Indels
Score 273; DB 22;
Pred. No. 1.4e-67;
0; Mismatches 75;
                                                                                                                                                                                                                                                                                               GTCCTGTGCCGCTGTGATGACGGTGGCTTCACC 635
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Best Local Similarity 80.9%;
Matches 318; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to PRO proteins and coding sequences. The present sequence is the coding sequence for one such PRO protein. It was found that the PRO genes are amplified in the genome of tumour cells. The gene amplification is expected to be associated with the overexpression of the gene product and contributes to tumourigenesis. Therefore, antagonists of PRO proteins are useful for the treatment of benign or malignant tuminurs, leuksemias, lymphoid malignancies and other disorders such as neuropal, astrocytal, hypothalamic, glandular, epithelial, inflammatogy and immunologic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 TCAATGGTGTGTGCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 TGCCCACAGGGGGTJACCCCTGGTGCTGGATGGCTGTGGCTGTAAAGTGTGTGCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533, useful for diagnosing and treating cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 273; DB 22; Length 1266; Pred. No. 1.4e-67; 0; Mismatches 75; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                       Hillan KJ,
                                                                                   Cytostatic; PRO protein; tumour; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                      Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 50; Fig 13; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 43.0%;
Best Local Similarity 80.9%;
Matches 318; Conservative
                                                                                                                                                                                  6660 GSD - OM66
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99WO-US28313
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                                                            PRO261 coding sequence
                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-091968/10.
P-PSDB; AAB68598.
                                                                                                                                  WO200105836-A1
                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                           13-SEP-1999;
15-SEP-1999;
05-OCT-1999;
                                   27-APR-2001
                                                                                                                                                                                 20-DEC-1999;
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08-SEP-1999;
                                                                                                                                                          25-JAN-2001
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30-NOV-1999
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                                                                                                                                                                                                                                 Human; anglogenesis-associated protein; PRO; endothelial cell growth, cardiac hypertrophy; cardiovascular disorder; endothelial disorder; anglogenic disorder; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer; Alzheimer's disease; Huntington's disease; stroke; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
CAGCCTGGGGCAGGCCCTGGCGGCCATGGGGCTGTGTGTCTTTGGATGAGGATGACGGT
                 244 CAGCCCGGGGCAGGACCCGGTGGCCGGGGGCCCTGTGCCTCTTGGCAGAGGACGACAGC
                                       AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAACCCAATTGCAGG
                                                 Goddard A;
ark MR, Marsters SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, wounds or cancer -
                                                                                                                                                                                                              Human angiogenesis-associated protein PRO261 cDNA, SEQ ID NO:107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N, Gerber H, G
J, Kuo SS, Mar
Williams PM,
                                                                               635
                                                                                                 364 ATCCGCTGCGCTGCGAGGACGCCGCCTTCACC 396
                                                                               GTCCTGTGCCGCTGTGATGACGGTGGCTTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ashkenazi AJ, Baker KP, Ferrara N,
Godowski PJ, Gurney AL, Hillan KJ,
Paoni NF, Pitti RM, Watanabe CK, W
                                                                                                                                                                                                                                                                                             gene therapy; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 58; Fig 41; 293pp; English.
                                                                                                                                                     BP
                                                                                                                                                  AAC97451 standard; cDNA; 1266
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99WO-US12252.
99US-0141037.
99US-0144758.
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99WO-US28409.
99WO-US28564.
99WO-US28565.
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                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-090793/10.
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183
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PRO agonist or antagonist; a retroviral gene therapy vector comprising a PRO agonist or antagonist; a retroviral gene therapy vector comprising a PRO nucleic acid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced anglogenesis via the administration of a PRO protein, or an agonist or antagonist thereof. PRO nucleic acids, PRO proteins, antibodies against PRO proteins, pRO agonists and PRO antagonists may be used as therapeutic agents to treat cardiovascular, endothelial or anglogenic disorders, such as therosolerosis, osteoporosis, myocardial infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, Huntington's endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's cisease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate cDNAs with sequence identity to PRO proteins, to map genes encoding PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 TCAAAGGTGCGTACCCAGCTGTGCCCGACATGTACCTGCCCCTGGCCACCACCTCCCCGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins comprising a PRO protein, agonists or antagonists of a PRO protein, and additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   543 AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAACCCAATTGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303 TCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 TGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTGTAAAGTGTGTGCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 AGGCTGGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGCCCAGGCCTGGTTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1266 BP; 216 A; 418 C; 390 G; 242 T; 0 other;
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Pred. No. 1.4e-67;
0; Mismatches 75;
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80.9%;
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protein of the invention.
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Matches 318; Conservative
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AAA77566
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184 CGGCTGGGGGAGCCTGCGACCAACTCCACGTCTGCGACGCCAGGCCTGGTCTGC
                                                                          TGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGTAAAGTGTGCACGG
                                                                                                                                  423 AGGCTGGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCCAGCCCAGGCCTTGTTGT
                                                                                                                                                                                                                                                   543 AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAACCCCAATTGCAGG
                                                                                                                                                                                          483 CAGCCTGGGGCCAGGCCCTGGCGCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGGT
                                                                                                                                                                                                                                                                                                                            603 GTCCTGTGCCGCTGTGATGACGGTGGCTTCACC 635
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                           Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating call proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 angigganic disorders in mammals (e.g. atheroselerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent nucleotide and protein sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerber H, Hillan KJ, Goddard A;
Kuo SS, Paoni NF, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals -
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Pred. No. 1.4e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the exemplification of the present invention.
PRO261 cDNA sequence SEQ ID NO:71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ferrara N,
Klein RD, F
, Wood WI;
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80.9%;
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Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-412154/35.
P-PSDB; AAB24402.
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                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                            12-MAR-1999;
28-APR-1999;
14-MAY-1999;
02-JUN-1999;
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01-SEP-1999;
08-SEP-1999;
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05-OCT-1999;
29-OCT-1999;
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15-SEP-1999
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Best Local S
 Human
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Novel human connective tissue growth factor 3 gene - useful for the diagnosis and treatment of e.g. cancer, arthritis, fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This nucleotide sequence codes for human connective tissue growth factor-3 (CTGF-3) protein (see AAW37946), a novel member of the growth factor superfamily. It was discovered in a cDNA library
                                                                                     Connective tissue growth factor-3; CTGF-3; human; cancer; arthritis; fibrosis; osteoporosis; diagnosis; therapy; ds
                                                                 Human connective tissue growth factor-3 gene.
                                                                                                                                          Location/Qualifiers
9..761
/*tsg= a
9..65
/*tag= b
66..758
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 1A-B; 87pp; English.
AAV29260 standard; DNA; 1285 BP
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                                           14-SEP-1998 (first entry)
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Gaps

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Indels

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Pred. No. 1.4e 0; Mismatches

Best Local Similarity 80.9 Matches 318; Conservative

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98US-0081695. 97US-0063704. 98US-0073612.

98WO-US22991.

29-OCT-1998; 14-APR-1998; 29-OCT-1997; 03-FEB-1998;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WNT-1 induced secreted protein; WISP-1; WISP-3; CTGF; tumour; connective tissue growth factor; cancer; melanoma; arteriosclerosis; leukaemia; lymphoid malignancy; haematopoiesis-related disorder: tissue-growth disorder; kind disorder; desmoplasia; fibrotic lesion; kidney disorder; bone-related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation, testicular-related disorder; anglogenesis; immunological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363 TGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTGTAAAGTGTGTGCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        423 AGGCIGGGGAGTCCIGCGACCACCTGCAIGTCIGCGACCCCAGCCAGGGCCTGGTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGCCTGGGGCAGGCCCTGGCGGCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   543 AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGCCTTTAAACCCCAATTGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
derived from human osteoblasts. The gene has also been identified in cDNA libraries from ovary, testis, heart, lung, skeletal muscle, adrenal medulla, adrenal cortex, thymus, prostate, small intestine and colon. A cDNA clone is deposited as ATCC 97756. Also provided are vectors, host cells and recombinant methods for producing CTGF-3 polypeptides. CTGF-3 nucleic acid sequences or their fragments, e.g. primers or probes, can be used to diagnose diseases where CTGF-3 expression is enhanced, e.g. cancer, arthritis, for a therosclerosis, or diseases where expression is decreased such as in osteoporosis. Disorders characterised by administering CTGF-3 polypeptides and anti-CTGF-3 antibodies,
                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                         Length 1285;
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                          Sequence 1285 BP; 237 A; 418 C; 389 G; 241 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human WISP-2 protein nucleotide sequence SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                   75;
                                                                                                                                                                                                                                                                                                                                                                     Score 273; DB 19;
Pred. No. 1.5e-67;
0; Mismatches 75;
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80.9%;
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                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.9
Matches 318; Conservative
                                                                                                                                                                                                                                                                              respectively
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The present invention describes Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-1 and MISP-1 wisp connective tissue growth factor (CTGF). Products from the present invention can be used to treat WISP-related disorders such as breast, ovarian, and colon cancer or melanoma. The products can be used to treat arteriosclerosis. The products can also be used to treat other diseases e.g. bendyn and malignant tumours, lead and lymphoid malignancies, neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, and blastococalic disorders, haematopoissis related disorders, tissue-growth disorders, bone-related disorders such as osteoporosis, trauma such as burns, inclsions, and other wounds, connective tissue disorders, and other wounds, connective tissue disorders, and other wounds, connective tissue disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            angiogenic and immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The products can be used in the production of transgenic or knock-out animals. Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 TCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAG
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                                                                                                                                                                                                New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and
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Wood WI;
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Pred. No. 1.5e-67;
                                                     AL,
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Roy MA,
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                                                                                                                                                                                                                                              Example 4; Page 174-175; 284pp; English.
                                                Goddard A,
Pennica D,
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80.9%;
                                                Cohen RL,
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(GETH ) GENENTECH INC.
                                                                                                                      WPI; 1999-337420/28.
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                                                Botstein DA,
Lawrence DA,
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RESULT 1
US-09-182-145-17
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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S-09-182-145-39
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S-09-25-316-3
S-09-142-569-3
S-09-142-569-1
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US-09-142-569-7
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Maximum Match 100%
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Guned, Audrey
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Pennica, Diane
APPLICANT: Poy, Margaret Ann
APPLICANT: Poy, Margaret Ann
APPLICANT: Poy, Margaret Ann
TITLE OF INVERTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US 60/063,704
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER PILING DATE: 1998-02-04
EARLIER PILING DATE: 1998-04-14
NUMBER: OF SEQ ID NOS: 156
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Sequence 2, Ap
Sequence 79, A
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               Sequence 1, Sequence 1, Sequence 24, Sequence 26, Sequence 26, Sequence 26, Sequence 26, Sequence 23,
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Pred. No. 1.1e-135;
0; Mismatches 41;
PCT-US96-08140-1
US-09-054-368-1
US-09-054-274-1
US-09-056-704-1
US-09-182-145-29
US-09-182-145-29
US-09-182-145-29
US-09-187-145-25
US-09-187-145-25
US-09-187-145-25
US-09-187-145-25
US-09-187-145-25
US-09-142-569-5
US-09-142-569-5
US-09-142-135-1
US-09-182-135-1
US-09-182-135-1
US-09-182-135-1
US-09-182-135-1
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US-09-103-840A-1
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US-08-781-891-79
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Patent No. 6387657
BARERAL INFORMATION:
APPLICANT: Botstein, David A.
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92.0%;
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Best Local Similarity 92.0
Matches 586; Conservative
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                                                         1488 ACACGGTGACAÑGAGGGCAACCCACTGATCCATTCTTCTGGCCATTTCCTTCTGCAT
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                                       TCCTAAAGTCTTAGCACTTGTGGTGGCTTGGGCTTCACACACTGTCA
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POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
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1128 CAGGGTTTTGTGGG
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Patent No. 6387657
GENERAL INFORMATION:
1662 TGTGGCAGTAG®
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US-09-182-145-13
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SEQ ID NO 13
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Best Local Similarity
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APPLICANT: Cohen, Robert
APPLICANT: Cohen, Robert
APPLICANT: Cohen, Robert
APPLICANT: Cohen, Robert
APPLICANT: Godard, Audrin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Lawrence, David A.
APPLICANT: Lawrence, David A.
APPLICANT: Lewine, Arnold J.
APPLICANT: Dennica, Diane
APPLICANT: Pennica, Diane
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REPERENCE: P1176R2
CURRENT APPLICANTON NUMBER: US/09/182,145B
CURRENT APPLICANTON NUMBER: US 60/063,704
EARLIER FILING DATE: 1998-10-29
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-04-14
EARLIER FILING DATE: 1998-04-14
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GACACCTTCTTGGTGGCCTCCTCGGCC-----TCAGGTTTGAAGCTGGCTCCACAAGGG
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Pred. No. 1.1e-135;
0; Mismatches 41; Indels 10;
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EQ ID NO 18
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APPLICANT: Gotoria, Robert

APPLICANT: Gotoria, Audievy

APPLICANT: Gotoria, Audievy

APPLICANT: Gotoria, Audievy

APPLICANT: Gotoria, Audievy

APPLICANT: Lawrence, David A.

APPLICANT: Lawrence, David A.

APPLICANT: Pennica, Diane

APPLICANT: Pennica, Diane

APPLICANT: Pennica, Diane

APPLICANT: ROY, Margaret Ann

APPLICANT: ROY, Margaret Ann

APPLICANT: POUNTON: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME

TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: PIJT6R2

CURRENT APPLICATION NUMBER: US/09/182,145B

CURRENT FILING DATE: 1998-10-29

EARLIER REPELOATION NUMBER: US 60/073,612

EARLIER PILING DATE: 1998-02-04

EARLIER PILING DATE: 1998-02-04

EARLIER PILING DATE: 1998-04-14

NUMBER OF SEQ ID NOS: 156
                                 1098 GGCTGGGGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGGCCTGGTCTGC
                                                                                                                                                                                        543 AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGACCTTTAAAACCCAATTGCAGG
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80.7%; Pred. No. 2.5e-66;
Live 0; Mismatches 76;
                                                                                                                                                                                                                                                                                                                          603 GTCCTGTGCCGCTGTGATGACGGTGGCTTCACC
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tent No. 6387657
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 39, Application US/09182145B Patent No. 6387657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 80.7
Matches 317; Conservative
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                                                                                                                                                                                                                                    APPLICANT: Botstein, David A.
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lavrence, David A.
APPLICANT: Lavrence, David A.
APPLICANT: Pennica, Diane
APPLICANT: ROY, Margaret Ann
APPLICANT: ROY, Margaret Non
APPLICANT: WOOG, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: PI176R2
CURRENT APPLICATION NUMBER: US 60/063,704
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER PILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
                                                                                                                                                                                                                                                     196 CGGCTGGGGGGAGCCCTGCGACCACGTCTGCGACGCCAGGGCCTGGGTCTGC
                                                                                                                                                                                                                                                                                                     CAGCCTGGGGCAGGCCCTGGCGGCCATGGGGCTGTGTCTTTGGATGAGGATGACGGT
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0; Mismatches
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ORGANISM: Homo sapiens
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; GENERAL INFORMATION:
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LENGTH: 1293
318;
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US-09-182-145-14
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Fri Aug 1 10:44:14 2003

	Qy 621 GACGGTGCTTCACC 635 	RESULT 7 US-09-253-316-3 Sequence 3, Application US/09253316 Patent No. 6595890 SERERAL INFORMATION	TITLE OF INVERTION: CONNECTUVE TISSUE GROWTH FACTOR HOMOLOGS FILER REPRENCE: 97-75 CURRENT APPLICATION WUMBER: US/09/283.316 CURRENT APPLICATION WUMBER: US/09/283.316 EMALLER APPLICATION WUMBER: US/075.300 EMALLER APPLICATION WUMBER: US/075.300 SECTIONS: 149-02-19 SECTIONS: 149-02-19 SECTIONS: 149-02-19 SECTIONS: 140-02 SECTION	- 0 C Z
	Qy     483 CAGCCTGGGGCAGGCCCTGGCGGCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGGT 542       1111 11111111111111111111111111111111	QY         543 AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGACCTTTAAACCCAATTGCAGG 602           Db         306 AGCTGTGAGGTGAACGGCCGCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCAGC 365           QY         603 GTCCTGTGCGCTGTGATGACGGTGCTTCACC 635           Db         366 ATCCTGTGCCGCTGTGATGACGGTGCTTCACC 635	RESULT 6  19.99-182-145-38  19.99-182-145-38  19.90-182-145-38  19.90-182-145-38  19.90-182-145-38  19.90-182-145-38  19.90-182-145-38  19.90-182-145-38  20.90-182-182-185-38  20.90-182-182-185-38  20.90-182-182-185-38  20.90-182-182-185-38  20.90-182-182-185-38  20.90-182-182-185-38  20.90-182-182-185-38  20.90-182-182-185-38  20.90-182-182-185-38  20.90-182-182-185-38  20.90-182-182-185-38  20.90-182-182-183-38  20.90-182-182-183-38  20.90-182-182-183-38  20.90-182-182-183-38  20.90-182-182-183-38  20.90-182-182-183-38  20.90-182-182-183-38  20.90-182-182-183-38  20.90-182-182-183-38  20.90-182-182-183-38  20.90-182-182-183-38  20.90-182-182-183-38  20.90-182-182-183-38  20.90-182-182-183-38  20.90-182-182-183-38  20.90-182-182-183-38  20.90-182-182-183-38  20.90-182-182-182-38  20.90-182-182-38  20.90-182-182-38  20.90-182-382-382  20.90-182-382-382  20.90-182-382-382  20.90-182-382-382  20.90-182-382-382  20.90-182-382-382  20.90-182	181 GACCAACTCCACGTCTGCGACGCCAGGCCTGGTCGCCGGGGCAGGACCC 501 GGCGGCATGGGGCTGTGTCTTGGATGAGGATGACGTTGCTGTGGGGTGAATGGC

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APPLICANT: Lau, Lester F.
TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
OTHER INFORMATION: "Human cyr61 cDNA coding sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois STATE: Illinois STATE: Illinois States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Best Local Similarity 54.5%; Pred. No. 3.4e-14;
Matches 168; Conservative 0; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,569
FILING DATE: 02-Apr-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:

NAME: Clough, David W.

REGISTRATION NUMBER: 36,107

REFRENCE/DOCKET NUMBER: 28758/33766

TELECOMMUNICATION INFORMATION:

TELEPRONE: 312/474-6300

TELERAX: 312/474-0448

TELEX: 25-3856
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STRANDEDNESS: single
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RESULT

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240 CTGGCGCTCTCCACCTGCCCGCCGCCTGCACTCTGGAGGCACCCAAGTGCGCC 299
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                                                                                     APPLICANT: Lau, Lester F. TITLE OF INVENTION: Extracellular Matrix Signalling Molecules NUMBER OF SEQUENCES: 17
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OTHER INFORMATION: "Mouse cyr61 cDNA coding sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                              Gerstein, Murray & Borun
South Wacker Drive
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                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/142,569
FILING DATE: US/2-Apr-1999
CLASSIFICATION: <unhaps.com/chown>
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28758/33766
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                         CITY: Chicago
STATE: Illinois
COUWTRY: United States of America
IP: 60606-6402
                                                                                                                                                                                ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
                   Application US/09142569
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
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STRANDEDNESS: single
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                                                                                                                                                           CORRESPONDENCE ADDRESS
                     Sequence 1, Application Patent No. 6413735 GENERAL INFORMATION:
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US-09-142-569-1
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316 CCCAGCTGTGCCGGACACCCTGTACCTTGGACACCACCCCAGTGCCCACAGGGGG 375
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  282 GTCAGAGGGCAĠACCCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCA 341
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                                                                                                                                                                                                                                                                                 APPLICANT: COhen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, Dayld A.
APPLICANT: Lewrence, Dayld A.
APPLICANT: Dennica, Daine
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
TITLE OF INVENTION WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: F1176R2
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Pred. No. 1.7e-12;
0; Mismatches 145; Indels
                                                                      590 ACCCAATTGCAGGGTCCTGTGCCGCTGTGATGACGGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT PELLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-04-14
                                                                                                                                                                                                Sequence 9, Application US/09182145B Patent No. 6387657
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Best Local Similarity 58.2%;
Matches 165; Conservative
                                                                                                                                                                                                                                                      David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 616 GTGATGACGG 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350 GACACCACCCAGGGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGTAA 409
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480 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGCTTCCAGCCCAACTGTAAACACCAG 539
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Pred. No. 6.7e-13;
0; Mismatches 163; Indels
                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Connective Tissue Growth Factor-2
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                            ADDRESSE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSE: CARELLA, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD CITY: ROSELAND STATE: NEW JERSEY COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: 18M PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,101A
FILING DATE: June 2, 1995
CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: DCT/US94/07736
FILING DATE: 12 JUL 94
ATTORNEY/AGENT INFORMATION:
NAME: FERRARG, GREGORY D.
REGISTRATION NUMBER: 36,134
                                                                      609 TGCCGCTGTGATGACGGTGGCTT 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                             Sequence 1, Application US/08459101A Patent No. 5945300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELERENX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1128 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.5%;
Best Local Similarity 52.1%;
Matches 177; Conservative (
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EDNESS: SINGLE
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                                                                                                                                                                       US-08-459-101A-1
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556 ATGGCCGCAGGTACCTGGATGGAGACCTTTAAACCCCAATTGCAGGGTCCTGTGCCGCT 615
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APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Pennica, Diane
APPLICANT: Noy, Margaret Ann
FILE REFERENCE: P176R2
CURRENT APPLICANION NUMBER: US/09/182,145B
CURRENT APPLICANION NUMBER: US 60/063,704
EARLIER FILING DATE: 1998-10-29
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICANION NUMBER: US 60/073,612
EARLIER APPLICANION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-04-14
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APPLICANT: Lewvine, Arnold J.
APPLICANT: Denvine, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
TITLE OF INVENTION WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2830;
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Pred. No. 1.2e-11;
0; Mismatches 148;
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CURRENT FILING DATE: 1999-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09182145B Patent No. 6387657
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52.6%;
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APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
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US-09-182-145-1
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Best Local S
Matches 164
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                                    GENERAL INFORMATION:
APPLICANT: Botstein, David A.
APPLICANT: Cohen, Robert
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Levine, Arnold J.
APPLICANT: Peonica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 1998-10-29
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 496 GCCCTGGCGGCCATGGGGCTGTGTCTCTTGGATGAGGATGACGGTAGCTGTGAGGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.3%; Score 78; DB 4; Length 1766; 53.2%; Pred. No. 1.7e-12; tive 0; Mismatches 145; Indels
Sequence 10, Application US/09182145B Patent No. 6387657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Unknown base,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 53.2
Matches 165; Conservative
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LOCATION: 1757
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2606 CCCAATTCTGCAAGTGGCCATGTGAGTGCCCGCCATCCCCACCCCGCTGCCGCTGGGGG 2547
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Patent No. 6395890
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR HOMOLOGS FILE REFERENCE: 97-75
CURRENT APPLICATION NUMBER: US/09/253,316
CURRENT FILING DATE: 1999-02-19
EARLIER APPLICATION NUMBER: US 60/075,300
EARLIER FILING DATE: 1998-02-20
                                                                                                                                                                                                                                              Query Match 11.8%; Score 75.2; DB 4; Length 28
Best Local Similarity 52.6%; Pred. No. 1.2e-11;
Matches 164; Conservative 0; Mismatches 148; Indels
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Pred. No. 2.7e-10;
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-04-14
EARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
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Best Local Similarity 51.1%;
Matches 164; Conservative
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LOCATION: (17)...(1078)
                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-182-145-2
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205 TGGAGTGAGCCTGGTGAGGATGGCTGTGGATGCTGTAAAATCTGTGCCAAGCAACCAGG 264
                                                  GGAGTCCTGCGAQCACCTGCATGTCTGCGACCCCAGCCAGGCCTGGTTTGTCAGCCTGG 490
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                                                                        491. GCCAGGCCCTGGGGCCCATGGGCTGTGTGTCTTGGATGAGGATGACGGTAGCTGTGA
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Job time : 37.7474 secs
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1 GACGCTICTGATCTCCAGAG......GTGATGACGGTGGCTTCACC 635
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                                                                                            July 28, 2003, 15:36:41; Search time 156.533 Seconds
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/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-112-267-18

US-10-010-408-3

US-10-010-408-12

US-09-915-582-14

US-09-915-682-14

US-10-146-726-319

US-10-146-726-319
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US-10-028-072-319
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Listing first 45 summaries
                                                              - nucleic search, using sw model
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seq length: 200000000
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Sequence 319, App Sequence 319	0000
US-10-140-470-319 US-10-175-918-319 US-10-175-918-319 US-10-175-918-319 US-10-137-865-319 US-10-140-474-319 US-10-140-474-319 US-10-140-002-319 US-10-142-419-319 US-10-142-423-319 US-10-141-755-319 US-10-141-755-319 US-10-123-262-319 US-10-123-263-319 US-10-123-263-319 US-10-123-263-319 US-10-123-263-319 US-10-123-263-319 US-10-123-263-319 US-10-123-263-319 US-10-123-263-319 US-10-123-319-319 US-10-123-319-319 US-10-123-319-319 US-10-123-319-319 US-10-123-319-319 US-10-123-319-319	-10-140-925-31 -10-160-498-31 -10-124-824-31 -10-127-825A-3
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## ALIGNMENTS

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REPULT 1. APPLICATION US/10010408

Sequence 1. Application US/10010408

Sequence 1. Application US/2002165185AII

PUBLICATION NO. US20020165185AII Heparin-Induced CCN-Like Molecules

TITLE OF INVENTION: NO. US20020165185AII Heparin-Induced CCN-Like Molecules

NUMBER OF SEQUENCES: 13

CORRESPONDER EADRESS:

STATE: Massachusetts

COMPUTR: Boston

STATE: Massachusetts

COMPUTR: USA

IIP: 02109

COMPUTR: USA

COMPUTR: USA
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SAME

US/09/182,145B

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TG-GGCAGTGGCTTGGAATGGAGGTCTTTATTACTGGGAACTGAGGAGCTAAGAGGCTCC
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APPLICANT: WOOD, WAILLIAM, I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME;
FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/10/112,267
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
PRIOR FILING DATE: EARLIER PELLING DATE: 1998-10-29
PRIOR FILING DATE: EARLIER PELLING DATE: 1998-10-29
PRIOR FILING DATE: EARLIER PILING DATE: 1999-10-29
PRIOR FILING DATE: EARLIER FILING DATE: 1999-10-29
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
NUMBER: OF SEQ ID NOS: 156
                                                                                                                                                                                                                                                                                     82.1%; Score 521.4; DB 15; Length 1734; 92.0%; Pred. No. 2.3e-140; 1ve 0; Mismatches 41; Indels 10;
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US-10-112-267-18/c
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les 586; Conserv
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                                                                                                                                                                                                      SEQ ID NO 17
LENGTH: 17
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Best Local S:
Matches 586
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100.0%; Score 635; I
Best Local Similarity 100.0%; Pred. No. 4.6
Matches 635; Conservative 0; Mismatches
                                                                                 NAME/KEY: CDS
LOCATION: 249..1001
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/10112267
Publication No. US20030068678A1
GENERAL INFORMATION:
    pairs
LENGTH: 1708 base pair:
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gurney, Austin L.
Hillan, Kenneth J.
Lawrence, David A.
Levine, Arnold J.
Pennica, Diane
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FILING DATE: 07-Dec-2001 CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617)227-7400
TELEPRA: (617)42-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                     Sequence 3, Application US/10010408 Publication No. US20020165185A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 753 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                  CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Flopp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 100.
Matches 387; Conservative
                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109
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                                                                                                                        US-10-010-408-3
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                                                                                                                                                 APPLICANT: ROY, MARGARET. AND APPLICANT: ROY, MARGARET. AND APPLICANT: WOOD, William I.

TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: P1176R2
CURRENT FILING DATE: 2002-03-27
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-0-30
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-0-30
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TG-GGCAGTGGCTTGGAATGGAGGTCTTTATTACTGGGAACTGAGGAGCTAAGAGGCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419 ACGGAGGTGGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGGCCCAGGGCCTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 521.4; DB 15
Pred. No. 2.3e-140;
0; Mismatches 41;
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92.0%;
                                                                        Gurney, Austin L.
Hillan, Kenneth J.
Lawrence, David A.
                                                                                                                      Levine, Arnold J.
Pennica, Diane
                          APPLICANT: Botstein, David A.
                                         Cohen, Robert
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         586; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
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Matches 586; Conserv
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                                                      APPLICANT:
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APPLICANT: John J. Castellot, Jr. IITLE OF INVENTION: No. US20020165185Alel Heparin-Induced CCN-Like Molecules and Uses Therefor
1188 CGGGAGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGGGGAGACCTTTAAACCCAATTG 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 753;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.25
                                                                                     1128 CAGGGTTTTGTGCCGCTGTGATGACGGTGGTTTCACC 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.9%; Score 387; DB 15; 100.0%; Pred. No. 1e-101;
                                         599 CAGGGTCCTGTGCCGCTGTGATGACGGTGGCTTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/044,273
FILING DATE: MATCh 19, 1998
APPLICATION NUMBER: <UNKnown>
FILING DATE: <UNKnown>
ATTORNEY/AGENT INFORMATION:
NAME: ANY B. Mandragouras
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                               LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. No. 1e-
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/10/010,408
                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD,
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..750
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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CAGCTGTGCCGGACACCCTGTACCTTGGACACCCACCCCACGGGGGGTA 60   378   CCCCTGGTGCTGGATGGCTGTGCTGTGTGCACGGGGGGTCC 437	rGGCmrCACC 635	7. O'THEN INFORMATION: n equals a,t,g, or c US-09-915-582-30  Query Match  43.8%; Score 278.4; DB 11; Length 1337;  Best Local Similarity 78.4%; Pred. No. 1.9e-70;  Matches 345; Conservative 3; Mismatches 84; Indels 8; Gaps 1;  Oy 196 CTCCACGGCCTCACTTCAGGTTTGAAGCTGGCTCCACAAGGGACATGAGG 53  Oy 256 GCACCCACGATTCACCTTCAGGCTCCACAAGGCACATGAGAG 53  Oy 256 GCACCCACGATCATCTTCTGGCCACTTCCTCTCTCTCTCT
Qy         429 GGGAGTCCTGCGACCACCTGCAAGTCTGCGACCCCAGGGCCTGGTTTGTCAGCCT         488           III	RESULT APPLICATION US/10010408  1 Sequence 12, Application US/10010408  1 PUBLICATION NO. US20020165185A11  1 GENERAL INFORMATION:  2 APPLICANT: John J. Castellot, Jr.  3 TITLE OF INVENTION: No. US20020165185A1el Heparin-Induced CCN-Like Molecules.  3 TITLE OF INVENTION: No. US20020165185A1el Heparin-Induced CCN-Like Molecules.  3 TATLE OF INVENTION: No. US20020165185A1el Heparin-Induced CCN-Like Molecules.  3 CORRESPONDENCE ADDRESS:  4 ADDRESSEE: LAHIVE & COCKFIELD, LLP  5 STATE: Massachusetts  COUNTRY: USA  2 IP: 02109  COMPUTER: EADAPLE FORM:  ADDIOM TYPE: Floppy disk  COMPUTER: IBM PC Compatible  COMPUTER: IBM PC Compatible  SOFTWARE: Patently Release #1.0, Version #1.25  CURRENT APPLICATION DATA:  APPLICATION NUMBER: 09/044,273  FILING DATE: MATCH ON TOWNER: CURROWN>  PRICESSIFICATION NUMBER: CURROWN>  RILING DATE: MATCH 19, 1998  APPLICATION NUMBER: CURROWN>  RESISTRATION:  NAME: AMY E. Mandragouras  NEDEL CANNERS AND TOWNER: 36,207  RESISTRATION NUMBER: 36,207	TELECOMMUNICATION INFORMATION:   TELECOMMUNICATION INFORMATION:   TELECOMMUNICATION INFORMATION:   TELEFATION (617)227-7400     TELEFATION FOR SEQ ID NO: 12:   SEQUENCE CHARACTERISTICS:   LENGTH: 681 base pairs     TYPE: nucleic acid     STRANDEDNESS: single     TYPE: nucleic acid     STRANDEDNESS: single     TYPE: nucleic acid     STRANDEDNESS: single     TAPE: nucleic acid     STRANDEDNESS: single     TAPE: nucleic acid     STRANDEDNESS: single     STRANDEDNESS: single     STRANDEDNESS: single     STRANDEDNESS: single     STRANDENESS: single     ST

Db 355 GGTGAACGGCCGCTGTATCGGGAAGGGGAGACCTTCCAGCCCACTGCAGCTG 414  Qy 611 CCGCTGTGATGACGTGGCTTCACC 635	Filvaroff, Elle Gao, Mary Gaddard, Madrey Gaddard, Audrey Goddard, Audrey Goddard, Audrey Goddard, Austrin Sherwood, Steve Smith, Victoria Stewart, Timoth Tumas, Daniel Watanabe, Collin Wood, William Zhang, Zeenen Wood, William Zhang, Secre Watanaton Secre Filor Date: 1997-09 LICATION NUMBER: NG DATE: 1997-10	APPLICATION 1
Qy         436 CCTGGGACCACTGGATGTCTGCGACCCAGGGCCTGGTTTGTCAGCCTGGGGCAG 495           1		=

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APPLICATION NUMBER: 60/064809
FILING DATE: 1997-11-07
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APPLICATION NUMBER: 60/063735
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FILING DATE: 1997-11-12
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APPLICATION NUMBER: 60/074086
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APPLICATION NUMBER: 60/079294
FILING DATE: 1998-03-25
APPLICATION NUMBER: 60/079663
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082999
FILING DATE: 1998-04-24
                              APPLICATION NUMBER: 60/063550
                                                 FILING DATE: 1997-10-28
APPLICATION NUMBER: 60/063561
                                                                                                  FILING DATE: 1997-10-28
APPLICATION NUMBER: 60/063704
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FILING DATE: 1997-10-29
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ILING DATE: 1997-11-24
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APPLICATION NUMBER: 60/069694
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APPLICATION NUMBER: 60/073612
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FILING DATE: 1998-02-09
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FILING DATE: 1998-04-09
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APPLICATION NUMBER: 60/081695
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APPLICATION NUMBER: 60/081817
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80.9%; Pred. No. 6.8e-69;
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PRIOR FILLING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084607
PRIOR APPLICATION NUMBER: 60/084627
PRIOR APPLICATION NUMBER: 60/084637
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-12
PRIOR PELING DATE: 1998-05-12
PRIOR PELING DATE: 1998-05-12
PRIOR PELING DATE: 1998-05-12
PRIOR PELING DATE: 1998-05-13
PRIOR PELING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/08579
PRIOR PELING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/086710
PRIOR PELING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/08810
PRIOR PELING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/08810
PRIOR PELING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/08810
PRIOR PELING DATE: 1998-06-11
PRIOR PELING DATE: 1998-06-11
PRIOR PELING DATE: 1998-06-13
PRIOR PELING DATE: 19
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Best Local Similarity
Matches 318; Conserv
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111    24 TGCCGCTGGGAGTACCCTGGTGCTGGTTGCTGCTGCTGCTGCTGCTGCACGG   123	RESULT 10  US-10-16-72-319  Sequence 319, Application US/10146727  Sequence 319, Application US/10146727  Sequence 319, Application No. US20030129691A1  Sequence 319, Application No. US20030129691A1  Septicant INFORMATION:  APPLICANT: Beresiali, Maureen  APPLICANT: Beresiali, Maureen  APPLICANT: Beresiali, Maureen  APPLICANT: Gao, Wel-Olang  APPLICANT: Girney, Amry E.  APPLICANT: Goldard, Audrey  APPLICANT: Goldard, Inforth A.  APPLICANT: Goldard, Marin L.  APPLICANT: Sherwood, Steven  APPLICANT: Goldard, Marin L.  APPLICANT: Wood, Milliam  APPLICANT: Wood, Milliam  APPLICANT: Wood, Milliam  APPLICANT: Wood, Milliam  APPLICANT: Matanabe, Colin K  APPLICANT: Matanabe, Colin K  APPLICANT: Monger: 2002-05-15  CURRENT APPLICATION NUMBER: US/10/146,727  CURRENT APPLICATION TATE: 2002-05-15  PRIOR PRIOR FILE OF TOWERTION TOWER: 2002-06-15  PRIOR PRIOR FILE OF TOWERTION TOWER: 2002-06-15  NUMBER OF SEQ. ID NOS: 550  SEQ. ID NO 319  CRANICAN: NO 319	į.	0; Gaps 0; 0y 303 TCAATGGTGTGTGCCGGCTGTGCCGGACCCTGTACCTGGACACCCCCCGGGACCCCCCCGGGACACCCTGTACCTTGGACACCCCCCGGGACACCCTTGCACCCCCCGGGACACCCTTGCACCCCCCGGACACCCTTGCACCCTGCCCTGGCCTTGCACCCTGCCCCTGGCCTTGCACCTCCCCGGACCCTCCCCGGACCCTCCCCGGACCCTCCCCCGGACCCTCCCCCGGACCCTCCCCCGGACCCTCCCCCGGACCCTCCCCCGGACCCTCCCCCGGACCCTCCCCCGGACCCTCCCCCGGACCCTCCCCCGGACCCTCCCCCGGACCCTCCCCGGACCCCGACCCGGACCCCGGACCCCGGACCCCGACCCAGCCACCA
	Qy 603 GTCCTGTGCCGCTGTGATGACGTGCCTTCACC 635	0%; Score 273; DB 14; 1 9%; Pred. No. 6.8e-69;	18; Conservative 0; Mismatches 75; Indels 0; Gaps 243 GGTGACATGAGGCCCCACTGATCTTCTGGCCACTTCCTTC

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                              303 TCAATGGTGTGTĞCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCACG 362
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACCORDING THE SAME
FILE REFERENCE: P3330R16397
CURRENT APPLICATION NUMBER: US/10/152,380
CURRENT FILING DATE: 2002-05-21
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
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                                                                                                                                   603 GTCCTGTGCCGCTGTGACGGTGGCTTCACC 635
                                                                                                       603 GTCCTGTGCCGCTGTGATGACGGTGGCTTCACC
                                                                                                                                                                                                                                                                                         Sequence 319, Application US/10152380 Publication No. US20030129694A1
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Tumas, Daniel
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Godowski, Paul J.
Gurney, Austin L.
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Gerritsen,Mary E.
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Wood, William
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DeForge, Laura
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Smith, Victoria
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Filvaroff, Ellen
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APPLICANT: Beresin1, Maur
APPLICANT: DeForge, Laura
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US-10-152-380-319
                                                                                                                                                                                                                                                                                                               Publication No. US20
GENERAL INFORMATION:
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US-10-152-380-319
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APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Tilvaroff, Ellen
APPLICANT: Gao, Wei-Giang
APPLICANT: Gao, Wei-Giang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Godd, William
APPLICANT: Wood, William
APPLICANT: Action K.
APPLICANT: 
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                                                                                                                           AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAAACCCAATTGCAGG 602
                                                                                                                                                         303 TCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAG 362
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                                                                         244 CAGCCCGGGGCAGGACCCGGTGGCCGGGGGCCCTGTGCCTCTTGGCAGAGGACGACAGC
                        CAGCCTGGGGCAGGCCCTGGGGGCTGTGTGTGTCTCTTGGATGAGGATGACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 GGTGACATGAGGGGCAGCCCACTGATCCATCTTGGCCCACTTCCTTGCCTTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
EQ ID NO 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 273; DB 14;
Pred. No. 6.8e-69;
0; Mismatches 75;
                                                                                                                                                                                                                             ; Sequence 319, Application US/10146788; Publication No. US20030129693A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin P.
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80.9%;
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US-10-146-788-319
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Best Local S
Matches 318
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Tumas,Daniel
                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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    US-10-028-072-319
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 TGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTAAAGTGTGTGCACGG
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wood,William
APPLICANT: Abang, Camin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333NRLC412
CURRENT APPLICATION NUMBER: 105,10/153,934
CURRENT FILING DATE: 2002-05-22
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Pred. No. 6.8e-69;
0; Mismatches 75; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prior Application removed - See file Wrapper or Palm NUMBER OF SEQ ID NOS: 550 SEQ ID NO 319
GTCCTGTGCCGCTGTGATGACGGTGGCTTCACC 635
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                                                                                         Sequence 319, Application US/10153934
Publication No. US20030129695A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.9%;
Matches 318; Conservative
                                                                                                                                                                                                                                                                                                                     Stewart, Timothy A. Tumas, Daniel
                                                                                                               GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
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Filvaroff, Ellen
Gao, Wei-Qiang
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Goddard, Audrey
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Wood, William
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Gurney, Austin L.
Sherwood, Steven
                                                                                                                                                                                                                                                                                                     Smith, Victoria
                                                                                                                                                                     DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-153-934-319
                                                           RESULT 13
US-10-153-934-319
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RESULT 14

CURRENT APPLICATION NUMBER: US/10/028,072 CURRENT FILING DATE: 2001-12-19 CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR PLING DATE: 1997-06-18
PRIOR PAPLICATION NUMBER: 60/059113
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PAPLICATION NUMBER: 60/059117
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PAPLICATION NUMBER: 60/059184
PRIOR PELING DATE: 1997-09-18
PRIOR PAPLICATION NUMBER: 60/059184
PRIOR PELING DATE: 1997-09-19
PRIOR PELING DATE: 1997-00-19
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063327
PRIOR APPLICATION NUMBER: 60/063327 Sequence 319, Application US/10028072 Publication No. US20030004311A1 GENERAL INFORMATION: APPLICATION NUMBER: 60/063561 FILING DATE: 1997-10-28 APPLICATION NUMBER: 60/063704 FILING DATE: 1997-10-29 Godowski, Paul J. Gurney, Austin L. Sherwood, Steven Smith, Victoria Stewart, Timothy A. Desnoyers, Luc Filvaroff, Ellen Gao, Wei-Qiang Gerritsen, Mary E. FILING DATE: 1997-10-28 APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura Watanabe, Colin K Goddard, Audrey Wood, William PRIOR

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APPLICATION NUMBER: 60/074092
FILING DATE: 1998-02-09
FILING DATE: 1998-03-12
FILING DATE: 1998-03-12
APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079294
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PPLICATION NUMBER: 60/073612
ILING DATE: 1998-02-04
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TLING DATE: 1998-02-27
RPLICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/080165
APPLICATION NUMBER: 60/080165
APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/081229
FILING DATE: 1998-04-09
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APPLICATION NUMBER: 60/081818
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/063733
FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063735
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PPLICATION NUMBER: 60/069212
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TLING DATE: 1998-02-09
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APPLICATION NUMBER: 60/083322
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FILING DATE: 1998-05-07
                                                                     APPLICATION NUMBER: 60/063738
                                                                                                     APPLICATION NUMBER: 60/063755
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FILING DATE: 1997-11-24
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APPLICATION NUMBER: 60/081817
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FILING DATE: 1998-05-07
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llarity 80.9%; Pred. No. 6.8e-69;
Conservative 0; Mismatches 75;
                                                                                                                                                                                                                                                      60/085579
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1998-05-15
APPLICATION UNBER, 60/085704
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/086414
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APPLICATION NUMBER: 60/086430
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
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FILING DATE: 1998-07-07
ER: 60/085323
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APPLICATION NUMBER: 60/
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/
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FILING DATE: 1998-06-1
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                                                          APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
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Pred. No. 6.8e-69;
0; Mismatches 75;
                                                                                                                                                        GTCCTGTGCCGCTGTGACGGTGGCTTCACC 635
                                                                                                                                                                      Sequence 319, Application US/10121049 Publication No. US20030022239A1 GENERAL INFORMATION:
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
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Stewart, Timothy A.
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Best Local Similarity 80.9%;
Matches 318; Conservative
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Wood, William
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Gurney, Austin L.
Sherwood, Steven
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BP037009 601456766
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BG720581 AGENCORT
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AC544380 AL544380
BQ719732 AGENCOURT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 940)
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Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.n column: 21
High quality sequence stop: 543.
Location/Qualifiers
ce
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National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                  BI161474
BQ279131 BQ278961 BQ073722 BB1826781
                   BG928868
BM043988
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BIR9200059
BGS8695
BIR23598
BIR237009
BIR337009
BIR3
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/clone=lb="NoT_CGAP_CO24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pcMv-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NoT_CGAP Library."
277 c 288 g 200 t 6 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 GGACACGGTGACATGAGGGCCAACCCACTTCTGGCCATTTCCTTCTTGC
                                                                                                                                                                                                                  CAGACACCTTCGTGGTGGCCTCCACGGCTCACCTTCAGGTTTGAAGCTGGCTCCACAAG
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                                                                                                                                                                                 Gaps
                                                                                                                                                                               10;
                                                                                                                                                     Ouery Match 67.1%; Score 425.8; DB 14; Length 940;
Best Local Similarity 90.9%; Pred. No. 1.5e-99;
Matches 488; Conservative 0; Mismatches 39; Indels 10;
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Eukaryota; Metazoa; Chordata; Craniata;
/organism="Mus musculus"
          /strain="FVB/N"
/db_xref="taxon:10090"
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AUTHORS
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BQ560868
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdnaelgaun grc.nia.nih.gov
Fils clone set has been freely distributed to the community. Please
visit http://lgaun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
Plate: H4067 Jow: A column: 01
Seq primer: -21M13 Reverse
High quality sequence stop: 537
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BB849097 GI:17090551
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                                                                                                                                                                                                                                                                                                                                    /dev_gtage="mixed"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: NotI; This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."
162 c 166 g 122 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 CAGACACCTTCGTGGTGGCCTCCACGGCCTCACCTTCAGGTTTGAAGCTGGCTCCACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 CCCCAGTGCCCAGAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTAAAGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTG-GGCAGTGGCTTGGAATGGAGGTCTTTATTACTGGGAACTGAGGAGCTAAGAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 537;
                                                                                                                                                                       Location/Qualifiers

1. 537
/organism="Mus musculus"
/organism="C57BL/6"
/db_xref="niaEST:H4067A01-5"
/db_xref="taxon:10090"
/clone="H4067A01"
/clone="H4067A01"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.7%; Score 385.2; DB 14;
.larity 92.1%; Pred. No. 3.7e-89;
Conservative 0; Mismatches 28;
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AL555144 1TI_NFL006_PL2 Homo sapiens cDNA clone CSODK007YO21 5
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                                                                                                                                                                                                                                                                                                                                                                                                                       167 CACACACTGTCAGACACCTTCGTGGTGGCCTCCACGGCCTCACCTTCAGGTTTGAAGCTG 226
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                   296 CCTGTGCCTGTCCTTGGACACCCCAGTGCCCACCGGGGGTACCCCTGGTGCTGGAT
                                                                                                                                              213 CAGGTTTGAAGCTGGCTCCACAAGGACACGGTGACATGAGGGGGCAGCCCACTGATCCAT
                                                                                                                                                                                                                               273 CTTCTGGCCACTTCCTTCCTCTGCCTTCTCTAATGGTGTGTGCCCAGCTGTGCCGGACA
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                                                             GGTGGCTTGGGCCTTCACACACTGTCAGACACCTTCGTGGTGGTGGCCTCCACGGCCTCACCTT
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Pred. No. 8.7e-67;
0; Mismatches 90; Indels
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Frul-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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AL555144
AL555144.1 GI:12896595
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Best Local Similarity 79.1%;
Matches 371; Conservative
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                                Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 424)

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawal, J., Kolima, Y., Kondo, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, Y., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Rahaira, S., Tanaka, T., Tomaru, A., Toya, T., Riken Bncyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Carninci, P., Sugahara Konno, H., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome_res@gsc.riken.go.jp,
UKL:http://genome.gsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayasu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehlro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 TGGGAACTGAGGAGCTAAGAGGCTCCTGTCAG---CTTGTCCTAAAGTCTTAGCACTTGT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="inner ear"
/dev_stage="adult"
/note="pooled tissues; (tissue_type=cerebellum,
dev_stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev_stage=0 day neonate,
sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=male), (tissue_type=hippocampus, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
a 124 c 132 g 103 t
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/clone_lib="RIKEN full-length enriched, adult inner ear"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length CDNA
encyclopedia: real-time sequence clustering for construction of
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 AGGGGCCTTGGCAAGGCTGCAGCCGCTG-GGCAGGGCTTGGAATGGAGGTCTTTATTAC
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Pred. No. 2e-76;
0; Mismatches 27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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392; Conservative
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/db_xref="taxon:9606"
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BQ961357
BQ961357.1 GI:22376835
                                                                                           Query Match
Best Local Similarity 78.9%;
Matches 370; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note—"Organ: Ovary (pool of 3); Vector: pCMV-SPORT6;
Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
                                                                                                                                                                                                    406
                                                                                                                                                                                                                                                                                                                                                                               583
                                                                                                                             CTTCCTCTGCCTTCTCTCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCC 346
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12361 row: f column: 15
TTGGACACCACCCCAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGCTG
                                                                                                                                                                                                                                                                                                         464 CCGGGTATGTGCACGCGGCGCTGGGGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAG
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                           587 TAAACCCAATTGCAGGGTCCTGTGCCGCTGTGATGACGGTGGCTTCACC 635
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/clone_lib="NIH_MGC_125"
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1. .1166
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Eukaryota; Metagoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metagoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthefia; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1251)

2 NIH-MGC http://mgc.noi.nih.gov/.

3 NIH-MGC http://mgc.noi.nih.gov/.

4 National Institutes of Health, Mammalian Gene Collection (MGC)

5 Onbert: Strausberg, Ph.D.

6 Contact: Robert Strausberg, Ph.D.

7 Tissue Procurement: DCTD/DPP

7 CONTACT: Robert Strausberg, Ph.D.

7 Tissue Procurement: DCTD/DPP

7 CONTACT: Robert Strausberg, Ph.D.

7 Tissue Procurement: DCTD/DPP

7 CONTACT: Robert Strausberg, Ph.D.

8 Danali Contaction: Rubin Laboratory

7 CONTACTION AGC Clone distribution information can be found through the In.A.G.E. Consortium/LLNL at:

8 Contaction/Outlifers

8 Contaction/Outlifers

9 Contaction/Outlifers

1 Contaction/Outlifers
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AGENCOURT_8929398 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6484532
                                                                                                                                                                                                                                                                                                       137 CACACACGGACAGGCACCCCCTTGGTGGCCCTTCACATTTCACCTTCAGGCTGAAAGCTG 196
constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036." 424 c 315~\rm g 207 t 4~\rm others
                                                                                                                                                                                                                                                                                                                                                                                     197 GCTCTGCAGGG------GACATGAGAGGCACACACACCTCCTCGCCTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 TTGGACACCACCCAGTGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               369 CCGGGTATGTGCACGCGCGCGGGGGACCCTGCGACCAACTCCACGTCTGCGACGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 CACACACTGTCAGACACCTTCGTGGTGGCCTCCACGCTCACCTTCAGGTTTGAAGCTG
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                                                      /note="Organ: prostate; Vector: pOTB7; Site_1: XhOI; Site_2: ECORI; cDNA made by Oligo-dT priming.
Directionally cloned into EcoRI/XhOI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Gallfornia, Berkeley) using ZAP-cDNA synthesis Kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library library (Unpublished (2000) Contact: Sonstegard TS
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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                                                                                                                                                                                                                                                                                                    423 AGGCTGGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGGCCCTGGTTTGT
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Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S.
                                                                                                                                                                                                                         Score 271.4; DB 14; Length 1251;
Pred. No. 1.5e-59;
0; Mismatches 76; Indels 0;
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                                                                                                                                                                               3 others
            /clone_lib="NIH_MGC_40"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                603 GTCCTGTGCCGCTGTGATGACGGTGGCTTCACC
/clone="IMAGE:6484532"
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                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.7%;
Matches 317; Conservative
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/db_xref="taxon:9913"

/db_xref="taxon:9913"

/clone_lib="BARC 5BOV"

/lab_host="pooled"

/lab_host="DH10B"

/note="vector: pCMV SPORT6; Site_l: NotI; Site_2: SalI;

Library made from pooled mRNA isolated from mammary

Lissues at eight physiological, developmental, and disease

states: "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA linear EST 05-MAR-2002 sapiens cDNA clone IMAGE:5725937
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 269.4; DB 10; Length 452;
Pred. No. 3.2e-59;
0; Mismatches 81; Indels 0;
cross_match with the
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BM805088
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v0.980904.e. Vector identified by and -minmatch 12 options.
PCR PRImers
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Contact: Robert Strausberg, Ph.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Invitrogen
                                                        FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 9 row: E column: 17
Seq primer: ATTTAGGGTGACACTATAG.
                                                                                                                                   Location/Qualifiers
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79.78;
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Matches 318; Conservative
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Kumar, S., (Sathe, G., 1
                                   Lark, M.W.
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                                                                                                                                                                                                /cloud-lime.nrighgC_125"
/lab_host="NHI_MGC_125"
/lab_host="NHI_MGC_125"
/lab_host="DH10B"
/note="Organ: ovary (pool of 3); Vector: pcMV-SPORT6;
Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."
19 a 423 c 294 g 200 t 2 others
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HNC57-1-D9.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 620)
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM12717 row: j column: 18
High quality sequence stop: 697.
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Pred. No. 1.4e-58;
0; Mismatches 79; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                        1. .1058
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5725937"
                                                                                                                            Location/Qualifiers
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BG928868.1 GI:14323391
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79.9%;
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BG928868
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UW2109
GlasoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_war-l@gsk.com
Seq primer: T7.
Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                           Identification and initial characterization of 5000 expressed sequenced tags. (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries osteoarthr. Cartil. 9 (7), 641-653 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NotI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="cartilage"
//tissue_type="cartilage"
//tissue_type="coli DH10 B"
/note="Vector: pSPORT I; Site_1: SalI; Site_2:
Directional"
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/clone_lib-"HNC (Human Normal Cartilage)"
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BM043988
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361 GCGAGGACGCCGCTTCACC 380
 BM921531.1 GI:19371910
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                                                                                                                                                                                                                                                                                                                                         /clone_InAGES:546794"
/clone_Ilb="NIH_MGC_40"
/tissue_type="carcinoma"
/tissue_type="carcinoma"
/lab_host="bll0b (phage-resistant)"
/note="Organ: prostate; Vector: poTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

12 a 267 c 246 g 125 t
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AGENCOURT_6708025 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5753009
5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                                   Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 TGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTGTAAAGTGTGTGCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 AGCTGGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCA-GCCAGGGCCTGGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 CGGCTGGGGGGGCCCTGCGACCAACTCCACGTCTGCGACGCATGCCAGGCCTGGTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               542 TAGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGACCTTTAAACCCAATTGCAG
             NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
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80.7%; Pred. No. 3.3e-57;
ive 0; Mismatches 75; Indels
                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1929 row: k column: 19
High quality sequence stop: 714.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                        Contact: Robert Strausberg, Ph.D.
 (bases 1 to 750)
                                                     Unpublished (1999)
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 CCTGCGACCAACTCCAGGTCTGCGACGCCAGGCCTGGTCTGCCAGCCCGGGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 TACCCCTGGTGCTGGATGGCTGTGGCTGTAAAGTGTGTGCACGGAGGCTGGGGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        496 GCCCTGGCGGCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGGTAGCTGTGAGGTGA
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                                                           1 (bases 1 to 1006)
NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                            Email: crapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can library Arrayed by: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMI2788 row. b column: 18
High quality sequence stop: 593.
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Pred. No. 4.7e-57;
0; Mismatches 74; Indels 0;
                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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80.5%;
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Matches 306; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
E I (bases 1 to 979)
E I (bases 1 to 979)
S NIH-MCC http://mag.nci.nih.gov/
National Institutes of Health, Mammallan Gene Collection (MGC)
L Unpublished (1989)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCA2045 row: k column: 04
High quality sequence stop: 752.
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/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: breast, Vector: pOTB7; Site_1: EcoRI;
Site_2: Xho1; DNA made by oligo-dr priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Strategene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                               BQ279131 979 bp mRNA linear EST 07-MAY-2002 AGENCOURT_7046721 NIH_MGC_107 Homo sapiens cDNA clone IMAGE:5805819
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                           449 GCATGTCTGCGACCCCAGGCCTGGTTTGTCAGCCTGGGGCAGGCCCTGGCGGCCA 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 CCATCTTCTGGCCA@TTCCTTCTCTCTCTCTCTCAATGGTGTGTGCCCAGCTGTGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref-"taxon:9606"
/clone="IMAGE:5805819"
/clone_llb="NIH_MGC_107"
                                                                                                                                                                                                                                                                                                              5', mRNA sequeñce.
BQ279131
BQ27913171 GI:20489339
                                                                                                                          CTTCACC 448
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JOURNAL
COMMENT
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KEYWORDS
SOURCE
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/db_xref="taxon:9606"
/clone="IMAGE:5019065"
/clone="IMAGE:5019065"
/clone="IMAGE:5019065"
/clone="IMH_MGC_42"
/tlssue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage_resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: xhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGA(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
                                                                   BI161474 1200-2001 928 bp mRNA linear EST 05-JUL-2001 602864871F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5019065 5',
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                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1833 row: m column: 18
High quality sequence start: 28
High quality sequence stop: 756.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322 GGGGCCCTGTGCCTCTTGCCAGAGGACGACAGCAGCTGTGAGGTGAACGCCCCCGTGTA 381
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 928)
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                                                                                                                                                                                                                                                                                                                             NHF-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 3.5e-56;
0; Mismatches 68; Indels
                                                                                                                                       BI161474
BI161474.1 GI:14621475
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11 Similarity 81.5%;
299; Conservative
                                                                                                                   mRNA sequence.
                                                                                                                                                                                                                                        Homo saptens
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Best Local Si
Matches 299;
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mRNA linear EST 02-APR-2002 sapiens cDNA clone IMAGE:5806602
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/tissue_type="epidermoid carcinoma, cell line"
/lab_host="epidermoid carcinoma, cell line"
/lab_host="epidermoid carcinoma, cell line"
/lab_host="epidermoid carcinoma, cell line"
/note="organ: ling; Vector: pOTB7; Site_1: ECORI; Site_2:
Xhoi; cDNA made by oligo-dT priming. Directionally cloned
into EcoRiXhoi sites using the following 5' adaptor:
GGCAGGAGG; Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
N'H MGC Library."
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                                                                                                                                                                                                                  Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1073)
                                                                                                                                TGGGGCAGGCCCTGGCGGCCATGGGGCTGTGTCTCTTGGATGAGGATGACGGTAGCTG
                                                                                                                                                                                                                                                                                548 TGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGCCTTTAAACCCAATTGCAGGGTCCT
                          ACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTAAAGTGTGTGCACGGAGGCT
                                                                                                            GGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGCCCAGGCCTGGTTTGTCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Apencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://maqg.llnl.gov
Plate: LLCM2047 row: k column: 19
High quality sequence stop: 517.
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Pred. No. 1.4e-55;
0; Mismatches 65;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5806602"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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384 c 347
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/lab_nost="DH10B (phage-resistant)"
/note="Organ: breast, Vector: pOTB7; Site_1: ECORI;
Site_2: Xho1; CDNA made by Oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the following s' adaptor: GGCAGAGG(0. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                     933 bp mRNA linear EST 07-MAY-2002 GENCOURT_7046697 NIH_MGC_107 Homo sapiens cDNA clone IMAGE:5805626 BQ278961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308 GGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTTGGACACCACCCCAGTGCCC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (Mases 1 to 933)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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CCACGTCTGCGACGCCAGGGCCTGGTCTGCCAGCCCGGGGCAGGACCCGGTGGACG
                                                                                                                           569 CCTGGATGGAGACCTTTAAACCCAATTGCAGGGTCCTGTGCCGCTGTGATGACGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL)
http://imago.llnl.gov
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/organism="Homo sapiens"
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/clone_lib="NIH_MGC_107"
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High quality sequence stop: 353.
Location/Qualifiers
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373 CTTCACC 379
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(4	336	62	366	122	456	182	516	242	576	302
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Search completed: July 29, 2003, 02:51:28 Job time: 1128.2 secs

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Description	AF25998 AR210325 AR210325 AF100778 AF126063 AX0764186 AX64186 AF083500	AR210322 Sequenc AR210323 Sequenc AR210323 Sequenc AR074604 Homo sa AR100780 Homo sa BC017782 Homo sa BR210337 Sequenc AR210338 Sequenc AR210338 Sequenc AR210338 Sequenc AC126895 Rattus		AF120275 Rattus AR194011 Sequence B13814 cDNA enco AF031385 Homo sa AF031385 Homo sa AF031385 Homo sa AF003594 Homo sa AF003594 Homo sa Deprotein COP-1 (Cop-1) mRNA, comple Craniata: Vertebrata: Euteleostom Sciurognathi; Muridae; Murinae; 3., Zhang, H., Jo, H., Dempsey, P.J.,
St. BD BD		6 AR210322 6 AR210323 9 AF100780 9 BC017782 6 AR210337 6 AR210337 6 AC126895 2 AC126895	2 AC095418 10 AL731698 2 AL699106 9 AL139352 CHKCEF 6 AR118595 6 AR118595 6 AR11810891 111636 111636 111636 9 HWCONGRC 9 HSCTGF 6 AR119211 6 AR119211 6 AR11921 6 AR11921 6 AR11921 7 AC000000000000000000000000000000000000	вй в оомна
Length D	1741 1734 1734 1734 1739 1266 1266 1266	1293 1293 1309 1427 1450 738 841 137964	226303 2161072 2161072 107260 11805 11805 2075 2075 2075 2075 2075 2075 2075 20	2345 2350 11887 1935 1935 . Vegicus . GI:773 . Vegicus .
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1 (bases 1 to 1734)

Botstein, D.A., Cohen, R.L., Goddard, A.D., Gurney, A.L., Hillan, K.J., Lawrence, D.A., Levine, A.J., Pennica, D., Roy, M.Ann. and Wood, W.I. WISP Polypeptides and nucleic acids encoding same
Patent: US 6387657-A 17 14-MAY-2002;
                                                                                                                                                                                                                     GCCCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCAAG
                                                                                                                                                                                                                                                                                          TGCGGCTGCCCAGGTGGGACTGCCCAAGAGAAAAAAAAGGGTGCCAGGAAAGTGCT
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Pred. No. 1.1e-165;
0; Mismatches 59;
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                           protein family
Coffey,R.J., Pardee,A.B. and Liang,P. Identification of rCop-1, a new member of the CCN protein famil as a negative regulator for cell transformation Mol. Cell. Biol. 18 (10), 6131-6141 (1998) 98414629 9742130 2 (bases 1 to 1741) Liang,P. Liang,P. Direct Submission Submitted (24-APR-2000) Cell Biology, Vanderbilt-Ingram Cancer Center, 649 MRB II, Nashyille, TN 37232, USA
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1. 1741
/organism="Rattus norvegicus"
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262. 1014
/gene="Cop-1"
/note="secreted protein"
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QY         359 CCAGTGCCCACAGGGGGTACCCCTGGTGCTGGTGGCTGCTGTAAAGTGTGTGT	QY         539 CGGTAGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGA		Db 787	RESULT 3 AR210325/C AR210325 AR210325 LOCUS DEFINITION Sequence 18 from patent US 6387657. ACCESSION AR210325 VERSION AR210325.1 GI:21512526 SEXPRORES CONTROL	NISM NCE ORS	TITLE WISP POLYPeptides and nucleic acids encoding same JOURNAL Patent: US 638767-A 18 11-MAY-2002; FEATURES Location/Qualifiers Source 11734  BASE COUNT 393 a 495 c 491 g 355 t	Query Match 82.4%; Score 727.6; DB 6; Length 1734; Best Local Similarity 91.9%; Pred. No. 1.1e-165; Matches 816; Conservative 0; Mismatches 59; Indels 13; Gaps Matches 816; Conservative 1: Mismatches 59; Indels 13; Gaps  3 CGCTCTGATCTCCAGAGGACCCTGGGACAGGGCCTTGGCAAGGCTGCAGCGCC  1722 CGCTCCTGATCTCCAGAGGACCCCGGGCTGGGACAGGGGCCTTGGCAAGGCTGCAGGCGTGCAGGCTGCAGGCGCTGGCAAGGGCTTGGCAAGGCGCTGCAGGCGCTGGCAGGCTGCAGGCGCTGCAGGCGCTGGCAGGCTGCAGGCGCTGCAGCTGCAGCTGCAGCTGCAGGCGCTGCAGCAGCAGCAGGAGCAGCAGCAGCAGCAGCAGCAGCAG	0.5   0.5

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Trill,J.J.; Hand,M.T.; Connor,J.R.; Dodds,R.A.; Ryan,P.J.; Trill,J.J.; Figher,S.M.; Nuttall,M.E.; Lipshutz,D.B.; Zou,C.; Hwang,S.M.; Vofta,B.J.; James,I.E.; Rieman,D.J.; Gowen,M. and ince,J.C.; Mang,S.M.; Vofta,B.J.; James,I.E.; Rieman,D.J.; Gowen,M. and factor-like cDNA from human osteoblasts encoding a novel regulator of osteoblast functions  
J. Biol. Chem. 274 (24), 17123-17131 (1999)
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/gene="Ctgfl"
/note='similar to the Mus musculus WISP-2 protein encoded
by the sequence presented in GenBank Accession Number
AR100778; putative growth factor; CTGF-L; contains IGF
binding (IGFBD), Von Willebrand Factor type C (VWC) repeat
and thrombospondin type I (TSP1) domains; member of the
CCN (ETSC/Cyrfl/Nov) family; lacks the fourth
carbogy-terminal (CT) domain present in other members of
the CGN family"
                                                                                                    726
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Submitted (04-FEB-1999) Bone & Cartilage Biology, UW 2109,
SmithKline Beegham, 709 Swedeland Rd., King of Prussia, PA 19406,
USA
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precugate"
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/db_xref="G1:4337060"
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Kumar, S. and Zou, C.
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Pred. No. 1.1e-165;
0; Mismatches 59; Indels 13;
                                              Genentech,
                                            Oncology,
                          Direct Submission
Submitted (23-OCT-1998) Molecular Oncolc
Way, South San Francisco, CA 94080, USA
Location/Qualifiers
                                                                                                                                                                 /tissue_type="mammary"
/note="transformed by Wnt-1"
1. .1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                       1. 1734
/organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="C57MG"
/cell_type="epithelial"
                                                                                                                                                                                                            /gene="Wisp2"
257. 1012
/gene="Wisp2"
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91.9%;
(bases 1 to 1734)
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/translation="MRGNPLIHLLAISFLCILSMVYSQLCPAPCACPWTPPQCPPGVP
LVLDGCGCCRVCARRLGESCDHLHVCDPSQGLVCQPGAGFSGRGAVCLFEEDDGSCEV
NGRRYLDGETFKPNCRVLCRCDDGGFTCLPLCSEDVRLPSWDCPRPRRIQVPGRCCPE
WVCDQAVMQPAIQPSSAQGHQLSALVTPASADGPCPNWSTAWGPCSTTCGLGIATRVS
NQNRPCQLIQRRLLSRPCLSRPGGSWNSAF"
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                                                                                                      GGCAGTGGCTTGGAATGGAGGTCTTTATTACTGGGAACTGAGGAGCTAAGAGGCTCCTGT
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No. 2.1e-163;
smatches 63;
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Mismatches
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                                                                                                                    Roy, M.A.
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                                                                                 Craniata; Vertebrata; E
Catarrhini; Hominidae;
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 linear
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 DNA
                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata
Mammalia; Eutheria; Primates; Catarrhi
1 (bases 1 to 1266)
Botstein,D., Goddard,A., Gurney,A.L.,
Wood,W.I.
                                                                                                                                                                                                                                                               Score 434.6; DB Pred. No. 1e-94;
                                                                                                                                        Polypeptidic compositions and methods Patent: WO 0105836-A 31 25-JAN-2001; Genentech, Inc. (US) Location/Qualifiers
                                                                                                                                                                                                                            ¥
                                                                                                                                                                                                                                                                                       Mismatches
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1266 bp
WO0105836.
                                                                                                                                                                                         1. .1266
/organism="Homo sapiens"
/db_xref="taxon:9606"
. 418 c 390 g 242
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/product="connective tissue growth factor-like protein precursor"

precursor"
/db_xref="d="a4670350.1"
/db_xref="d1:3462836"
/translation="mmGTPKTHILAESLCILSKVRTQLCPTPCTCPWPPRCPLGVP
LVLDGGGCCRVCARRLGEPCDQLHVCDASQGLVCQPGAGFGGRGALCLLAEDDSSCEW
WNCGGGGCLRVCARRLGEPCDQLHVCDASQGLVCSDVRLPSWNCPHPRRVEVLGRCCPE
WNCGGGGGLGTQPLPAQGPQFSGLVSSLPPGVPCPEMSTAWGPCSTTGGLGMATRVSN
ONRFGBLETQNRLCBRRCPPSRGRSSQNSAF"

418 c 389 g 241 t
                                                                               o mRNA linear PRI 04-NOV-1998
growth factor-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="CTGF-L; encodes IGF binding (IGFB), von Willebrand factor type C (VWC) and thrombospondin type I (TSP1) domains; member of the CCN (CTGF/Cyr61/nov) family; lacks the fourth carboxy-terminal domain present in other members of the CCN family"
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Mammalia; Buthéria; Primates; Catarhini; Hominidae; Homo.

1 (bases 1 to 1283)

Kumar, S., Hand, A.T., Connor, J.C., Dodds, R.A., Ryan, P.J.,

Trill, J.G., Fisher, S.M., Slemmon, J.R., Lipshutz, D.B.,

Bartholomew, V., James, I.E., Rieman, D.J., Gowen, M. and Lee, J.C.

Identification and cloning of CTGF-L from human osteoblasts, a

novel cysteine Titch protein containing an IGF binding domain

Bone 23 (5), $240 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 CGCTGGGGGGGGCCTGCGACTAACTCCACGTCTGCGACGCCAGGCCTGGTTGC
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Submitted (11-AUG-1998) Bone & Cartilage Biology, UW 2109,
SmithKline Beecham, 709 Swedeland Road, King of Prussia, E
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Pred. No. 1e-94;
0; Mismatches 129; Indels
   644
 /cell_type="primary osteoblast"
9. .761
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
                                                                             Homo sapiens connective tissue g
precursor, mRNA, complete cds.
AF083500
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Local Similarity 79.9%;
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                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                           Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E., Gao, W.Q., Geritleen, M. E., Goddard, A., Godowski, P.J., Gurney, A.L., Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K., Wood, W.L. and Zhang, Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 434.6; DB 6;
Pred. No. 1e-94;
); Mismatches 129;
                                   DNA
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                                 1266 bp 1
Sequence 319 from Patent WO0140466.
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                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
418 c 390 g 247
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Location/Qualifiers
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AX464186.1 GI:21899109
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1427)

2 Pennica,D., Swañson,T.A., Welsh,J.W., Roy,M.A., Lawrence,D.A., Lee,J., Brush,J., Taneyhill,L.A., Deuel,B., Lew,M., Watanabe,C., Cohen,R.L., Melĥem,M.F., Finley,G.G., Ouirke,P., Goddard,A.D., Hillan,K.J., Gumer,A.L., Botstein,D. and Lewine,A.J. WiSp genes are members of the connective tissue growth factor family that are,up-requiated in wnt-1-transformed cells and aberrantly expréssed in human colon tumors

L. Proc. Nati. Acad. Sci. U.S.A. 95 (25), 14717-14722 (1998)
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                                                                                                                                                                                                                                                                                 243 GGTGACATGAGGĞGCAGCCCACTGATCCATCTTCTGGCCACTTCCTTCCTCTGCCTTCTC 302
                                                                                                                                                              61 TCAAAGGTGCGTACCCAGCTGTGCCCGACATGTACCTGCCCCTGGCCACCTCCCCGA 120
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Pred. No. 1e-94;
0; Mismatches 129;
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Homo sapiens connective tissue growth factor-related protein
Precursor (CT58) mRNA, complete cds.
AF074604
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/db_xref="GI:3328192"
/translation="MRGTPKTHLLAFSLLCLLSKVRTQLCPTPCTCPWPPPRCPLGVP
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WGRLYRRGETPOPHCSIRCNCEDGGFTCVPLCSEDVRLPSWDCPHPRRYEVLCRCCPE
WVCGQGGGGTGTQPLPAQGPQFSGLVSSLPPQYPCPEWSTAWGPCSTTCGLGMAIRVSN
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/product="connective tissue growth factor-related protein
precursor"
                                                                                                                                                                                             CCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGGCGCTCCACGGCGCAAGGA 782
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Rowles, J. and Gendler, S.
CT58, a new member of the connective tissue growth factor family, interacts with the breast cancer associated mucin MUC1
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Submitted (25-JUN-1998) Biochemistry and Molecular Biology, Mayo
Clinic Scottsdale, 13400 E. Shea Blvd., Scottsdale, AZ 85259, USA
Localion/Qualifiers
1. .1309
/organism="Homo sapiens"
/db_xref="taxon:9606"
1. .1309
                                                                       CACCAACTITCIGCCCTIGTCACTCCTGCTCTGCTGATGCTCCTTGTCCAAATTGGAGC
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les, J. and Gendler, S.
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/db_xref="GI:4028583"
/translation="MRGTPKTHLLAFSLLCLLSKVRTQLCPTPCTCPWPPPRCPLGVP
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MARLYRAEGETPOPHCS IR FOREBGGFTCVPLCSEDVRLPSWDCPHPRRYEVLGKCCPE
WVCGGGGGTLGTPDPAGQPQFSGLVSSLPPGYPCPEWSTAWGPCSTTCGLGMATRVSN
ONRFCRLETQRRLCLSRPCPPSRGRSPQNSAF"
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                        Oncology, Genentech, Inc., 1
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         Direct Submission
Submitted (23-OCT-1998) Molecular Oncold
Way, South San Francisco, CA 94080, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                Score 434.6; DB Pred. No. 1e-94;
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                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                     /map="20q12-q13.1"
/tissue_type="lung"
/dev_stage="fetus"
                                                                                                                                                                                                                                                                                                              417 9
                                                                                              /chromosome="20"
                                                                                                                                                                                          /codon_start=1
                                                                                                                                                     /gene="WISP2"
156. .908
                                                                                                                                                                             'gene="WISP2"
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79.9%;
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Email: cgapbs-refamil.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
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LVLDGCGCCRVCARRLGEPCDQLHVCDASQGLVCQPGAGGGGRGALCLLAEDDSSCEV
INGRLYREGETFQPHCSIRCKEDGGFTCVPLCSEDVRLPSWDCPHPRKVEVLGKCCPE
WVCGQGGGLGTQPLPAQGPQFSGLVSSLPPCYPCPEWSTAWGPCSTTCGLGMATRVSN
ONRFCRLETQRRLCLSRPCPPSRGRSPQNSAF"
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                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
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Direct Submission
Submitted (03-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                               Homo sapiens, WNT1 inducible signaling pathway protein 2, clone MGC:22271 IMAGE:4691574, mRNA, complete cds.
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/protein_id="AAH17782.1"
/db_xref="GI:17389483"
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Catarrhini; Hominidae; Homo
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Pred. No. 1e-94;
0; Mismatches 129;
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/tissue_type="Lung"
/clone_lib="NIL_MGC_77"
/lab_host="DH10B"
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/db_xref="LocusID:8839"
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165. .917
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Mammalia; Eutheria; Primates;
1 (bases 1 to 1450)
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Best Local Similarity
Matches 512; Conser
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Query Match 47.6%;
Best Local Similarity 79.6%;
Matches 510; Conservative (
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Unclassified.
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Lotstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.
WISP polypetides and nucleic acids encoding same
Patent: US 6387657-A 38 14-MAY-2002;
Location/Qualifiers
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TCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAG
                                            AGGCTGGGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGGGCCTGGTTTGT
                                                                                                                                                               AGCTGTGAGGTGAACGGCCGCCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCAGC
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Pred. No. 7e-92;
0; Mismatches 125;
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Sequence 38 from patent US 6387657.
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1 (bases 1 to 841)

Botsein, D.A., Cohen, R.L., Goddard, A.D., Gurney, A.L., Hillan, K.J.,
Lawrence, D.A., Levine, A.J.,
Pennica, D., Roy, M.Ann. and Wood, W.I.
WISP Polypeptides and nucleic acids encoding same
Patent: US 638 § 657-A 39 14-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         422
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                                                                                                                                                                                                   TGCCCACAGGGGGTACCCCTGGTGCTGGCTGTGGCTGCTGTAAAGTGTGTGCACGG
                                       GACCACCTGCATGTCTGCGACCCCAGGCCTGGTTTGTCAGCCTGGGGCCCT
                                                                               GGCGGCCATGGGGCTGTGTGTCTTTGGATGAGGATGACGGTAGCTGTGAGGTGAATGGC
                                                                                                                       CCCAGGTACCTGGATGGAGAGACCTTTAAACCCAATTGCAGGGTCCTGTGCCGCTGTGAT
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Pred. No. 2.6e-91;
0; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                           41 bp
6387657.
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AR210338
AR210338.1 GI:21512543
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297 c 280 g
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185	482	245	542	305	602	365	662	425	722	485	782	543	842	603		
126 TGCCCGCTGGGAGTACCCCTGGTGGTGGTGGCTGTGGCTGCTGCCGGGTATGTGCACGG	423 AGGCTGGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGGCCTGGTTTGT	186 CGGCTGGGGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCCAGGGCCTGGTCTGC	CAGCCTGGGGCAGGCCCTGGCGGCATGGGCTGTGTCTCTTGGATGAGGATGACGGT	CAGCCGGGGCAGGACCGGGGGGGGGGCCCTGTGCTTTTGTTTG	AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAACCCCAATTGCAGG	AGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	GTCCTGTGCCGCTGTGATGACGGTGCCTTCACCTGCCGCCTGTGCAGGATGTG	366 ATCCGCTGCCGCTGCGACGCGCGCTTCACCTGCCTGCCGCTGTCGCTGTGCGGCGGTGTGTGT	CGGCTGCCCAGCTGCGCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGC	CGCTGCCCACCACCCCCACCCCAGGGGTCGAGGTCTGGGGTCGTGGCTGCTGCTGCTGCTGCTGCTGCTGC	CCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCGCAAGGA	CCTGAGTGGGTGTGCGCCCAAGGGGGGACTGGGGTCTCCGTCCTTCCAGCCCAAGGA	CACCAACTITCTGCCCTTGTCACTCCTGCCTGATGCTCCTTGTCCAAATTGGAGC	CCCCAGTTTTCTGGCCTTGTTTCTTCCCTGCCCCTGGTGTGTCCCCTGCCCAGAATGGAGC		604 ACGCCTGGGACCTGGCTCGACCTGTGGGCTGGGCTT 644
126	423	186	483	246	543	306	603	366	663	426	723	486	783 (	544	843	604
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Nucleic acid sequences encoding rat heparin-induced CCN-like protein, used in methods to identify modulators or in diagnostic applications

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                                                                     RESULT 2
                                                                               AAX76488
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                                                                                                            Agents that stimulate or inhibit HICP protein activity or expression, antisense HICP nucleic acid molecules and HICP antibodies, can be used to modulate cell-associated activity. HICP modulators can be used to treat disorders characterized by aberrant HICP protein activity or expression. Probes capable of hybridizing to HICP mRNA or antibodies specific for HICP can be used to detect HICP activity in a biological sample. HICP can be used to treat disorders, such as a cardiovascular or fibrotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                        This cDNA encodes a rat heparin-induced CCN-like protein (HICP)
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                                                                                                                                                 Length 1708;
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                                                                                                           disorder, characterized by aberrant cell proliferation.
                                                                                                                              Sequence 1708 BP; 362 A; 486 C; 478 G; 382 T; 0 other;
                                                                                                                                                100.0%; Score 883; DB 20; 100.0%; Pred. No. 6.7e-235;
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                                                                                                                                                                   0; Mismatches
         Fig 1; 108pp; English
                                                                                                                                                                    Matches 883; Conservative
                                                                                                                                                          Similarity
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          Claim
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The present invention describes Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-1, and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-1, wisp polypeptides, designated WISP-1, WISP-2 products from the present invention can be used to treat WISP-related disorders such as breast, ovarian, and colon cancer or melanoma. The products can be used to treat arteriosclerosis. The products can also be used to treat other diseases e.g. benign and malignant tumours, leukaemia and lymphoid malignancies, neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, and blastococalic disorders, haematopolesis-related disorders, tissue-growth disorders, bone-related disorders such as other wounds, connective tissue disorders, burns, inclsions, and other wounds, connective tissue disorders, catabolic states, testicular-related disorders, and inflammatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenic and immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The products can be used in the production of transgenic or knock-out animals. Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       connective tissue growth factor; cancer; melanoma; arterioscierosis; leukaemia; lymphoid malignancy; haematopolesis related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic leaion; kidney disorder; bone-related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation; testicular-related disorder; angiogenesis; immunological disorder; sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF;
                                GCACAGCCTGGGGCCCCTGCTCAACCACCTGTGGGCTGGCAT 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gurney AL, Hillan
Roy MA, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse WISP-2 protein nucleotide sequence SEQ ID NO:17.
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Pennica D,
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97US-0063704.
98US-0073612.
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Levine AJ,
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Lawrence DA,
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29-OCT-1997;
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841
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Length 1734;

20; DB

Score 727.6;

82.48;

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The invention provides a rat heparin-induced CCN-like protein (HICP) protein. Agents that stimulate or inhibit HICP protein activity or expression, antisense HICP nucleic acid molecules and HICP antibodies, can be used to modulate cell-associated activity. HICP modulators can be used to treat disorders characterized by aberrant HICP protein activity or expression. Probes capable of hybridizing to HICP manA or antibodies specific for HICP can be used to treat disorders, such as a cardiovascular of fibrotic disorder, characterized by aberrant cell proliferation. The
                  Heparin-induced CCN-like protein; HICP; cell-associated activity; ss; cardiovascular disorder; aberrant cell proliferation; fibrotic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGTGTCCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAGTGCCCA
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                                                                                                                                                                                                                     Nucleic acid sequences encoding rat heparin-induced CCN-like protein, used in methods to identify modulators or in diagnostic applications
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Pred. No. 3.3e-166;
0; Mismatches 0;
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100.0%; Pre
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635; Conser
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                                               TG-GGCAGTGGCTTGGAATGGAGGTCTTTATTACTGGGAACTGAGGAGCTAAGAGGCTCC
                                                                                       TGTCAG----CTTGTCCTAAAGTCTTAGCACTTGTGGTGGCTTGGGCTTCACACACTGTCA
                                                                                                                            GACACCTTCGTGGTGGCCTCCACGGCCTCACCTTCAGGTTTGAAGCTGGCTCCACAAGGG
                                                                                                                                                                    TCTCTCAATGGTGTATTCCCAGCTGTGCCCAGCACCCTGTGCCTGTCCTTGGACACCACC
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                  Indels
9e-192;
- 59;
        ed. No. 9e-1
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                                                                                                                                                                                                                                   CCTGGCGGCCATGGGGCCTGTGTGTCTCTTGGATGAGGATGACGGTAGCTGTGAGGTGAAT
                                                                                              GGCCGCAGGTACCBGGATGGAGACCTTTAAAACCCAATTGCAGGGTCCTGTGCCGCTGT
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Pennica D,
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97US-0063704.
98US-0073612.
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Levine AJ,
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Lawrence DA,
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                                                                                 The invention provides a rat heparin-induced CCN-like protein (HICP) protein. Agents that stimulate or inhibit HICP protein activity or expression, antisense HICP nucleic acid molecules and HICP antibodies, can be used to modulate cell-associated activity. HICP modulators can be used to treat disorders characterized by aberrant HICP protein activity or expression. Probes capable of hybridizing to HICP motel activity specific for HICP can be used to detect HICP activity in a biological sample. HICP can be used to treat disorders, such as a cardiovascular of fibrotic disorder, characterized by aberrant cell proliferation. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCCTGGTGCTGGATGGCTGTGGTGTGTGTGTGTGCACGGAGGCTGGGGGGAGTCC 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                        Heparin-induced CCN-like protein; HICP; cell-associated activity; ss; cardiovascular disorder; aberrant cell proliferation; fibrotic disorder.
CCCAGCTGGGACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGCCCCGAG
                                   TGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCGAAGGACACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGCTGTGCCGGACACCCTGTACCTTGCACACCACCCCCAGTGCCCACAGGGGGTA
                                                                     CTTTCTGCCCTTGTCACTCCTGCTCTGATGCTCCTTGTCCAAATTGGAGCACAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid sequences encoding rat heparin-induced CCN-like protein, used in methods to identify modulators or in diagnostic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence represents the coding sequence of rat HICP mature
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100.0%; Pred. No. 4.5e-147;
ive 0; Mismatches 0;
                                                                                                                             TGGGGCCCCTGCTCAACCACCTGTGGGCTGGGCAT 883
                                                                                                                                                                                                                                                                  Rat HICP mature polypeptide coding sequence.
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                                                                                                                                                                                              AAZ07521 standard; cDNA; 681
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                                     CTTGTCACTCCTGGCTCTGCTGATGCTCCTTGTCCAAATTGGAGCACAGCCTGGGGGCCCC
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Roy MA,
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Fri Aug

153 GCCTGGGGCCCCTGCTCAACCACCTGTGGGTTGGGCAT 116

BP.

AAX16595 standard; cDNA; 1522

RESULT 6 AAX16595

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disorders such as breach invention and colon cancer or melanoma. The products such as breach ovariant and colon cancer or melanoma. The products can be used to treat arteriosclerosis. The products can also be used to treat diseases e.g. benign and malignant tumours, used to treat other diseases e.g. benign and malignant tumours, leakach of the products and plant, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, and blastocoelle disorders, heamatopolesis-related disorders, tissue-growth disorders, bone-related disorders such as osteoporosis, trauma such as disorders, including such disorders, and other wounds, connective tissue disorders, catabolic states, testicular-related disorders, and inflammatory, angiogenic and immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The products can be used in the production of transgenic or knock out animals.
                                                                                                               The present invention describes Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-3 have homology to connective tissue growth factor (CTGF). Products from the present invention can be used to treat WISP-related
New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3
                                                            Page 179-180; 284pp; English.
                                                            Disclosure;
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Sequence 753 BP; 159 A; 229 C; 238 G; 127 T; 0 other;

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                                  GTGTGCCCAGCTGTGCCGGACACCCTGTACCTTGCACCACCACCCCAGTGCCCA
                                                                              CAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTAAAGTGTGTGCACGGAGGCTG
                                                                                                                 GGGCCAGGCCCTGGCGGCCATGGGGCTGTGTCTCTTGGATGAGGATGACGTAGCTGT
                                                                                                                                                                                      GAGGTGAATGGCCGCAGGTACCTGGATGGAGACCTTTAAACCCAATTGCAGGGTCCTG
                                                                                                                                                                                                                              GAGGTGAATGGCCGCAGGTACCTGGATGGGGAGACCTTTAAACCCAATTGCAGGGTTTTG
                                                                                                                                                                                                                                                TGCCGCTGTGATGACGGTGGCTTCACCTGCCTGCCGCTGTGCAGGATGTGCGGCTG
                                                                                                                                                                                                                                                         CCCAGCTGGGACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGCCCCGAG
                                                                                                                                                                                                                                                                                            CAACTITCTGCCCTTGTCACTCCTGCTCTGCTGATGCTCCTTGTCCAAATTGGAGCACA
                                                                                                                                                                                                                                                                                                                                                               213 CAACTITCIGCCTIGICACTCCTGCATCTGCCGATGGCCCCTGTCCAAACTGGAGCACA
                                                                                                                                          Gaps
                   3;
Length 753;
                   43; Indels
DB 20;
Score 553.2; DB 20
Pred. No. 1.6e-143;
                 0; Mismatches
62.7%;
92.8%;
        al Similarity 92.8
592; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes human growth factor-like protein (HGFLP) which has homology to connective tissue growth factor (CTGF) and fisp-12, which are members of the platelet-derived growth factor (PDGF) and superfamily of growth factors. Antisense oligonucleotides and HGFLP antagonists can be used to treat or prevent cancer, and connective fissue disorders including ankylosing spondylitis, atherosclerosis, Dupuytren's contracture, eosinophilic fascilitis, Felty syndrome, Goodpasture's disease, Hunter syndrome, Hurler syndrome, keloids, Marfan syndrome, nodular fascilitis, osteogenesis imperfecta, polyarthritis and restenosis following angiophasty. HGFLP antibodies and polynucleotides can also be used in diagnostic assays for conditions or
                                                                                                         Human, growth factor-like protein; HGFLP; fisp-12; CTGF; PDGF family; connective tissue growth factor; platelet-derived growth factor; keloid; connective tissue growth factor; cancer; ankylosing spondylitis; scleroderma; atherosclerosis; Dupuytren's contracture, eosinophilic fasciitis; atherosclerosis; Dupuytren's contracture, Hunter syndrome; Hunter syndrome; Hunter syndrome; modular fasciitis; osteogenesis imperfecta; restenosis; rheumatoid arthritis; systemic lupus erythematosus; ss.
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                                                                              Human growth factor-like protein encoding cDNA.
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78.8%;
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                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Fig 1; 63pp;
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                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-1997;
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                                              29-APR-1999
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                                                                                                                                                                                                                                                                      CCTGGGCAAGTGCTGCCTGAGTGGGGTGTGGCGCCAAGGAGGGGGACTGGGGACCCAGCC 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted protein; immunosuppressive; antiarthritic; antirheumatic; antipoliferature; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; human; opthalmalogical; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                         TTGTCCAAATTGGAGCACAGCCTGGGGCCCCTGCTCAACCACCTGTGGGCTGGGCAT 883
                                                            CCGGGTATGTGCACGCGGGGGGGGGAGCCCTGCGACCCACGTCCACGTCTGCGACGCCAG
                                                                                                                                                                                                                                    CICCACGGCGCAAAGACACCAACTITCIGCCCTIGICACTCCTGCCTGTGTGCTCC
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GCTCTGCAGGG-----GACATGAGAGGCACACCGAAGACCCACCTCCTGGCCTTCTC
                          294 CCTCCTCTGCCTCCTCTCAAAGGTGCGTACCCAGCTGTGCCCGACACCATGTACCTGCCC
                                                  347 TTGGACACCACCCCAGTGCCCAACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGCTG
                                                                                    TAAAGTGTGTGCACGGAGGCTGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAG
                                                                                                                       CCAGGGCCTGGTTTGTCAGCCTGGGGCAGGCCCTGGGGGCCATGGGGCTGTGTGTCTCTT
                                                                                                                                594 CCAGCCCCACTGCAGCATCCGCTGCGCTGCGAGGACGGCGGCTTCACCTGCGTGCCGCT
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                  CTTCCTCTGCCTTCTCTCTATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein encoding cDNA (clone Id HBODE48)
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                                                                                                                                                                                                                                                                                                                                                                                           BP
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The invention provides novel human secreted proteins and polynucleotides encoding them. The secreted proteins can be expressed by standard recombinant methodology. The secreted proteins and polynucleotides are used to prevent, treat or ameliorate a medical condition in e.g. humans, also be used in disgnésing a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in disgnestic immunoassays e.g. radioimmunoassays or enzyme also be used in manosorbent gassays (ELISA). Disorders which are disgnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardioasscular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. foconeal infections caused by bacteria, viruses and fungi and coular disorders e.g. foconeal infection. The polypeptides can also be used at also decreased to repensate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present sequence represents a human secreted protein encoding cDNA.
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                         Fiscella
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used to preventing, t<u>r</u>eating or ameliorating a medical condition
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                         Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1337 BP; 257 A; 427 C; 396 G; 252 T; 5 other;
                         Shi Y,
                                                                                                                                                                                                                                                                  482pp; English.
                      Duan DR,
                      Ebner R,
Barash SC;
                                                                                                                                                                                                                                                                  Claim 1; Page 427-428;
                                                                                                    2001-476220/51
Moore PA, ho.
                   Wei P,
                                                                                                                                  P-PSDB; AAB85542
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The invention provides novel human secreted proteins and polynucleotides encoding them. The secreted proteins can be expressed by standard concoding them. The secreted proteins and polynucleotides are recombinant methodology. The secreted proteins and polynucleotides are used to prevent, treat or ameliorate a medical condition in e.g. humans, also be used in diagnosing a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the cliented include autoimmunoassays or aradioimmunoassay or enzyme disorders and in diagnostic immunoassays or, aradioimmunoassays or enzyme clinked include autoimmune diseases e.g. reducing arthritis, created include autoimmune diseases e.g. rheumatoid arthritis, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, verborovascular disorders e.g. cardiac arrest, verborovascular disorders e.g. corneal infection. The polypeptides can also be cused to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for
                                                                      593
                                                                                                          852
                                                                                                                             Secreted protein; immunosuppressive; antiarthritic; antirheumatic; anticholiferature; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; human; opthalmalogical; gene therapy; ss.
GGGACTGCCCCCACCAGGAGGGTCGAGGTCCTGGGCAAGTGCTGCCCTGAGTGGGTGT
                                                      CCCTTGTCACTCCTGCCTCTGCTGTTCCTTGTCCAAATTGGAGCACAGCCTGGGGGCC
                                   GTGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCAAGGACACCAACTTTCTG
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i GH, Fiscella M;
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Shi Y, Ch
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DR,
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PA, Wei P, Ebner R,
Ruben SM, Barash SC;
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04-FEB-2000; 2000US-0180628.
12-SEP-2000; 2000US-0231968.
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                                                                                                                                                                              54
 to regenerate tissues and in
           chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present sequence represents a human secreted protein encoding cDNA.
                                                                                                                                                                                                                                                                               115 GCGTACCCAGCTGTGCCCGAACATGTACCTGCCCCTGGCCACCTCCCCGATGCCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 GTGGCCTCCACGGCCTCACCTTCAGGTTTGAAGCTGGCTCCACAAGGGACACGGTGACAT
                                                                                                                                                                                                                                                                                                                                                  175 GGGAGTACCCCTGGTGCTGGATGGCTGTGGCTGCCGGGTATGTGCACGGCGGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                            GGTATGTGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCAAGGACACCAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCTGCCCTTGTCACTCCTGCTGTGTTCCTTCTCCAAATTGGAGCACAGCTG
                                                                                                                                                                                                        251 GAGGGGCAGCCACTGATCCATCTTCTGGCCACTTCCTTCTCTGCTTCTCTCAATGGT
                                                                                                                                                                                                                                    GTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCACCAGTGCCCACA
                                                                                                                                                                                                                                                                                                                        371 GGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGTAAAGTGTGTGCACGGAGGCTGGG
                                                                                                                                                                                                                                                                                                                                                                              GGCAGGCCCTGGCGGCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGGTAGCTGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          551 GGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAAACCCAATTGCAGGGTCCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355 GGTGAACGGCCGCCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCAGCATCCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                511 CCGCTGTGATGACGGTGGCTTCACCTGCCGCTGTGCAGTGAGGATGTGCGGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGCTGGGACTGCCCACGCCCCAAGAATACAGGTGCCAGGAAAGTGCTGCCCCGAGTG
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                                                                                                                                                                  = = = = = = =
                                                                                            Score 439.8; DB 22; Length 1352;
                                                                  Sequence 1352 BP; 268 A; 431 C; 399 G; 254 T; 0 other;
                                                                                                          Pred. No. 6e-112;
; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      687
                                                                                                                                                                                                                                                                                                                                   culture of primary tissues,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGACCCTGCTCGACCACCTGTGGGCTGGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGCCCCTGCTCAACCACCTGTGGGCTGGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO261 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA30048 standard; cDNA; 1266
                                                                                            49.8%;
                                                                                                           78.48;
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                                                                                                                          Conservative
                                                                                                           Best_Local Similarity
Matches 543; Conserv
supporting cell
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                                                                                               Query Match
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843 ACAGCCTGGGGCCCC
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                                                                                       723 CCCGAGTGGGTATG
                                                                                                                     484 CCTGAGTGGGTGE
                                                                                                                                                                       Human cDNA sequence en
   364 ATCCGCTGCCG
                                                                           424 CGGCTGCCCAGC
                                                                                                                                                                                                                                               604 ACGCCTGGGGA©
                                              CGGCTGCCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a human PRO261 nucleotide sequence. PRO261 is a growth factor. The invention relates to isolated antibodies which bind to a polypeptide. The "PRO" polypeptides are encoded by genes which are over expressed in the genome of tumour cells. Vectors and host cells comprising the nucleic acid encoding the antibodies are used in the production of the antibodies. The antibodies and nucleic acids encoding them are used for diagnosing a tumour in a mammal. The antibodies are used for inhibiting the growth of tumour cells and identifying compounds that inhibit a blological or immunological activity of and/or expression of a PRO187, PRO533, PRO214, PRO210, PRO211, PRO230, PRO261, PRO261, PRO261, PRO217, PRO261, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 TCAAAGGTGCGTACCCAGGTGTGCCCGACACCATGTACCTGCCCCTGGCCACCTCCCCGG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 TCAATGGTGTGTGCCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGCCTGGGGCCAGGCCCTGGCGGCCATGGGGCTGTGTTTGGATGAGGATGACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGCCTTTAAAACCCAATTGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                   New isolated antibodies which bind to specific polypeptides used for diagnosis and treatment of neoplastic cell growth and proliferation
                                                                                                                                                                                                                         Botstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 434.6; DB 21; Length 1266;
Pred. No. 1.6e-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 129; Indels
antibody dependent enzyme mediated prodrug therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1266 BP; 216 A; 418 C; 390 G; 242 T; 0 other;
                                                                                                                                                                                                                            Wood WI,
                                                                                                                                                                                                                              MA,
                                                                                                                                                                                                                              Roy
                                                                                                                                                                                                                            Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                Example 7; Fig 13; 200pp; English.
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                                                                                                                     99WO-US20594.
                                                                                                                                                 98US-0099803
98WO-US18824
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512; Conservative
                                                                                                                                                                                                                            Gurney AL,
                                                                                                                                                                                               (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                         WPI; 2000-271386/23
                                                                                                                                                                                                                                                                        P-PSDB; AAY88573.
                                                         WO200015666-A2
                             Homo sapiens
                                                                                                                     08-SEP-1999;
                                                                                                                                                   10-SEP-1998;
                                                                                                                                                                  10-SEP-1998;
                                                                                       23-MAR-2000
                                                                                                                                                                                                                            Goddard A,
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GCGAGGACGCCGCTTCACCTGCCTGCCGCTGTGCAGCGAGGATGTG 423
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                                                                                                                            SEGACTECCCCCACCCCAGGAGGTCGAGGTCCTGGGCAAGTGCTGC 483
                                                                                                                                                                                FIGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCAAGGA 782
                                                                                                                                                                                                                                                                                                                     GCCTTGTCTTCCTGCCCCTGGTGTCCCCTGCCCAGAATGGAGC 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate, cervical; tumour necrosis factor-alpha; TMR-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                                                                                                                                                          CCTTGTCACTCCTGCTCTGCTGATGCTCCTTGTCCAAATTGGAGC
                                                                                                                                                                                                                                   GCGCCCAAGGAGGGGGACTGGGGACCCAGCCCTTCCAGCCCAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                    CITCLE TITITITITITITITITI
                                                                                                                                                                                                                                                                                                                                                                                           CTGCTCAACCACCTGTGGGCTGGGCAT 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coding for PRO261 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS21403 standard; cDNA; 1266 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32678
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782

723 CCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGGATCCAGCGCTCCACGCCCAAGGA

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AAS21244-AAS21518 encode for novel human secretory and transmembrane
PRO polypeptides. The PRO polypeptides are useful to detect other
PRO polypeptides, to link bloactive molecules to cells expressing
PRO polypeptides, to modulate biological activities of cells expressing
PRO polypeptides, and to detect the presence of mammalian lung, colon,
breast, prostate, rectal, cervical or liver tumours by comparing PRO
polypeptide expression in a cell sample to that in a control sample.
Some of the 275 sequences are also useful to stimulate the release of
tumour necrosis factor-alpha (TNF-alpha) from human blood, the
proliferation or differentiation of chondrocytes, the proliferation of gene expression in pericyte cells, the release of proteoglycans from
cartilage, the proliferation of inner ear utricular supporting cells or T-lymphocytes, the release of a cytckine from peripheral blood
monocytes (PBMCs), or the proliferation of endothelial cells. Some of
the RPO polypeptides may modulate glucose or free fatty acid uptake by
skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
to factor VIIA. The PRO polypeptides can be used in assays to identify
mon collinear and a promoter and a procession of the colling and a procession of the cells or by adipocytes; or inhibit binding of A-peptide
non collinear and a procession of the proliferation or any action of the proliferation or inhibit binding of A-peptide
non collinear and a procession of the proliferation of moneyers (BMCs).
                3
                                                                                                                                                                                            ated, secretory and transmembrane PRO polypeptide used to detect
or PRO polypeptides, link bloactive molecules to cells expressing
polypeptides, and detect the presence of mammalian tumours e.g.
                Gao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
             Filvaroff E, (
                                                                    Shang
          Deforge L, Desnoyers L, Filvaro
A, Godowski PJ, Gurney AL, Sher
Fumas D, Watanabe CK, Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1266 BP; 216 A; 418 C; 390 G; 242 T; 0 other;
                                                              Tumas D,
                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                              lung, breast, prostate, cervical
Beresini M, De
ME, Goddard A,
                                                                                                                                                                                                                                                                                                                          Claim 3; Fig 319; 813pp;
                                                            Stewart TA,
                                                                                                                  2001-408281/43.
                                                                                                                                        P-PSDB; AAU12331
          Baker KP, Bere
Serritsen ME,
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other PRO
                                                              Smith V,
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                                                                                                                                                                                                                                                           602
                                                                                                                                                                                                                                                                                                                                               722
                                                                                                                             363 TGCCCACAGGGGGTACCCCTGGTGCTGGTGGCTGCTGTAAAGTGTGTGCACGG 422
                                                                                                                                                                                                                 CAGCCTGGGGCAGGCCCTGGCGGCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGGT 542
                                                                                                                                                                                                                                      CAGCCCGGGGCAGGACCCGGTGGCCGGGGGCCCTGTGCCTCTTGGCAGAGACGACAGC 303
                                                                                                                                                                                                                                                                                                                                                        AGCTGTGAGGTGAACGGCCGCCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCAGC 363
                                                      AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGCCTTTAAAACCCAATTGCAGG
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Score 434.6; DB 22; Length
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CACCAACTTTCTGCCCTTGTCACTCCTGCCTCTGCTGATGCTCCTTGTCCAAATTGGAGC
                                                                                                     New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533, useful for diagnosing and treating cancers -
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                                              TGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGTAAAGTGTGTGCACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                   Human; anglogenesis-associated protein; PRO; endothelial cell growth; cardiac hypertrophy; cardiovascular disorder; endothelial disorder; anglogenic disorder; atherosclerosis, osteoporosis; hypertension; mayocardial infarction; diabetic retinopathy; rheumatoid arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cance Alzheimer's disease; Huntington's disease; stroke; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                     Human anglogenesis-associated protein PRO261 cDNA, SEQ ID NO:107.
                                                                                                                                                                                                                                                                                                  gene therapy; transgenic animal; ss
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99WO-US12252.
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The Invention relates to novel numan anglogenesis associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding PRO proteins. The Invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein. PRO antibodies specific for a PRO protein, fusion proteins comprising a PRO nucleic acid, the recombinant production of a PRO protein, agonists or antagonists of a PRO protein, and comprising a PRO protein, agonists or antagonists of a PRO protein, and additionally encompasses methods of identifying modulators of PRO compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO compactions in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or anglogenic disorder via the administration of a PRO protein, PRO nucleic acid; and methods of inhibiting or stimulating endothelial or PRO agonist or antagonist; are troviral gene therapy vector comprising a cardiovascular, and methods of inhibiting or stimulating endothelial or pRO nucleic acid; PRO protein, or an agonist or antagonist; and protein, or an agonist or stimulating endothelial or angionist and PRO antagonists may be used as therapeutic agents to treat cardiovascular, endothelial or angioned angionesis, such as the administration of a PRO proteins, antibodies against PRO proteins, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, poorlasis, of and arthritis, cardiovascular, endothelial or angiogenic disconder, such as a thereosclerosis, volcers, wounds, cancer, Alzhelmen's disease, buttington's disease, or stroke. PRO nucleic acids are additionally useful in the cecombinant production of PRO proteins, an also be used to produce transgenic company. The process and also produce transgenic company the process and also process.
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ark MR, Marsters
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N. Hillan KJ, Kuo SS, Mark MR, Mc
Watanabe CK, Williams PM, Wood WI;
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99WO-US21547.
99WO-US23089.
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99WO-US28564.
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99US-0145698
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                                                                                                                                                                                                                                                                                                                                            Human; PRO; promotion; Inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; anglogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine; ss.
                     TGCCCGCTGGGAGTACCCCTGGTGCTGGTGGCTGTGGCTGCTGCTGCCGGGTATGTGCACGG
                                          184 CGGCTGGGGGGGGCCTGCGACCAACTCCACGTCTGCGACGCCAGGCCAGGCCTGGTCTGC
                                                              CAGCCTGGGGCAGGCCCTGGCGGCCATGGGGCTGTGTCTCTTGGATGAGGATGACGGT
                                                                      AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAAACCCAATTGCAGG
                                                                                                  CGGCTGCCCAGGTGGGACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGC
                                                                                                                                                          CCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCAAGGA
                                                                                                                                                                                    CACCAACTTTCTGCCCTTGTCACTCCTGCTGTGATGCTCCTTGTCCAAATTGGAGC
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                                   AGGCTGGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGCCCAGGGCCTGGTTTGT
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                                                                                                                                                                                                                                    Human PRO261 cDNA sequence SEQ ID NO:71
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                                                                                                                                                                                                                                                                                    AAA77566 standard; cDNA; 1267
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99US-0115554.
99WO-US05028.
99US-0123957.
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99US-0145698.
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                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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12-MAR-1999;
28-APR-1999;
14-MAY-1999;
02-JUN-1999;
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26-JUL-1999;
01-SEP-1999;
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12-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for preventing, diagnosing and treating diagnosing porticities and cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with imappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors associated with decreased PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24335 represent nucleotide and protein sequences used in
                                                                                                                                                                                 Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes nucleic acids encoding PRO polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 TCAAAGGTGCGTACCCAGCTGTGCCCGACACCATGTACCTGCCCCTGGCCACCTCCCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGCTGCCCAGCTGGGACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGC
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                                                                                                                                                                               I, Hillan KJ, Goddi
Paoni NF, Smith V;
                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial angiogenic disorders in mammals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21; Length 1267;
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Pred. No. 1.6e-110;
0; Mismatches 129;
                                                                                                                                                                                    Gerber
                                                                                                                                                                                                         Kuo SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the exemplification of the present invention.
                                                                                                                                                                               Ferrara N,
Klein RD, F,
, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                        61; Fig 29; 315pp; English
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                                          99WO-US21547.
99WO-US23089.
99US-0162506.
99WO-US20944
99WO-US21090
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                                                                                                                                                                               Baker KP,
Gurney AL,
Williams PM,
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Matches 512; Conservative
                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                           WPI; 2000-412154/35.
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Godowski PJ, (
Watanabe CK, 1
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administering CTGF-3 polypeptides and anti-CTGF-3 antibodies
                                  Sequence 1285 BP;
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                                                                               CGGCTGCCCAGCTGGGACTGCCCCCACCCCAGGAGGGTCGAGGTCCTGGGCAAGTGCTGC 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This nucleotide sequence codes for human connective tissue growth factor: 3) protein (see AAM37946), a novel member of thee factor: 3) forfer; 1) twas discovered in a cDNA library derived from human osteoblasts. The gene has also been identified in cDNA libraries from novary, testis, heart, lung, skelterial muscle, adrenal medulla, adrenal cortex, thymus, prostate, small intestine and colon. A cDNA clone is deposited as ATCC 97756. Also provided colon. A cDNA clone is deposited as ATCC 97756. Also provided CTGF-3 polypeptides. CTGF-3 nucleic acid sequences or their fragments, e.g. primers or probes, can be used to diagnose diseases thereoffs-3 polypeptides is enhanced, e.g. cancer, arthritis, fibrosis or atherosclerosis, or diseases where expression is decreased such as in osteoporosis. Disorders characterised by
                                 CCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGGCGCTCCACGGCGCAAGGA
                                                                CACCAACTITICTGCCCTTGTCACTCCTGCCTGCTGATGCTCCTTGTCCAAATTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human connective tissue growth factor 3 gene - useful for the diagnosis and treatment of e.g. cancer, arthritis, fibrosis, osteoporosis
                                                                                                                                                                                                                                                                           Connective tissue growth factor-3; CTGF-3; human; cancer; arthritis; fibrosis; osteoporosis; diagnosis; therapy; ds
                                                                                                            ACGCCTGGGGACCCTGCTCGACCACCTGTGGGCTGGGCAT 644
                                                                                                                                                                                                                                                       connective tissue growth factor-3 gene.
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9..761
/*tag= a
/*tag= b
66..758
/*tag= c
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P-PSDB; AAW37946.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 AGCTGTGAGGTGAACGCCGCCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCAGC
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                                                                                                                      303 TCAATGGTGTGTGTGCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAG
                                                                                                                                                                                                                                                                                                                                                                               543 CCCCAGTTTTCTĞGCCTTGTCTCTTCCCTGCCCCCTGTGTCTCCCTGCCCAGAATGGAGC
                                                                                                                                                           3 GGGGACATGAGAGGCACACCGAAGACCCACCTCCTGGCCTTCTCCCTCTCTGCCTCCTC
                                                                                                                                                                                                                                                                             TGCCCACAGGGGGAACCCCTGGTGCTGGATGGCTGTGGCTGTAAAGTGTGTGCACGG
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                                        Length 1285;
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                                                                               Indels
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  T; 0 other,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   603 ACGCCTGGGGA@CCTGCTCGACCACCTGTGGGCTGGGCAT
                                        DB 19;
                                      tch 49.2%; Score 434.6; DB 19; al Similarity 79.9%; Pred. No. 1.6e-110; 512; Conservative 0; Mismatches 129;
  C; 389 G; 241
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237 A;
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Best Local S.
Matches 512
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The present invention describes Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-1 have homology to connective tissue growth factor (CTGF). Products from the present invention can be used to treat WISP-related disorders such as breast, ovarian, and colon cancer or melanoma. The products can be used to treat atteriosclerosis. The products can also be used to treat other diseases e.g. benign and malignant tumours, leukaemia and lymphoid malignancies, neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial stromal, and blastocoelic disorders, desmoplasia, fibrotic lesions, kidney disorders, and other wounds, connective tissue disorders, catabolic states, testicular-related disorders, and inflammatory, anglogenic and immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The products can be used to transgenic or knock-out animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 CAGCCCGGGGCAGGACCCGGTGGCCGGGGGCCCTGTGCCTCTTGGCAGGACGACGACAGC 315
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                                                                                                                                                                                                                                                                 New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.2%; Score 434.6; DB 20; Length
79.9%; Pred. No. 1.6e-110;
Live 0; Mismatches 129; Indels
                                                                                                                                                                                 Hillan
                                                                                                                                                                                 Gurney AL, Hillan
Roy MA, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1293 BP; 232 A; 425 C; 393 G; 243 T; 0 other;
                                                                                                                                                                                                                                                                                         Example 4; Page 174-175; 284pp; English.
                                                                                                                                                                                Goddard A,
Pennica D,
                                                                                             98US-0081695
                                                                                                           97US-0063704.
                                                                  98WO-US22991
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                                                                                                                                                                                Cohen RL,
Levine AJ,
                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                      WPI; 1999-337420/28.
                                                                                                                                                                                                                                      P-PSDB; AAY17649
                                                                                                                                                                                Botstein DA,
Lawrence DA,
                                                                  29-OCT-1998;
                                                                                            14-APR-1998;
                                                                                                              29-OCT-1997;
03-FEB-1998;
                                      06-MAY-1999
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CGGCTGCCCAGCTGGGACTGCCCAAGGCCCCAAAGAAATACAGGTGCCAGGAAAGTGCTGC
                                                                                CACCAACTTTCTGCCCTTGTCACTCCTGCCTCTGCTGATGCTCCTTGTCCAAATTGGAGC
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Sequence 23, Appl
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APPLICANT Colon, Robert
APPLICANT Goddard, Audrey
APPLICANT Goddard, Audrey
APPLICANT Gurner
APPLICANT Gurner
APPLICANT Hillan, Kenneth J.
APPLICANT Lewine, Arnold J.
APPLICANT Lewine, Arnold J.
APPLICANT Pennica, Diane
APPLICANT Pennica, Diane
APPLICANT POY, MATGATER Ann
APPLICANT POY, MATGATER Ann
APPLICANT POY, MATGATER Ann
APPLICANT POY, MATGATER AND
APPLICANT POY, MATGATER POXPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1976R2
CURRENT APPLICATION NUMBER: US 60/063,704
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER PILING DATE: 1998-00-04
EARLIER PILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 CGCTCCTGATCTCCAGAGGACCCCGGGCTGGGACAGGGGCCTTGGCGAGGCTGCAGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 TG-GGCAGTGGCTTGGAATGGAGGTCTTTATTACTGGGAACTGAGGAGCTAAGAGGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACACCTTCGTGGTGGCCTCCACGGCCTCACCTTCAGGTTTGAAGCTGGCTCCACAAGGG
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Sequence 3; Ag
Sequence 3, Ag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 727.6; DB 4;
Pred. No. 1.2e-189;
0; Mismatches 59;
US-09-182-145-1
US-09-182-145-2
US-09-253-316-1
US-09-253-316-1
US-09-182-145-34
US-09-182-145-35
US-09-182-145-31
US-09-182-145-23
US-09-182-145-29
US-09-182-145-29
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1 US-09-103-840A-1
US-08-710-249-3
US-09-220-157A-3
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Patent No. 6387657
GENERAL INFORMATION:
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91.9%;
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Best Local Similarity 91.9
Matches 816; Conservative
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                    version 5.1.6 - 2003 Compugen Ltd.
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US-09-182-145-18
US-09-182-145-14
US-09-182-145-39
US-08-162-145-39
US-08-162-145-39
US-08-162-145-39
US-08-17-12-10
US-08-712-302-1
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Gapop 10.0 , Gapext 1.0
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; SEQ ID NO 18 ; LENGTH: 1734 ; TYPE: DNA ; ORGANISM: Mus musculus US-09-182-145-18	Query Match 82.4%; Score 727.6; DB 4; Length 1734; Best Local Similarity 91.9%; Pred. No. 1.2e-189; Matches 816; Conservative 0; Mismatches 59; Indels 13; Gaps 4	QY         3 CGCTTCTGATCTC@AGAGCCCTGGGGTGGGACAGGGCCTTGGCAAGGCTGCAGCCG 62	Qy         63 TG-GGCAGTGGCTTGGBATGGAGGTCTTTATTACTGGGAACTGAGGAGCTAAGAGGCTCC 121	Qy 122 TGTCAGCTTGTCCTAAAGTCTTAGCACTTGTGGTGGCTTCACACACTGTCA 178	Qy         179 GACACCTTCGTGGTGGCCTCCACGCCTCACCTTCAGGTTTGAAGCTGGCTCCACAAGGG 238	Oy 239 ACACGGTGACATGAGGGCAGCCCACTGATCCATCTTCTGGCCACTTCCTTC	Qy 299 TCTCTCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACC 358	Qy 359 CCAGIGCCCACAGGGGTACCCCIGGTGCTGGATGGCTGCTGTAAAGTGTGC 418	Qy         419 ACGGAGGCTGGGGGAGTCCTGCGACCATGTTCTGCGACCCCAGCCAG	Qy         479 TTGTCAGCCTGGGGRAGGCCCTGGCGGCCTGGGGCTGTGTGTCTTGGATGAGATGA 538	Oy 539 CGGTAGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGA	Oy 599 CAGGGTCCTGTGCTGATGACGGTGGCTTCACCTGCCGCTGTGCAGTGAGGA 658	Oy 659 TGTGCGGCTGCCCAĞCTGGGACTGCCCCAGGCCCCAAGAGAATACAGGTGCCAGGAAAGTG 718 11111111111111111111111111111111111	Oy 719 CTGCCCCAGTGGGTATGTGACCAGGGAGTGACACCGGGATCCAGGGCTCCAGGGC 775   111111111111111111111111111111111	QY 776 GCAAGGACACCAACTTCTGCCCTTGTCACTCTCTCTCTGCTGATGCTCTTGTCCAAA 835	Qy 836 TTGGAGCACAGCCTGGGGCCCTGCTGTAACCACCTGTGGGCTGGGCAT 883	RESULT 3 US-09-182-145-13
Db 193 GACACCTTCTTGGTGGCCTCCTCGGCCTCAGGTTTGAAGCTGGCTCCACAAGGG 246  Qy 239 ACACGGTGACATGAGGGCAGCCCACTGATCTTCTGGCCACTTCCTTC	Qy 299 TCTCTCAATGGTGTGCCCAGCTGTGCCGACACCCTGTACCTGTGCACACCACC 358	Qy 359 CCAGTGCCCACAGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTAAAGTGTGTGC 418	Qy         419 ACGGAGGCTGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGGCCTGGT 478	Qy 479 TIGICAGCCIGGGCAGGCCCTGGCGGCCATGGGGCTGTGTGTCTCTTGGATGAGGATGA 538	Qy 539 CGGTAGCTGTGAGTGAATGCCCGCAGGTACCTGGATGGAGACCCTTTAAACCCAATTG 598	Oy 599 CAGGTCTGTGCCGCTGTGACGTGGCTTCACCTGCCTGCCGTGTGCAGTGAGGA 658	Oy 659 IGTGCGGCTGCCCAGCTGGCCCCCCCCAAGAGAATACAGGTGCCAGGAAAGTG 718	Oy 719 CIGCCCGAGTGGGTATGTGACCAGGGAGTGACACCGGGGATCCAGGGGTCCAGGGC 775	Qy 776 GCAAGGACACCAACTTTCTGCCCTTGTCACTCCTGCTGTGTGTTGTTCTTGTCCAAA 835	Qy         836         TIGGAGCACCAGCCCCTGCTCAACCACCTGTGGGCTGGGC	RESULT 2 US-09-182-145-18/c ; Sequence 18, Application US/09182145B	Patent No GENERAL I APPLICAN	APPLICAN APPLICAN APPLICAN	APPLICANT: Levine, Arnold J. APPLICANT: Pennica, Diane APPLICANT: ROy, Margaret Ann APPLICANT: Noy, Margaret Ann APPLICANT: UCAG William I	TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME; FILE REFERENCE: P1176R2; CURRENT APPLICATION NUMBER: US/09/182,145B	CORRENT FILLNO LDATE: 1299-110-29  EARLIER APPLICATION NUMBER: US 60/063,704  EARLIER FILLNO DATE: 1997-10-29  EARLIER APPLICATION NUMBER: US 60/073,612	; BARLIER FILING DATE: 1998-02-04 ; BARLIER APPLICATION NUMBER: US 60/081,695 ; BARLIER FILING DATE: 1998-04-14 ; NUMBER OF SEQ ID NOS: 156

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1218 TCAAAGGTGCGTACCCAGCTGTGCCCACACCATGTACCTGCCCCTGGCCACCTCCCCGA
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                                                                                                                                                                                         APPLICANT: Botstein, David A.
APPLICANT: Cohen, Robert
APPLICANT: Cohen, Robert
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Levine, Arnold J.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
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                                        Score 434.6; DB 4;
Pred. No. 1.3e-109;
); Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT PELICATION NUMBER: US/09/182,145B;
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-04-14
                                                                                                                                       ; Sequence 14, Application US/09182145B; Patent No. 6387657; GENERAL INFORMATION:
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Best Local Similarity
Matches 512; Conserv
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                                                                                                                                                                                                                                 SAME
                                                                                                                                                                                                                                 ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1293;
                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOSTSEIN, David A.
APPLICANT: COHON, Robert
APPLICANT: COHON, Robert
APPLICANT: Garney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lewine, David A.
APPLICANT: Lewine, Arnold J.
APPLICANT: Lewine, Arnold J.
APPLICANT: Denica, Diane
APPLICANT: Denica, Diane
APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Bood, William I.
TILE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCO
FILE REFERNCE: P1176R2
CURRENT FILING NETE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1998-10-29
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-04-14
NUMBER OF EXQ ID NOS: 156
SEQ ID NO 13
LENGTH: 1293
LENGTH: 1293
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Pred. No. 1.3e-109;
0; Mismatches 129;
3, Application US/09182145B 6387657
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llarity 79.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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512; Conserv
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   Sequence 13,
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Matches 512
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APPLICANT: Cohen, Robert
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, Dayld A.
APPLICANT: Lawrence, Dayl
TGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGCCCCGAGTGGGTATGTGAC
                                                                                                                                                                                      GGCGATCCAGCGCTCCACGCGCAAGGACACCAACTTCTGCCCTT
                                                                                                                                                                                                                                 SGGGACCCAGCCCTTCCAGCCCAAGGACCCCAGTTTTCTGGCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.6%; Score 420.6; DB 4;
79.6%; Pred. No. 7.5e-106;
ave 0; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1-841 OTHER INFORMATION: Sequence is synthesized tent No. 6387657
                                                                                                                                                                                                                                                                                                                                                                                                   SCTGGGCAT 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39, Application 0S/09182145B Patent No. 6387657
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ORGANISM: Artificial séquence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 510; Conservative
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                                                                                                                                                                                                                                                                                    GTCACTCCTGCCTG
                                                                                                                                      421 TGCCCCCACCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-09-182-145-39
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US-09-182-145-39
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Botstein, David A.
APPLICANT: Cohen, Robert
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Lawrence, David A.
APPLICANT: Pennica, Diane
APPLICANT: Pennica, Diane
APPLICANT: ROY, Margaret Ann
APPLICANT: ROY, Margaret Ann
APPLICANT: ROY, Margaret Ann
APPLICANT: WOO, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILER REPERENCE: PI176R2
CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER PILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GACCAACTCCACGTCTGCGACGCCAGCCCAGGCCTGGTCTGCCAGCCCGGGCAGGACCC
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                                                                                           CACCAACTITCIGCCCTIGICACTCCTGCCTCTGCTGAIGCTCCTTGTCCAAATIGGAGC
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Pred. No. 1.6e-106;
0; Mismatches 125; Indels
                                                                                                                                                                                                         ACGCCTGGGGACCCTGCTCGACCACCTGTGGGCTGGGCAT 638
                                                                                                                                                                                         ACAGCCTGGGCCCCTGCTCAACCACCTGTGGGCTGGGCAT 883
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79.9%;
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Best Local Similarity 79.99
Matches 498; Conservative
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; ORGANISM: Homo sapiens
US-09-182-145-38
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542 TAGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGCCTTTAAACCCAATTGCAG 601
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APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                 Score 128.4; DB 1;
Pred. No. 7.7e-26;
0; Mismatches 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-386-680-1
; Sequence 1, Application US/08386680
Patent No. 5585270
; GENERAL INFORMATION:
                                                                                                                                                                                 14.5%;
52.2%;
                                                                                                                                                                                 Query Match 14.5
Best Local Similarity 52.2
Matches 338; Conservative
                                            MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: DB60R32
FEATURE:
                                                                                                                                 130..1177
   nucleic acid
        STRANDEDNESS: SIN
                                                                                                                               ; LOCATION:
US-08-167-628-1
                                                                                                                 NAME/KEY:
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126 TGCCCGCTGGGAGTACCCCTGGTGGTGGATGGCTGTGGCTGCTGCCGGGTATGTGCACGG 185
                                                                                                CAGCCTGGGGCAGGCCCTGGCGCCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGGT
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                               Sequence I, Application US/08167628
Patent No. 5408040
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Spensley Horn Jubas & Lubitz
4225 Executive Square, Suite 1400
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REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/752,427
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STREET: 422.
TTW: La Jolla
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   CCCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCAAGG 781
                                                         672 TTACCGACTGGAAGACACGTTTGGCCCAGACCCAACTATGATTAGAGCCAACTGCCTGGT 731
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                                                                                                                                                                                                                                            732 ccagaccacagagiggagcgccigirccaagaccigigggargggcar 779
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APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
WUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS;
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92037
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PCP-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,717
FILING DATE: 02-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUBBER:
FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: WETHERLI, Jr. FP.D., John W.
REGISTRATION NUMBER: 31,678
TREECHOLY COCKET NUMBER: PD-1294
TREECHONUNICATION INFORMATION:
TELEPHONE: 619-455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08459717
Patent No. 5770209
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MOLECULE TYPE: CDNA
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CLONE: DB60R32
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US-08-459-717-1
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                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,680
FILING DATE: 10-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph. D., John W.
REGISTRATION NUMBER: 31,678
REPRENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: DUCLIEC acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 52.2*
Matches 338; Conservative
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STRANDEDNESS: single
                                                      COMPUTER READABLE FORM:
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; LOCATION: 130..1177
US-08-386-680-1
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MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: DB60R32
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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-rhes 301;
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Pred. No. 7.7e
0; Mismatches
                                                                            PD-1294
RESULT 11
US-08-880-031-1
'Sequence 1, Application US/08880031
'Patent No. 5916756
'GENERAL INFORMATION:
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Best Local Similarity 52.2%;
Matches 338; Conservative
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130..1177
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CLONE: DB60R32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
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                                             195 GCCGGCCGTCGGCCAGAACTGCAGCGGGCCGTGCCGGTGCCCGGACGAGCCGGCGCCGCG 254
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Patent. No. 5783187
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
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NAME: Wetherell, Jr. Ph.D., John W.
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APPLICATION NUMBER: US/08/167
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FILING DATE: 11.5EP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,680
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APPLICATION NUMBER:
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US-08-712-302-1
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          732 CCAGACCACAGAGTGGAGCGCCTGTTCCAAGACCTGTGGGATGGGCAT 779
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APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS.
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APPLICATION NUMBER: US/09/097,179
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STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
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REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
INFORMATION FOR REQ ID NOG 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
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APPLICATION UNDBER: US 08/386,680
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US/08/167,628
FILING DATE:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PCFDOS/MS-
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
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US-09-097-179-1
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MOLECULE TYPE:
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Pred. No. 7.7e-26;
0; Mismatches 301; Indels
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
UNDBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,031
                                                                                                                                                                       E: Spensley Horn Jubas & Lubitz 4225 Executive Square, Suite 1400
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REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION:
TELEPHONE: 619-455-5100
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APPLICATION NUMBER: US/08/167,628
FILING DATE:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 52.2%;
Matches 338; Conservative (
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; LOCATION: 130..1177
US-08-880-031-1
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CITY: La Jolla
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                                                                                                             CTCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCACAA 361
                                                                                                                                      GTGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTGAAAGTGTGTGCACG 421
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                              Gaps
Length 2075;
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APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
WUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  DB 3;
Score 128.4; DB 3;
Pred. No. 7.7e-26;
0; Mismatches 301;
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STREET: 4225 Executive Square, Suite 1400
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Patent No. 6190884
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 14.5%;
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              Similarity
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Matches 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTAAAGTGTGTGCACG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432 TCCCTGCATCTTCGGTGGTACGGTGTACCGCAGCGGAGAGTCCTTCCAGAGCAGCTGCAA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGCGCAAGG 781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 GCAGCTGGGCGAGCTGTGCAGCGCGACCCCTGCGACCGCGCACCGCACAAGGGCCTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 TGACTTCGGCTCCCCGGCCAACCGCAAGATCGGCGTGTG---CACCGCCAAAGATGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542 TAGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAAACCCAATTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 128.4; DB 4
Pred. No. 7.7e-26;
                                                                                                        NAME: Wetherell, Jr. Ph.D., John W. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-510
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                   FILING DATE:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
                   US/08/167,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.5%;
52.2%;
                                                                                            ATTORNEY/AGENT INFORMATION
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PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
130..1177
                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY:
; LOCATION:
US-09-080-715-1
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671
    662 GCGGCTGCCCAGCTGGGCACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTG 721
                                                                                                                                                                                     552 TCGTCTGCCCAGCC@TGACTGCCCCTTCCCGAGGGGTCAAGCTGCCCGGGAAATGCTG 611
                                                                                                                                                                                                                             CCCCGAGTGGGTAT@TGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCAAGG 781
                                                                                                                                                                                                                                                                                                           782 ACACCAACTITCTG©CCTTGTCACTCCTGCCTCTGC-----TGATGCTCCTTGTCCAAA 835
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                                                                                                                                                                                                                                                                                                                                                                                         836 TIGGAGCACCAĞGGCCCCTGCTCAACCACTGTGGGCTGGGCAT 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: University of South Florida
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE S.12
ADDRESSEE: FISH & RIGHARDSON P.C.
STREET: 4225 Execution Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 128.4; DB 5;
Pred. No. 7.7e-26;
0; Mismatches 301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US96/08140 FILING DATE: 30-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application PC/TUS9608140 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC*FODS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEX/AGENT INFORMATION:
NAME: Halle, b. b. b. b.sa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 52,2%;
Matches 338; Conservative
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SEQUENCE CHARACTERISTICS
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130..1177
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TOPOLOGY: 1:
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PCT-US96-08140-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGACTTCGGCTCCCCGGCCAACCGCAAGATCGGCGTGTG---CACCGCCAAAGATGGTGC 431
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                                                                                                                                                           APPLICANT: Lau, Lester F.
TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
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732 CCAGACCACAGAGTGGAGCGCCTGTTCCAAGACCTGTGGGGATGGGCAT 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
OTHER INFORMATION: "CTGF cDNA coding sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                  STATE: Illinois
COUNTRY: United States of America
ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
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Pred. No. 7.7e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28759/33766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/142,569
FILING DATE: 02-Apr-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                Sequence 7, Application US/09142569 Patent No. 6413735 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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52.2%;
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MOLECULE TYPE: DNA
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Matches 338; Conservative
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                                                                                                                                                                                                                                                                                    CITY: Chicago
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                                                                                US-09-142-569-7
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		Qy 302		Оу 362	Db 255	Qy 422	315	Qy 482		Oy 542										Qy 836	Db 732	

Search completed: July 28, 2003, 21:35:54 Job time : 52.24 secs

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July 28, 2003, 15:36:41; Search time 217.668 Seconds (without alignments) 8368.853 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                1439767 seqs, 1031500376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                        - nucleic search, using sw model
                                                                                                                                                                                                     US-10-010-408-1_COPY_1_883
                                                                                                                                                                                                                                                                                                             IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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length: 2000000000
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                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB s
Maximum DB s
                                                                                        OM nucleic
                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

(cgn2\_6/ptodata/2/pubpna/USO9\_NEW\_PUB.seq:\*
(cgn2\_6/ptodata/2/pubpna/USO9\_NEW\_PUB.seq:\*
(cgn2\_6/ptodata/2/pubpna/USO9\_NEW\_PUB.seq:\*
(cgn2\_6/ptodata/2/pubpna/USO9\_NEW\_PUB.seq:\*
(cgn2\_6/ptodata/2/pubpna/USO9\_PUBCOMB.seq:\*
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(cgn2\_6/ptodata/2/pubpna/USO9\_PUBCOMB.seq:\*
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(cgn2\_6/ptodata/2/pubpna/USO0\_PUBCOMB.seq:\*
(cgn2\_6/ptodata/2/pubpna/USO0\_PUBCOMB.seq:\*
(cgn2\_6/ptodata/2/pubpna/USO0\_PUBCOMB.seq:\*
(cgn2\_6/ptodata/2/pubpna/USO0\_PUBCOMB.seq:\*

	Description	Sequence 1, Appli	Sequence 17, Appl	18,	3,	12	30,	Sequence 14, Appl	Sequence 319, App	319,	Sequence 319, App						
SUMMARIES	ΠD	US-10-010-408-1	US-10-112-267-17	US-10-112-267-18	US-10-010-408-3	US-10-010-408-12	US-09-915-582-30	US-09-915-582-14	US-10-137-866-319	US-10-146-726-319	US-10-146-727-319	US-10-146-788-319	US-10-152-380-319	US-10-153-934-319	US-10-028-072-319	US-10-121-049-319	US-10-123-904-319
	80	15	15	15	15	15	11	11	14	14	14	14	14	14	15	15	15
	Query Match Length DB	1708	1734	1734	753	681	1337	1352	1266	1266	1266	1266	1266	1266	1266	1266	1266
ф	Query Match	100.0	82.4	82.4	71.9	64.1	49.8	49.8	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2
	Score	883	727.6	727.6	635	266	440	439.8	434.6	434.6	434.6	434.6	434.6	434.6	434.6	434.6	434.6
	Result No.	7	7	с С	4	γ	9	7	80	O	10	11	12	13	14	15	16

Sequence 319, App Sequence 319	319, 319,
US-10-140-470-319 US-10-175-746-319 US-10-175-746-319 US-10-137-865-319 US-10-137-865-319 US-10-140-474-319 US-10-142-413-319 US-10-142-413-319 US-10-142-419-319 US-10-142-419-319 US-10-142-419-319 US-10-121-050-319 US-10-121-050-319 US-10-121-051-319 US-10-123-261-319 US-10-123-261-319 US-10-123-261-319 US-10-123-261-319 US-10-123-261-319 US-10-123-261-319 US-10-123-261-319 US-10-123-261-319 US-10-123-261-319 US-10-123-28-319 US-10-123-38-319 US-10-123-38-319 US-10-123-38-319 US-10-123-38-319 US-10-123-38-319 US-10-123-38-319 US-10-123-38-319 US-10-123-38-319 US-10-123-38-319 US-10-123-38-319	-10-124-824-31 -10-127-825A-3
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11112222222222222222222222222222222222	44 45

## ALIGNMENTS

RESULT 1

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Sequence 1, Application US/10010408
Publication No. US20020165185A1
GENERAL INFORMATION:
APPLICANT: John J. Castellot, Jr.
APPLICANT: John US20020165185Alel Heparin-Induced CCN-Like Molecules and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFICATION: <university Country of the control of the country of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREFT: 28 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/044,273
FILING DATE: March 19, 1998
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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TELEFAX: (617)742-4214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 13
US-10-010-408-1
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TGTCAG---CTTGTCCTAAAGTCTTAGCACTTGTGGTGGCTTGGGCTTCACACACTGTCA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 CGCTCCTGATCTCCAGAGGACCCGGGCTGGGACAGGGGCCTTGGCGAGGCTGCAGCTGC 72
                                                                                                                                       APPLICANT: GUUTEN, AUSTIN.
APPLICANT: GUTEN, AUSTIN.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lavine, Arnold J.
APPLICANT: Lavine, Arnold J.
APPLICANT: Lavine, Arnold J.
APPLICANT: Lavine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: ROY, Margaret Ann
APPLICANT: ROY, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: PIJ662
CURRENT FILING DATE: 2002-03-27
CURRENT FILING DATE: BARLIER FILING DATE: 1998-10-29
PRIOR FILING DATE: BARLIER FILING DATE: 1998-02-04
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
PRIOR FILING DATE: BARLIER FILING DATE: 1998-02-04
PRIOR FILING DATE: BARLIER FILING DATE: 1998-02-04
PRIOR FILING DATE: BARLIER FILING DATE: 1998-04-04
PRIOR FILING DATE: BARLIER FILING DATE: 1998-02-04
PRIOR FILING DATE: BARLIER FILING DATE: 1998-02-04
PRIOR FILING DATE: BARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 TGTCAGGCTCCTGTCCTAAACTCTTGGCACTGGGGTGGCTTGGGCTTCACACTGTCA
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 841 GCACAGCCTGGGGCCCCTGCTCAACCACCTGTGGGCTGGGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 727.6; DB 15;
Pred. No. 6.2e-203;
0; Mismatches 59;
                                                                Sequence 17, Application US/10112267
Publication No. US20030068678A1
GENERAL INFORMATION:
APPLICANT: Botstein, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.4%;
llarity 91.9%;
Conservative
                                                                                                                       Cohen, Robert
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mus musculus US-10-112-267-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 816; Conserv
                                                    US-10-112-267-17
                                                                                                                                  APPLICANT:
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                                                                                                                                             Length 1708
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                                                                                                                                           Query Match 100.0%; Score 883; DB 15; Best Local Similarity 100.0%; Pred. No. 2.2e-248; Matches 883; Conservative 0; Mismatches 0;
                                                                                  COCATION: 249..1001
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-010-408-1
 pairs
            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
LENGTH: 1708 base
                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                         61
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TITLE OF INVENTION: No. US20020165185A1el Heparin-Induced CCN-Like Molecules and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1662 TGTGGCAGTAGCTTGGGATGGAGGTCTTTCTTGCTGGGAACTGAGGAGCTGAGAGGTCC 1603
                                                                                                               1068 TGTGCGGCTGCCCAGGACTGCCCACGCGCCAGGAATACAGGTGCCAGGAAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAAGGACACCAACTTTCTGCCCTTGTCACTCCTGCATCTGCCGATGGCCCTGTCCCAAA
                                479 TTGTCAGCCTGGGGCAGGCCCTGGCGGCCATGGGGCTGTGTGTCTCTTGGATGAGGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1188 CGGGAGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGGGAGACCTTTAAAACCCAATTG
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Publication No. US20020165185A1
GENERAL INFORMATION:
APPLICANT: John J. Castellot, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: LAHIVE & COC
STREET: 28 State Street
CITY: Boston
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COUNTRY: USA
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                              TTGTCAGCCTGGGGCCCCCAGTGGCCGTGGTGCTGTGTGCCTCTTCGAAGAGGATGA
                                                                                 CTGCCCCGAGTGGGTATGTGACCAGGGAGTGA---CACCGGCGATCCAGGCTCCACGGC
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TTGTCAGCCTGGGGCAGGCCCTGGGGGCCATGGGGCTGTGTGTTTGGATGAGGATGA
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Sequence 18, Application US/10112267
Sequence 18, Application US/20030068678A1
SEBERAL INFORMATION:
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Lawrence, David A.
APPLICANT: Lawrence, David A.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Malliam I.
APPLICANT: Roy, Malliam I.
APPLICANT: Roy, Malliam I.
APPLICANT: Roy, Malliam I.
APPLICANT: Roy, Mulliam I.
APPLICANT: Roy, Wangeret Expression NUMBER: US/10/112,267
CURRENT FILING DATE: EARLER FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: EARLER APPLICATION NUMBER: US 60/01
PRIOR APPLICATION NUMBER: EARLER FILING DATE: 1998-10-29
PRIOR FILING DATE: EARLER FILING DATE: 1998-02-04
PRIOR FILING DATE: EARLER FILING DATE: 1998-02-04
PRIOR FILING DATE: EARLER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
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816; Conserv
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US-10-112-267-18/c
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LENGTH: 1734
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Matches 81
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Sequence 12, Application US/10010408
Publication No. US20020165185A1
GENERAL INFORMATION:
APPLICANT: John J. Castellot, Jr.
TITLE OF INVENTION: No. US20020165185Alel Heparin-Induced CCN-Like Molecules
 318 CAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCCCCAGTGCCCACAGGGGGTA 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT PATENTION DATA:
APPLICATION NUMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION OF APPLICATION OF APPLICATION NUMBER: 09/044,273
FILING DATE: March 19, 1998
APPLICATION NUMBER: CUNKNOWN>
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                           601 TGGGGCCCCTGCTCAACCACCTGTGGGCTGGGCAT 635
                                                       849 TGGGGCCCCTGCTCAACCACCTGTGGGCTGGGCAT
                                                                                                                                                                                                                                                                                                                            ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
                                                                                                                                                                                                                                                                      and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..681
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 681 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: Massachusetts
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CORRESPONDENCE ADDRESS:
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LOCATION:
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US-10-010-408-12
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Best Local S:
Matches 566
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                                   SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 71.9%; Score 635; DB 15; I
Best Local Similarity 100.0%; Pred. No. 6.6e-176;
Matches 635; Conservative 0; Mismatches 0;
                                                                                                                                 APPLICATION NUMBER: 09/044,273
FILING DATE: MATCH 19, 1998
APPLICATION NUMBER: cUnknown>
FILING DATE: CUnknown>
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPRAN: (617)227-7400
                                                                  APPLICATION NUMBER: US/10/010,408 FILING DATE: 07-Dec-2001 CLASSIFICATION: <Unknown>PRIOR APPLICATION DATA:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..750
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 753 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Qy 498 CCTGGCGCCATGGGGCTGTGTCTCTTGGATGAGGATGACGGTAGCTGTGAGGTGAAT 557	Db 181 CCTGGCGGCCATGGGGCTGTTTTTTTTTGATGATGAGGTGGTGTGTGT	Db 241 GGCCGCAGGTACTGGAGAGACCTTTAAACCCAATTGCAGGGTCCTGTGCGCCGCTGT 300 Qy 618 GATGACGGTGCTTCACCTGCCGCTGTGCAGGGTGCCGGCTGCCAGCTGG 677	Db 301 GATGACGGTGCCTTGCCTGCCGCTGTGCAGTGAGGATGTGCGGCTGCCCAGTGG 360	Qy 678 GACTGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGCCCCAGTGGGTATGT 737	Qy 738 GACCAGGGAGTGACACGGCGATCCAGGCGCTCCACGGCGCAAGGACACTTTCTGCC 797	798 CTTGTCACTCCTGCCTGTGATGCTCCTTGTCCAAATTGGAGCACCAGCGGGCCCC	Db 481 CTTGTCACTCCCTGCCTCTGCTCCTTGTCCAAATTGGAGCACAGCCTGGGGCCCC 540	Qy         858 TGCTCAACCACCTGTGGGCTTGGGCAT 883	D COLLLES C	08-09-915-582-30 ; Sequence 30, Application US/09915582	ո ն	APPLICANT: Rosen et al.  TITLE OF INVENTION: 17 Human Secreted Proteins FILE REFERENCE: PS72391  CURRENT APPLICATION NUMBER: US/09/915,582	PRIOR FILING DATE: 2001-01		PRIOR FILING DATE: 2000-03		SEQ ID NO 30 LENGTH: 1337			; COTHER INFORMATION: n equals a,t,g, or c US-09-915-582-30	49.8%; Score 440; DB 11; Length 1337; 78.3%; Pred. No. 8e-119;	196		6	54 GCACACCGAAGACCCACCTCCTGGCCTTCTCCCTCTCTCT	QY 316 CCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCCCCCAGTGCCCACAGGGGG 375

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C151
CURRENT APPLICATION NUMBER: US/10/137,866
CURRENT FILING DAIE: 2002-05-03
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Publication No. US20030129689A1
GENERAL INFORMATION:
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303 TCAATGGTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAG 483 CAGCCTGGGGCAGGCCCTGGCGGCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGGT 543 AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGCCCTTTAAACCCAATTGCAGG CACCAACTITICTGCCCTTGTCACTCCTGCTGTTGTTGTTGTTGTTGGAGC CGGCTGCCCAGCTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGC CCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGCGCGCAAGGA Gaps Length 1266; ö Indels DB 14; 49.2%; Score 434.6; DB 14; 79.9%; Pred. No. 3e-117; ative 0; Mismatches 129; PRIOR FILLING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 66/08810
PRIOR PLING DATE: 1998-06-10
PRIOR PLING DATE: 1998-06-11
PRIOR PLING DATE: 1998-06-11
PRIOR PAPLICATION NUMBER: 66/08953
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 66/08997
PRIOR PILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-18
PRIOR PLING DATE: 1998-06-19
PRIOR PLING DATE: 1998-06-19
PRIOR PAPLICATION NUMBER: 60/09049
PRIOR PLING DATE: 1998-06-24
PRIOR PAPLICATION NUMBER: 60/09045
PRIOR PLING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-26
PRIOR PLING DATE: 1998-06-26
PRIOR PLING DATE: 1998-06-27
PRIOR PLING DATE: 1998-07-01
PRIOR PLING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-07
PRIOR PLING DATE: 1998-07-07
PRIOR PLING DATE: 1998-07-07 APPLICATION NUMBER: 60/088741 Conservative Similarity 512; 424 723 783 Query Match Best Local Matches q g ò a 셤 ò 임 ò g ò g g ŏ à ò ò ò

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TGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTGTAAAGTGTGTGCACGG
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79.9%; Pred. No. 3e-117;
:1ve 0; Mismatches 129; Indels
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Publication No. US20030129691A1
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Filvaroff, Ellen
Gao, Wel-Qiang
Gerritsen, Mary E.
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Godowski, Paul J
Gurney, Austin L
Sherwood, Steven
Sinith, Victoria
Stewart, Timoghy A
Tumas, Daniel
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Matches 512; Conservatiĝe
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APPLICANT: Beresini, Maura
APPLICANT: DeForge, Laura
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ORGANISM: Homò Sapien
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R16308
CURRENT APPLICATION NUMBER: US/10/146,726
CURRENT FILING DATE: 2002-05-15
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3e-117;
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           CURRENT FILING DATE: 2002-05-15
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
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Pred. No. 3e-
                                                                                                          Sequence 319, Application US/10146726 Publication No. US20030129690A1 GENERAL INFORMATION:
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Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel.
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Flyaroff, Ellen
Gao, Wei-Olang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Peul J.
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Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Best Local Similarity 79.9
Matches 512; Conservative
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ORGANISM: Homo Sapien
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    64 TCAAAGGTGCGTACCCAGCTGTGCCCGACACCATGTACCTGCCCCTGGCCACCTCCCCGGA 123
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                                       CCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGGGCTCCACGGCGCAAGGA
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C397
CURRENT APPLICATION NUMBER: US/10/152,380
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                              TGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGTAAAGTGTGTGCACGG
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NUMBER OF SEQ ID NOS: 550
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith Victoria
Stewart, Timothy A.
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Wood, William
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Filvaroff, Ellen
Gao, Wei-Qiang
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US-10-152-380-319
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                                                       AGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGCCTTTAAAACCCAATTGCAGG
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Abang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C322
CURRENT APPLICATION NUMBER: US/10/146,788
CURRENT FILING DATE: 2002-05-15
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Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
Goddard, Audrey
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
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Filvaroff, Ellen
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ORGANISM: Homo Sapien
US-10-146-788-319
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TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C4412 CURRENT APPLICATION NUMBER: US/10/153,934 CURRENT FILING DATE: 2002-05-22 Prior Application removed - See file Wrapper NUMBER OF SEQ ID NOS: 550 LENGTH: 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 319, Application US/10028072
Publication No. US20030004311A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Flvaroff, Ellen
APPLICANT: Gao, Mai-Oiang
APPLICANT: Gerittsen, Mary E.
                                                                                                                                    tch 49,2%;
al Similarity 79,9%;
512; Conservative (
                                                                                          ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-153-934-319
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US-10-028-072-319
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Best Local S:
Matches 512,
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OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
                                     Gaps
               Length 1266;
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                                    Indels
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            Score 434.6; DB 14;
Pred. No. 3e-117;
0; Mismatches 129;
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Publication No. US20030129695A1
GENERAL INFORMATION:
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DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
            49.2%;
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Stewart, Timothy A.
Tumas, Daniel
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Wood, William
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                                    Matches 512; Conservative
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                        Similarity
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or Palm
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Pred. No. 3e-117;
0; Mismatches 129;
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R APPLICATION NUMBER: 60/065186
R FILING DATE: 1997-11-12
R PELLING DATE: 1997-11-17
R APPLICATION NUMBER: 60/066364
R FILING DATE: 1997-11-21
R R PELLING DATE: 1997-11-21
R APPLICATION NUMBER: 60/066453
R FILING DATE: 1997-11-24
                                                                                                                                                                                                                                                                                                                                       A APPLICATION NUMBER: 60/072320
R FILING DATE: 1998-01-23
A APPLICATION NUMBER: 60/073612
R APPLICATION NUMBER: 60/074086
R FILING DATE: 1998-02-09
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PPLICATION NUMBER: 60/083545
ILING DATE: 1998-04-29
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FILING DATE: 1997-12-11
APPLICATION NUMBER: 60/069694
FILING DATE: 1997-12-16
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FILING DATE: 1998-02-27
APPLICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/081818
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082999
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FILING DATE: 1997-11-24
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FILING DATE: 1997-12-11
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FILING DATE: 1998-02-09
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FILING DATE: 1998-03-12
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FILING DATE: 1998-04-09
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FILING DATE: 1998-04-09
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APPLICATION NUMBER: 60/083322
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FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/085149
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APPLICATION NUMBER: 60/085323
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APPLICATION NUMBER: 60/085579
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APPLICATION NUMBER:
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                CURRENT APPLICATION NUMBER: US/10/028,072 CURRENT FILING DATE: 2001-12-19 FRICN APPLICATION NUMBER: 60/049911 PRIOR FILING DATE: 1997-06-18 PRIOR APPLICATION NUMBER: 60/056974
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APPLICATION NUMBER: 60/059115
FILING DATE: 1997-09-17
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APPLICATION NUMBER: 60/063329
FILING DATE: 1997-10-27
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APPLICATION NUMBER: 60/059113
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FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059122
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APPLICATION NUMBER: 60/062250
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APPLICATION NUMBER: 60/062285
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APPLICATION NUMBER: 60/062287
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APPLICATION UNMBER: 60/063082
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APPLICATION NUMBER: 60/063127
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APPLICATION NUMBER: 60/063327
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                                                            Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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Wood, William
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                Sodowski, Paul J. Surney, Austin L.
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                                                Sherwood, Steven
Goddard, Audrey
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND ITITLE OF INVENTION: ACTOS ENCODING THE SAME
FILE REFERENCE: P3330R1617
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
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llarity 79.9%; Pred. No. 3e-117;
Conservative 0; Mismatches 129;
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Publication No. US20030022239A1
GENERAL INFORMATION:
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Filvaroff, Ellen
Gao, Wei - Olang
Gerritsen, Mary
Goddard, Hodiey
Goddard, Hodiey
Gurney, Austin L.
Sherwood, Stewen
Smith, Victoffla
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Stewart, rimmethy A.
Tummas, Daniell
Watanabo, Collin K
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Pred. No. 3e-117;
0; Mismatches 129; Indels
R APPLICATION NUMBER: 60/085697
R PILING DATE: 1998-05-15
A APPLICATION NUMBER: 60/085704
R FILING DATE: 1998-05-15
R FILING DATE: 1998-05-17
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R APPLICATION NUMBER: 60/086430
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R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089907
R FILING DATE: 1998-06-18
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FILING DATE: 19/98-06-11
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APPLICATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/091360
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APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
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FILING DATE: 1998-07-07
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E. (Dasses I to 1058)

I. (Dasses I to 1058)

I. Onpublished (1999)

Contact: Robert Strausberg, Ph.D. Email: capapbs-rémail.nih.gov
Tissue Procurement: Invitrogen

CONA Library Preparation: Life Technologies, Inc.

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Location/Qualifiers

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AGENCOURT_6490429 NIH_MGC_125 Homo saplens cDNA clone IMAGE:5725937
5', mRNA sequence.
                                                            HNC57-1-D
603185689
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BQ778961
BQ778961
BM751866
BM751866
BM751869
BG9000009
BM88499
BG900020
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828
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367.2
367.2
363.4
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349.6
335.8
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297.8
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223.6
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BQ937887 AGENCOURT
BQ279131 AGENCOURT
BQ07722 AGENCOURT
BM043988 603620978
BM921531 AGENCOURT
                                                                   July 28, 2003, 18:02:17; Search time 1565.76 Seconds (without alignments) 9133.322 Million cell updates/sec
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                                                                                                        Description
                                                                                                                                                                                                         32308132
         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                   16154066 seqs, 8097743376 residues
                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                                OM nucleic - nucleic search, using sw model
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BQ937887
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BQ073722
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                                                                                                                                                    IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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em_gss_other:*
em_gss_pro:*
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Maximum Match 100%
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em_gss_hum:*
em_gss_inv:*
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em_gss_fun:*
em_gss_mam:*
                                                                                                                                                                                                                                                                                                                                                                                          gb_est1:*
gb_est2:*
gb_htc:*
gb_est3:*
gb_est4:*
gb_est5:*
em_estfun:*
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length: 2000000000
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48.2
47.5
46.8
45.4
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429.2 425.8 419.8 413 400.6

Score

Result No.

Minimum DB seq Maximum DB seq

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Database

Scoring table:

Searched:

Perfect score:

Run on:

sequence:

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Local Similarity
les 488; Conserv
            house mouse
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                                             /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: Not1; RNA source pool of three ovaries, from females ranging in age from 36 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size angle 1.35 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036.
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BQ937887
BQ937887.1 GI:22353365
                                                                                                                                        2 others
                                                                                                                                                                                       0; Mismatches 133; Indels
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                                                                                                                                                                    DB 14;
                                                                                                                                                                  Score 429.2; DB 10
Pred. No. 3.7e-99;
                                                                                                                                       200 t
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/clone_lib="NIH_MGC_125"
/lab_host="DH10B"
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                       294 g
                                                                                                                                                                    48.68;
79.38;
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                                                                                                                                                                             al Similarity 79.3
509; Conservative
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Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (pases 1 to; 940)

RS NIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabs: femail.nih.gov

Tissue Procurement: The Cepko Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAM14017 row: n column: 21

High quality séquence stop: 543.

RES

1. 940

1. 940
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Ada_xxde="taxon:10090"

/clone="taxon:10090"

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llarity 90.9%; Pred. No. 2.6e-98;
Conservative 0; Mismatches 39;
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Fri Aug

g

628 372 688 808

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1. .1073
/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ Ab_Lerf="LaxAcn:9606"
/ Clone="Inb="NIH_MGC_101"
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/ Liseue_type="epidermoid carcinoma, cell line"
/ Lab_host="PDH10B (phage-resistant)"
/ Lab_host="DH10B (phage-resistant)"
/ Lab_host="DH10B (phage-resistant)"
/ Lab_host="DH10B (phage-resistant)"
/ Lab_host="DH10B (phage-resistant)"
/ Lab_host="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
/ Abol: CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/AhoI sites using the following 5' adaptor:
GGCACGAG(G) Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ073722 1073 bp mRNA linear EST 02-APR-2002
AGENCOURT_7046577 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:5806602
                                                                                                                                                                                432
                                                                                                                                                                                                                                                                                  493 GGGACTGGGGACCCCATCCCAGCCCAAGGACCCCAGTTTTCTGGCCTTGTCTTT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         809 TGCCTCTGCTGATGCTCCTTGTCCAAATTGGAGCACACAGCCTGGGGCCCCTGCTCAACCA 868
                                                                                                                                                                                                                                            CCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGCCCCGAGTGGGGTATGTGACCAGGGAGT 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     553 CCTGCCCCTGGTGTCCCCTGCCCAGAATGGAGCACGGCCTGGGGACCCTGCTGGACCAC 612
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2047 row: k column: 19
High quality sequence stop: 517.
Location/Qualifiers
                                                                                                                                                       749 GACACCGGCGATCCAGCGCTCCACGGCGCAAGGACACCAACTTTCTGCCCTTGTCACTCC
   569 CCTGGATGGAGAGCCTTTAAAACCCAATTGCAGGGTCCTGTGCCGCTGTGATGACGGTGG
                                  CTTCACCTGCCTGCCGCTGTGCAGTGAGGATGTGCGGGCTGCCCAGCTGGGACTGCCCACG
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Pred. No. 5.2e-95;
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80.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGTGGGCTGGGCAT 883
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BQ073722
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JOURNAL
COMMENT
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BQ073722
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/note="Organ: breast; Vector: poTB7; Site_1: poTB7; Si
                                                                                                        979 bp mRNA linear EST 07-MAY-2002
5', mRNA sequence.
BQ279131 GI:20489339
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-refmail.nih.gov
Tissue Procurement: Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2045 row: K column: 04

High quality sequence stop: 752.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGATGGCTGTGCTGTAAAGTGTGTGCACGGAGGCTGGGGGAGTCCTGCGACCACCT 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 CCAGGTCTGCGACGCCAGGCCTGGTCTGCCAGCCCGGGGCAGGACCGGTGGACG 252
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                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 979)
NIH-MGC http://mgc.ncl.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
GTTTGTCAGCCTGGGGCAGGCCCCAGTGGCCGTGGTGCTGTGTGCCTCTGTGCTANG 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 CCACCTCCTGGCCTTCTCCCTCTCTCTCTCTCAAAGGTGCGTACCCAGCTGTGCCC
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511
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BQ279131
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/db_xief="taxon:9606"
/clone="IMAGE:5446794"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 CCAGCCCGGGCAGGACCCGGTGGACGGGGGCCCTGTGCCTCTTGGCAGAGGACGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 CAGCTGTGAGGTGAACGGCCGCCTGTATCGGGAAGGGGAGACCTTCCAGCCCCAGCCCAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363 TGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGTAAAGTGTGTGCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 CGGTGGGGGGAGECCTGCGACCAACTCCACGTCTGCGACGCCATGCCAGGGCCTGGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     482 TCAGCCTGGGGCAAGCCCTGGCGCCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              542 TAGCTGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAACCCAATTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 45.4%; Score 400.6; DB 13; al Similarity 79.5%; Pred. No. 6.6e-92; 511; Conservative 0; Mismatches 129;
                                                                   sapiens"
  sequence stop: 714
                  Location/Qualifiers
1. 750
/organism="Homo sapi
  High quality
                                                                                                                                                                                                                                                                                                                                                                                    112
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NIH-MGC http://mgc.nci.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.linl.gov
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ACCESSION BM921531 VERSION BM921531.1 GI:19371910 VERSION BM921531.1 GI:19371910 KEYWORNS SOURCE ONGANISM Homo sapiens EUKATYOCE: Home. ORGANISM Homo sapiens EUKATYOCE: Marmalla; Eutheria; Primates; Catarrhin; Hominidae; Homo. AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Emall: cgapbs:r@mall.nih.gov Tissue Procurement: Life Technologies, Inc. COMMENT PROCUREMENT: Life Technologies, Inc.	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAMI2788 row.b column: 18 High quality sequence stop: 593. High quality sequence stop: 593. I. 1006 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="INDAGE:5753009" /clone="INDAGE:5	insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."  BASE COUNT 148 a 368 c 317 g 169 t 4 others  OUETY MATCH  OUETY MATCH  Best Local Similarity 78.7%; Pred. No. 7.6e-92;  MATCHES 489; Conservative 0; Mismatches 131; Indels 1; Gaps 1;  April		ATGGCCGCAGGTACCTGGATGGAGACCTTTAAACCCAATTGCAGGTCCTGTGCCGT

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: ATC.
GNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
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    /organism="Homo sapiens"
/db_xref="taxon:9606"

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/clone_lib="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_hest="high (phage-resistant)"
/lab_hest="high (phage-resistant)"
/note="forman pancreas; Vector: pOTB); Site_1: XhoI;
Site_2 EcorI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXAhoI sites using the following 5' adaptor: GCACGGG(6). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Califona, and Superscript II RT (Life Technologies).
Note: Ens is a NIH-MGC Library. |" Life Technologies).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheriå; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTAAAGTGTGTGGAGGCTGGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 391.8; DB 13;
Pred. No. 1.1e-89;
0; Mismatches 122;
/clone≱"IMAGE:5258159"
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ilarity 70.5%;
Conservative (
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161
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                                DEFINITION
                                                                                                                   ORGANISM
                                                                                                                                                                       AUTHORS
TITLE
JOURNAL
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ORIGIN
                                                           ACCESSION
                                                                                                                                                            REFERENCE
     BI161474
                                                                                       KEYWORDS
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                                                                                                                                                    Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
Plate: H4067 row. A column: 01
Seq primer: -21M13 Reverse
High quality sequence stop: 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 CAGACACCTICTIGGIGGCCTCCTCGGCC----TCAGGITTGAAGCTGGCTCCACAAG 297
1 (bases 1 to 537)
VanBuren,V., Plao,Y., Dudekula,D.B., Qian,Y., Carter,M.G., Martin,P.R., Stagg,C.A., Bassey,U., Alba,K., Hamatani,T., Kargul,G.J., Luo,A.G. and Ko,M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."
1 162 c 166 g 122 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                        Assembly, verification, and initial annotation of NIA 7.4K mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 CAGACACCTTCGTGGTGGCCTCCACGGCCTCACCTTCAGGTTTGAAGCTGGCTCCACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                              Contact: Yong Qian
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 14; Length 537;
                                                                                                                                                                                                                                                                                                                                         /clone="H4067A01"
/clone_lib="NIA Mouse 7.4K cDNA Clone Set"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.6%; Score 385.2; DB
llarity 92.1%; Pred. No. 5e-88;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                             /db_xref="niaEST:H4067A01-5"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                       1. .537
/organism="Mus musculus"
                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     /sex="mixed"
/dev_stage="mixed"
                                                                                                                                                                                                                                                                                               /strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                              /lab_host-"DH10B"
                                                                                    Unpublished (2002)
                                                                       cDNA clone set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 442; Conserv
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RESULT 10

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:5019065"
/clone=lib="MIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/tissue_type="epithelioid carcinoma pancreas; Vector: porm?; Site_1: XhoI;
Site_2: Eccns: pancreas; Vector: porm?; Site_1: XhoI;
Site_2: Eccns: pancreas; Vector: porm?; Site_2: Eccnsing the
following 5 adaptor: GGCAGGGGG(6). Site_selected >SODbp
for average insert size l Sikb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "Life Technologies).
BI161474 101-2001 928 bp mRNA linear EST 05-JUL-2001 602864871F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5019065 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 GGGGCCCTGTGCCTCTTGGCAGAGGACGACAGCTGTGAGGTGAACGCCCGCTGTA 381
                                                                                                                                                                                                                                             Chordata, Craniata, Vertebrata, Euteleostomi, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 GACACCCTGTACCTGTCCTTGGACACCACCCCAGGGCGCACAGGGGGTACCCCTGGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 GGATGGCTGTGCTGCCGGGTATGTGCACGGCGGCTGGGGGAGCCCTGCGACCT
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                                                                                                                                                                                                                                                                                                        1 (bases 1 to 928)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M. AG.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov m column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 374.6; DB 13; Length 928;
Pred. No. 3.3e-85;
0; Mismatches 134; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence start: 28
High quality sequence stop: 756.
Location/Qualifiers
                                                                                                                     BI161474.1 GI:14621475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 42.4%;
Best Local Similarity 77.7%;
Matches 478; Conservative
                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .928
                                                    mRNA sequence.
BI161474
                                                                                                                                                                                                                          Homo sapiens
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388

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 888)

I (contact: Robert Strausberg, Ph.D.

Email: Gapbs-rémail.nih.gov

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-rémail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CLONG distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC Clone distribution information can be http://image.llnl.gov

Plate: LLAMI1408 row: n column: 07

High quality sequence stop: 877.
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                                                                                                                                                                                                                                                                          194 CCACGTCTGCGACGCCA-GCCTGGTCTGCCAGCCCGGGGCAGGACCCGGTGGCCG 252
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                        CCATCTTCTGGCCACTTCCTTCTTCTCTCTCTCATGGTGTGTGCCCAGCTGTGCCG 328
                                                                                                                                                                                                                569 CCTGGATGGAGACCTTTAAACCCAATTGCAGGGTCCTGTGCCGCTGTGATGACGGTGG 628
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                                                                                                                                                                                                                                                                                                                                                      253 GGGGCCCTGTGCCTCTTGGCAGACGACGACGACGCTGTGAGGTGAACGCCCCCTGTA
                                              14 CCACCTCCTGGCCTTCTCCCTCTCTCTCTCTCTCAAAGGTGCGTACCCAGCTGTGCCC
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                                                                                                  GACACCCTGTACCTTGGACACCACCCCAGTGCCCACAGGGGGTACCCCTGGTGCT
                                                                                                                                                                                                                                                        GCATGTCTGCGACCCCAGCCAGGCCTGGTTTGTCAGCCTGGGGCAGGCCCTGGCGGCCA
                                                                                                                                                                                                                                                                                                                                  509 TGGGGCTGTGTGTCTCTTGGATGAGGATGACGGTAGCTGTGAGGTGAATGGCCGCAGGTA
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BI825652.1 GI:15937202
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                                      CTTCACCTGCCTGCCGCTGTGCAGTGAGGATGTGCGGCTGCCCAGCTGGGACTGCCCACG
                                                                                                              689 CCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGCCCCGAGTGGGTATGTGACCAGGGAGT
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Pred. No. 2.4e-83;
); Mismatches 124;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5169065"
/clone=lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
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Best Local Similarity 79.0
Matches 486; Conservative
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Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mac
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M.
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Primates; Catarrhini; Hominidae; Homo
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/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/note="Vector: pSPORT I; Site_1: SalI; Si
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709 Swedeland Road, P.O. Box 1539, King of
710 Swedeland Road, P.O. Box 1539, King of
721: 610-270-7245
Fax: 610-270-5598
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Pred. No. 4.4e-83;
); Mismatches 110;
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                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                         Email: sanjay_kumar-10gsk.com
Seq primer: T7.
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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HNC57-1-D9.R HNC (Human Normal Cartilage) Homo sapiens CDNA, mRNA
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                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="INAGE:5164614"
/clone=lib="NIH_MGC_119"
/tissue_type="medulia"
/lab_host="DH108"
  Location/Qualifiers
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AGENCORT_6492297 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5589134 57, mRNA sequence.
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    180 GACGCCAGCCA-GGCCTGGTCTGCCAGCCGGGGGCAGGACGGGGGGGGCCCTG 238
                                                                                                 239 TGCCTCTTGGCAGAGGACGACAGCAGCTGTGAGGGGAACGGCCGCTGTATCGGGAAGGG 298
                                                                                                                                                                                              299 GAGACCTTCCAGCCCCACTGCAGCATCCGCTGCCGCTGCGAGGAGGAGGCGGCTTCACCTGC 358
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Eukaryota: Metazoa: Chordata: Catarrhini; Hominidae: Homo.
1 (bases 1 to 1166)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capaba-riemail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Library Sequence and Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://mage.librarysequence.stop: 647.
High quality sequence stop: 547.
                                                                                                                                                                                                                                                                   639 CTGCCGCTGTGCAGTGAGGATGTGCGGCTGCCCAGCTGGGACTGCCCACGCCCCAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                539 GTGTGTCCCCTGCCCAGAATGGAGCACGCCTGGGGACCCTGCTCGA-CACCTGTGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        759 ATCCAGCGCTCCACGCGCGCAAGGACACCAACTTTCTGCCCCTTGTCACTCCTGCCTCTGCT
                                                                                                                                                                      579 GAGACCTTTAAACCCAATTGCAGGGTCCTGTGCCGCTGTGATGACGGTGGCTTCACCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xtef="taxon:9606"
/clone="IMAGE:5589134"
/clone_lib="NIH_MGC_125"
/lab_host="DH108"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: porpr; Site_l: XhoI;
Site_2: ECORI; CDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGGAGAGA(6). Size-selected 5800bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Gallfornia, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                           BI457367 916 bp mRNA linear EST 21-AUG-2001
603185689F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5258398 5',
    783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM180 row: a column: 23
High quality sequence stop: 778.
Location/Qualifiers
1. 918
Corganism="Hono sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5558398"
/clone="IMAGE:5558398"
/clone="IMAGE:5558398"
/clone="IMAGE:5558398"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 ACCTGTCCTTGGACACCACCCGGTGCCCACGGGGGTACCCCTGGTGCTGGATGCTGT 398
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                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 916)

N'H-MGC http://mgc.nci.nih.gov/

NH-MGC http://mgc.nci.nih.gov/
Uppublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
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                        CCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCAAGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTGCTGTAAAGTGTGTGCACGGAGGCTGGGGGAGTCCTGCGACCACCTGCATGTCTGC
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Pred. No. 2.4e-82;
0; Mismatches 122; Indels 4;
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                                                                                                                                                                                                                                                                                                                               369 CCGGGTATGTGCACGCGCGCTGGGGACCCTGCGACCAACTCCACGTCTGCGACCCCA 428
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constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036." $^{\prime\prime}$ 424 c 315.g 207 t 4 others
                                                                                        9; Gaps
                                                               DB 13; Length 1166
                                                            Score 361.2; DB 13; Length
Pred. No. 9.9e-82;
0; Mismatches 114; Indels
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                                                            40.9%;
78.8%;
                                                            Query Match
Best Local Similarity 78.8
Matches 458; Conservative
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-MODEL-framet-p2n.model -DEP-x1h
-MODEL-framet-p2n.model -DEP-x1h
-MODEL-framet-p2n.model -DEP-x1h
-MODEL-framet-p2n.model -DEP-x1h
-DB-GenEmbl -QEPMT-fastap -SUFFTX=P2n.rge -MINNATCH=0.1 -LOOPCL=0 -LCOPEXT=0
-UNITS=b1ts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1 -LIST=45
-UNITS=b1ts -START=1 -END=-1 -MATRIX=b109 um62 -TRANS=human40.cd1 -LIST=45
-UNITS=b1ts -START=1 -END=-1 -MATRIX=b109 um62 -TRANS=human40.cd1 -LIST=45
-UNITS=b1ts -START=1 -LIST=6 - THE MAX.END-100 - ALIST=10 - ALIST=45
-USER-USI0010408_CGCN_1_1_2496_Cunat_25072003_101855_17924 -NCPU-6 -ICPU-3
-NO_MARP -LISTS_NEGEQUERY -NGG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7
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1 MRGSPLIHLLATSFLCLLSM......LCLPRPCLAARSHSSWNSAF 250
                       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    nucleic search, using frame_plus_p2n model

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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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AR210324 Sequence
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AF100778 Mus muscu
AF126063 Mus muscu
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AR119211 Sequence
AR151276 Sequence
AF463517 Gallus ga
AJ298335 Gallus ga
U4324 Xenopus lae
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A2844 nov mRNA se
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J04496 Chicken CEF
AC126895 Rattus no
U83916 Sus scrofa
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AF120275 Rattus no
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AB023068 Rattus no
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AJ271167 Notophtha
AR018957 Sequence
AR130891 Sequence
AX206708 Sequence
I11636 Sequence
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I113210 Sequence I
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M70642 Mouse FISP-
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Homo sapien
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AR201286 Sequence
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AF100780 H
BC017782 H
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AF100778
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ALIGNMENTS

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PAT 20-JUN-2002
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Botstein, D.A., 'Cohen.R.L., Goddard, A.D., Gurney, A.L., Hillan, K.J., Lawrence, D.A., 'Levine, A.J., Pennica, D., Roy, M.Ann. and Wood, W.I. Wisp polypeptides and nucleic acids encoding same
Patent: US 6387657-A 17 14-MAY-2002;

Location/Qualifiers
1. 1734
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Conservative:
Mismatches:
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                                                                                Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                l (bases 1 to 1741)

Zhang, R., Averboukh, L., Zhu, W., Zhang, H., Jo, H., Dempsey, P.J.,
Coffey, R.J., Pardee, A.B. and Liang, P.
Identification of rCop-1, a new member of the CCN protein family, as a negative regulator for cell transformation
MOI. Cell. Biol. 18 (10), 6131-6141 (1998)
98414629
                                                                                                                                                                                                                        Direct Submission
Submitted (24-APR-2000) Cell Biology, Vanderbilt-Ingram Cancer
Center, 649 MRB II, Nashville, TN 37232, USA
Location/Qualifiers
1. .1741
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
1. .1741
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            AF259981 1741
Rattus norvegicus CCN family
                                                   AF259981.1 GI:7739780
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                                                                       Rattus norvegicus.
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                                        AF259981
           AF259981
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                                                                                                               Rattus.
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KEYWORDS
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 US-10-010-408-2 (1-250) x AR210325 (1-1734)	Qy 1 MetargGlySerProLeuIleHisLeuLeuAlaThrSerPheLeuCysLeuLeuSerMet 20	Db 1478 ArcAGGGCAACCACTGATCCTTCTGGCCATTCCTTCTTGCATCTTCTCTAATG 1419	Oy 21 ValCysAlaGlnLeuCysArgThrProCysThrCysProTrpThrProProGlnCysPro 40	1418 GTGTATTCCCAGCTGTGCCCAGCACCTGTGCCTGTGCTTGGACACCACCCCAGTGCCCA	VY 4.1 G.HOLYVALF.POLGUASPOLYV.VSCLYV.VSCLYSVSVALVYSALANJARIGAEGU OU  1358 CCGGGGGTACCTGGTGGTTGGTTGGTTGCTTGCGAGTTGTAGAGGGTG 1299	61 GlyGluSerCysAspHisLeuHisValCysAspProSerGlnGlyLeuValCysGlnPro 80	Db 1298 GGGAGTCCTGCGACCACGCATGTCTGCGACCCCAGGCCTGGTTTGTCAGCCT 1239	Oy 81 GlyalaGlyProGlyGlyHisGlyalaValCysLeuLeuAspGluAspAspGlySerCys 100	101 GluValAsnGlyArgArgTyrLeuAspGlyGluThrPheLysProAsnCysArgValLeu 120	Db 1178 GAGGTGAATGGCCGCAGGTACCTGGATGGGGAGACCTTTAAACCCAATTGCAGGTTTTG 1119	Qy 121 CysArgCysAspAspGlyGlyPheThrCysLeuProLeuCysSerGluAspValArgLeu 140	1118		Oy 161 TrpValCysAspGlnGlyValThrProAlalleGlnArgSerThrAlaGlnGlyHis 179	Db 998 TGGGTGTGTGTGAGGCAGTGATGCAGCCGCAATCCAGCCCTCTCAGCCCAAGGACAC 939	Oy 180 GlnLeuSerAlaLeuValThrProAlaSerAlaAspAlaProCysProAsnTrpSerThr 199	938	Additional transfer of the control o	Oy 220 AsnargPheCysGlnLeuGlulleGlnArgArgLeuCysLeuProArgProCysLeuAla 239 	Oy 240 AlaArgSerHisSerSerTrpAsnSerAlaPhe 250 :::	T 4 778	LOCUS AF100778 1734 bp mRNA linear ROD 17-DEC-1998 DEFINITION Mus musculus connective tissue growth factor related protein WISP-2 (Wisp2) mRNA, complete cds.	N AF100778 AF100778.1 GI:4028578	ALYWUKUDS SOUTRCE Mus musculus ORGANISM Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. REFERENCE 1 (bases 1 to 1734) AUTHORS Pennica,D., Swanson,T.A., Welsh,J.W., Rov,M.A., Lawrence,D.A.,	Lee,J., Brush,J., Taneyhill,L.A., Deuel,B., Lew,M., Watanabe,C., Cohen,R.L., Melhem,M.F., Finley,G.G., Quirke,P., Goddard,A.D., Hillan,K.J., Gurney,A.L., Botstein,D. and Levine,A.J. TITLE WISP genes are members of the connective tissue growth factor	
Qy 41 GlnGlyValProLeuValLeuAspGlyCysGlyCysGysLysValCysAlaArgArgLeu 60	Db 377 CCGGGGGTACCCCTGGTGCTGGTGGCTGCTGTGTGTGTGT	61 GlyGluSerCysAspHisLeuHisValCysAspProSerGlnGlyLeuValCysGlnPro	437 GGGGAGTCCTGCGACCTGCATGTCTGCGACCCCAGGCCTGGTTTGTC	OY 81 GlyAlaGlyProGlyGlyHisGlyAlaValCysLeuLeuAspGluAspAspGlySerCys 100	101 GluValAsnGlyArgArgTyrLeuAspGlyGluThrPheLysProAsnCysArgValLeu	Db 557 GAGGTGAATGGCCGCAGGTACCTGGATGGGGAGACCTTTAAACCCAATGCAGGGTTTTG 616	CysArġCysAspAspGlyGlyPheThrCysLeuProLeuCysSerGluAspValAr	Db 617 TGCCGCTGTGATGACGGTGGTTTCACCTGCCGCGTGTGCAGTGAGGATGTGCGGCTG 676 Ov 141 ProSetTrDAspCvsProArdProLvsArgT1GG1nVa1PrcG1vtvsCvsCvsPrcG1u 160		>		Oy 180 GinLeuSerAlaLeuValThrProAlaSerAlaAspAlaProCysProAsnTrpSerThr 199 11	200 AlaTrpGlyProCysSerThrThrCysGlyLeuGlylleAlaThrArgValSerAsnGln 2	Db 857 GCCTGGGGCCCCTGCFCACCTGTGGGTTGGGCATAGCCACCAGTATCCAACCAG 916	Qy 220 AsnArgPheCysGlnLeuGluIleGlnArgArgLeuCysLeuFroArgProCysLeuAla 239	Db 917 AACCGATTCTGCCAACTGGAGATCCAGCGTCGCCTGTGTCTGCTCCAGACCCTGGCA 976	Qy 240 AlaArgSerHisSerSerTrpAsnSerAlaPhe 250  Option 1	STATE STATE OF THE	LOCUS AR210325/C AR210325 1734 bp DNA linear PAT 20-JUN-2002 DEFINITION Sequence 18 from patent US 6387657. ARCESSION AR210325 VERSION AR210325 1 GT:21512526	S Unknown. ISM Unknown.	Unclassified.  REFERENCE 1 (bases 1 to 1734) AUTHORS Betstein, D.A., Cohen, R.L., Goddard, A.D., Gurney, A.L., Hillan, K.J.,	Lawrence, D.A., Levine, A.J., Pennica, D., Roy, M.Ann. and Woc WISP polypeptides and nucleic acids encoding same L. Patent: US 6387657-A 18 14-MAY-2002;	FEATURES Location/Qualifiers Source 1.1734	BASE COUNT 393 a 495 C 491 g 355 t	3.97e-67 Length: 1308.50 Matches:	Percent Similarity: 93.63% Conservative: 9 Best Local Similarity: 90.04% Mismatches: 15 Query Match: 6 Gaps: 1	

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SM Mus musculus , Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Mus. E. 1 (bases 1 to '1739)

Kumar,S., Hand,A.T., Connor,J.R., Dodds,R.A., Ryan,P.J., Trill,J.J., Figher,S.M., Nuttall,M.E., Lipshuz,D.B., Zou,C., Hwang,S.M., Votta,B.J., James,I.E., Rieman,D.J., Gowen,M. and Lee,J.C.
Identification and cloning of a connective tissue growth factor-like coph from human osteoblasts encoding a novel regulator of osteoblast functions

L. J. Biol. Chem. 274 (24), 17123-17131 (1999)
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AF126063.1 GI:4337059
                                                                                           161 TrpValCysAspGlnGlyVal --- ThrProAlaileGlnArgSerThrAlaGlnGlyHis 179
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Swedeland Rd., King of Prussia, PA 19406,
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precurŝor"
                            240 AlaArgSerHisSerSerTrpAsnSerAlaPhe 250
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Kumar, S. and Zou, C.
Direct Submission
Submitted (04-FBB-1999) Bs
SmithKline Beecham, 709 Sw
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family that are up-regulated in wnt-1-transformed cells and aberrantly expressed in human colon tumors Proc. Natl. Acad. Sci. U.S.A. 95 (25), 14717-14722 (1998) 99061933
                                                                                                                                                                Direct Submission
Submitted (23-OCT-1998) Molecular Oncology,
Way, South San Francisco, CA 94080, USA
Location/Qualifiers
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Botstein, D., Goddard, A., Gurney, A.L., Hillan, K.J., Roy, M.A. Wood, W.I.
Polypeptidic compositions and methods for the treatment of the Patent: WO 0105836-A 31 25-JAN-2001;
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/db_xref="taxon:9606"
418 c 390 q 242
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121 CysArgCysAspAspGlyGlyPheThrCysLeuProLeuCysSerGluAspValArgLeu 140	LeuseralaLeuvalThrProalaSeralaAspalaProCysProAsnTrpSerThrAla		Direct Submission Submitted (11-200-1998) Bone & Cartilage Biology, UW 2109, Submitted (11-200-1998) Bone & Cartilage Biology, UW 2109, SmithKline Beecham, 709 Swedeland Road, King of Prussia, PA 19406, USA Location/Qualifiers   Organism="Homo sapiens"
60 60 60 60 60 60 60 60 60 60 60 60 60 6	. TOS	LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL JOURNAL SOURCE SOURCE
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1 (bases 1 to 1293)
Botstein,D.A., Cohen.R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.
WISP polypeptides and nucleic acids encoding same
Patent: US 6387657-A 13 14-MAY-2002;
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to $1309)
Rowles,J. and Gandler.S.
Rowles,J. and Gandler. S.
Interacts with the breast cancer associated mucin MUCl
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Submitted (25-JgN-1998) Biochemistry and Molecular Biology, Mayo
Clinic Scottsdalle, 13400 E. Shea Blvd., Scottsdale, Az 85259, USA
Location/Qualifiers
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/produ¢t-"connective tissue growth factor-related
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Rowles, J. and Gendler, S.
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Botstein, D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.
WISP polypeptides and nucleic acids encoding same
WISP polypeptides and nucleic acids encoding same
Patent: US 6387657-A 14 14-MAY-2002;
Location/Qualiflers
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Mismatches:
Indels:
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Proc. Natl. Acad. Sci., U.S.A. 99061933 9843955 2 (bases 1 to 1427) Pennica,D. Direct Submission Submitted (23-0CT-1998) Molecu Way, South San Francisco, CA 9 Location/Qualifiers in 1427 / Organism="Homo sapie / Ab_rref="taxon:9606" / Chromosome="20912-q13.1" / Lissue_type="lung" / Gene="Wispe" / Gene="Wispe" / Gene="Wispe" / Gene="Wispe" / Condon startel / Condon startel	#18P-020 #18P-020  #18P-020  #18P-020  #18P-020  #18P-020  #18P-020  #18P-020  #18P-020  #18P-020  #18P-020  #18P-020  #18P-020  #18P-03  #18P-03	Imilarity: 73.60%   Mismatches: 73.89%   Indels: 73.89%   Indels: 6aps: 8-2 (1-250) x AF100780 (1-1427)   MetargGlySerProLeulleHisLeuLeualaThrS	41 GlnGlyValProLeuValLeuAspGlyCysGlyCysCysLysValCysAlaArgArgLeu 60
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL FEATURES SOUICE GENE	BASE COUNT ORIGIN Alignment Pred. No.: Score:	Best Local Simi. Query Match: DB: US-10-010-408-2 QY 1 M Db 156 A Db 216 G	
MetArgGlySerProLeuIleHisLeuLeuAlaThrSerPheLeuCysLeuLeuSerMet	GAGGTGAACGCCCCTGTATCGGGAAGGGAGACCTTCCAGCCCCACTGCAGCATCCGC CysArgCysAspAspGlyGlyPheThrCysLeuProLeuCysSerGluAspValArgLeu [	181 LeuSerAlaLeuValThrProAlaSerAlaAspalaProCysProAsnTrpSerThrAla 200	AF100780  AF100780  AF100780  AF100780  AF100780  AF100780  AF100780.1 G1:4028582  Homo sapiens.  Homo sapiens.
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/transpartion="mrcTpkThildePsilcilskvrTolcptpcTcPwppprcplGvp
lvLdcGcCcrvCarrigePcDQLHvCDaSqGlvCqPGaGGGGALCLLAEDDSSCEV
nGRLYREGETPQPHCSTRCRCBGGFTCVPLCSEDVRLPSWDCPHPRNEVLGKCCPE
WCGGGGGLGTQPLPAGGPGSGLVSTLPGCVPCPEWSTAWGPCSTTCGLGMATRVSN
WNRCORLETQRRLCSRPCPPSRGRSPQNSAF"

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Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dlokson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (03-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                    BC017782 1450 bp mRNA linear PRI 06-DEC-2
Homo sapiens, WNT1 inducible signaling pathway protein 2, clone
MGC:22271 IMAGE:4691574, mRNA, complete cds.
                                                                                                                   ArgPheCysGlnLeuGluIleGlnArgArgLeuCysLeuProArgProCysLeuAlaAla
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Mammalia; Eutheria; 1
1 (bases 1 to 1450)
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TITLE
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COMMENT
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704 200 764 220 824 884

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1450 184 17 49 0

Matches:

284

us-10-010-408-2.p2n.rge

Oy 225 LeuGluIleGlnArgArgLeuCysLeuProArgProCysLeuAlaAlaArgSerHisSer 244	Alignment Scores:  Pred. No.:  Score: Score: Percent Similarity: Best Local Similarity: Percent Similarity:  Rest Local Similarity:  72.73\$ Mismatches:  Gaps: Conservative: 172.60\$ Mismatches: 6 Gaps: Conservative: 172.60\$ Mismatches: 6 Gaps: 1 NetArgGlySerProLeuIleHisLeuLeuAlaThrSerPheLeuCysLeuLeuSerMet 20	Db	101 GluvalAsnGlyArgArgTyrLeuAspGlyGluThrPhelysProAsnCysArgValLeu 101 GluvalAsnGlyArgArgTyrLeuAspGlyGluThrPhelysProAsnCysArgValLeu 101 GluvalAsnGlyArgArgTyrLeuAspGlyGluThrPhelysProAsnCysArgValLeu 111 [111111111111111111111111111111111
DEFINITION   Sequence 38 from patent US 6387657.   AR210337   AR		Qy         65 AspHisLeuHisValCysAspProSerGlnGlyLeuValCysGlnProGlyAlaGlyPro         84           III         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	CysprodryProlysArgileGinValProGlyLysCysCysproGluTrpValCysAsp 

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603 CACGGCCTGGGGACCCTGCTCGACCTGGGCTGGGCTGGG	9 qa	
198 rThralafrpGlyProCysSerThrThrCysGlyLeuGlyIlealaThrArgValSerAs 218	Oy 1	
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roAlaSerAlaAspAla	Oy 1	
492 TGGGTGTGCGGCCCAAGGAGGGGGACTGGGGACCAGCCCTTCCAGCCCAAGG 542	Db da	

Search completed: August 1, 2003, 04:21:56 Job time: 2649 secs

SUMMARIES

## GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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August 1, 2003, 01:17:19; Search time 237 Seconds (without alignments) 2375.526 Million cell updates/sec
                                                                                                                              US-10-010-408-2
1440
1 MRGSPLIHLLATSFLCLLSM......LCLPRPCLAARSHSSWNSAF 250
OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                     2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                         Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
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                                                                                                                                                                                                                       BLOSUM62
                                                                                                                                 Title:
Perfect score:
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Command line parameters:
-WODEL-frame+\_p2n.modal -DEV-xlh
-WODEL-frame+\_p2n.modal -DEV-xlh
-Q-/cgn2\_1/USPFO\_spool/US10010408/runat\_25072003\_101855\_17876/app\_query.fasta\_1.391
-Q-/cgn2\_1/USPFO\_spool/US10010408/runat\_25072003\_101855\_17876/app\_query.fasta\_1.391
-DB-N.Geneseq\_101002 -QFWT-fastap -SUFFIX-p2n.rng -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-blts -START-1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR\_SCORE-pct -THR\_MAX-100 -THR\_MIN-0 -ALIGN-15
-WODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US10010408\_CGGN\_1\_1\_263\_CRUNAT\_25072003\_101855\_17876 -NCPU-6 -ICPU-3
-NO\_MAAP -LARGEQUERY -NGG\_2CORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-FGAPDEY\_TIMEOUT-120 -WARN\_THEOUT-30 -THREADS-1 -XGAPDP=10 -XGAPDFT-0.5 -FGAPOP=6

/SIDS2/gcgdata/geneseg/genesegn-embl/NA1991.DAT:\*/SIDS2/gcgdata/geneseg/genesegn-embl/NA1992.DAT:\*/SIDS2/gcgdata/geneseg/genesegn-embl/NA1993.DAT:\* /SIDS2/gcgdata/geneseq/geneseqn-embl/Na1989.DAT:\*/SIDS2/gcgdata/geneseq/geneseqn-embl/Na1990.DAT:\* /SIDS2/gcgdata/geneseq/geneseqn-emb1/Na1994.DAT:\*/SIDS2/gcgdata/geneseq/geneseqn-emb1/Na1995.DAT:\* /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:\*/SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:\*/SIDSZ/gcgdata/geneseq-embl/NA1981.DAT:\*/SIDSZ/gcgdata/geneseq-embl/NA1983.DAT:\*/SIDSZ/gcgdata/geneseq-embl/NA1983.DAT:\*/SIDSZ/gcgdata/geneseq-geneseqn-embl/NA1984.DAT:\*/SIDSZ/gcgdata/geneseq-geneseqn-embl/NA1985.DAT:\*/SIDSZ/gcgdata/geneseq-geneseqn-embl/NA1985.DAT:\*/SIDSZ/gcgdata/geneseq-geneseqn-embl/NA1986.DAT:\*/SIDSZ/gcgdata/geneseq-geneseqn-embl/NA1987.DAT:\*/SIDSZ/gcgdata/geneseq-geneseqn-embl/NA1987.DAT:\*/SIDSZ/gcgdata/geneseq-geneseqn-embl/NA1988.DAT:\*/SIDSZ/gcgdata/geneseq-geneseqn-embl/NA1988.DAT:\*/SIDSZ/gcgdata/geneseq-geneseqn-embl/NA1988.DAT:\*/SIDSZ/gcgdata/geneseq-geneseqn-embl/NA1988.DAT:\*/SIDSZ/gcgdata/geneseq-geneseqn-embl/NA1988.DAT:\*/SIDSZ/gcgdata/geneseq-geneseq-geneseqn-embl/NA1988.DAT:\*/SIDSZ/gcgdata/geneseq-g N\_Geneseq\_101002:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:\* /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:\* /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:\*

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ription	t HICP	HICP polypep	HCP mature p	WISP-2 prot		Human WISP-2 prote	EGF-like homologue		ပ	PRO261 coding sequ		Š	Human WISP-2 prote	Connective tissue	Human secreted pro	eq	Ęa	O	Human WISP-2 prote	7	ctive ti	Human connective t	Connective tissue	connective				_	-	connective	Human benign prost	٠.	12 CDN	fibrobla	for beta-IG-	sequence diff	Rat connective tis	encod	Chicken nov coding	edneuc	Chicken nov gene f	ヸ	tis	ective	)
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AAZ07517 standard; cDNA; 753 AAZ07517; RESULT 1 AAZ07517

BP.

ALIGNMENTS

26-NOV-1999 (first entry)

Rat HICP polypeptide coding sequence.

Heparin-induced CCN-like protein; HICP; cell-associated activity; ss; cardiovascular disorder; aberrant cell proliferation; fibrotic disorder 

Rattus sp.

W09947556-A2

23-SEP-1999.

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                                                                                                                                                                             The invention provides a rat heparin-induced CCN-like protein (HICP) protein. Agents that stimulate or inhibit HICP protein activity or expression, antibense HICP nucleic acid molecules and HICP antibodies, can be used to modulate cell-associated activity. HICP modulators can be used to treat disorders characterized by aberrant HICP protein activity or expression. Probes capable of hybridizing to HICP protein activity specific for HICP can be used to detect HICP activity in a biological sample. HICP can be used to treat disorders, such as a cardiovascular or fibrotic disorder, characterized by aberrant cell proliferation. The present sequence represents the coding sequence of rat HICP.
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                                                                                                                                                            Claim 5; Fig 1; 108pp; English.
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P-PSDB; AAY27434.
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                                                                                                                                                                                                                                                                            Heparin-induced CCN-like protein; HICP; cell-associated activity; ss; cardiovascular disordèr; aberrant cell proliferation; fibrotic disorder.
                                              TrpGlyProCysSerThrThrCysGlyLeuGlyIleAlaThrArgValSerAsnGlnAsn
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99WO-US05999

18-MAR-1999;

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                                                                                       GlnGlyValProLeuValLeuAspGlyCysGlyCysCysLysValCysAlaArgArgLeu
                                                                     GAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAACCCAATTGCAGGGTCCTG
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                                                                                                                     Nucleic acid sequences encoding rat heparin-induced CCN-like protein, used in methods to identify modulators or in diagnostic applications
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                                                                                                                                                    Disclosure; Fig 2; 108pp; English
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P-PSDB; AAY27440.
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Percent Similarity:
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Query Match:
DB:
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                                                 (TUFT ) TUFTS
                                                                    Castellot JJ;
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Products from the present invention can be used to treat WISP-related disorders such as breast, ovarian, and colon cancer or melanoma. The products can be used to treat arteriosclerosis. The products can also be used to treat other diseases e.g. benign and malignant tumours, leukaemia and lymphold malignancies, neuronal, gilal, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, and blastocoelic disorders, desmoplasia, fibrotic lesions, kidney disorders, bone-related disorders such as osteoporosis, trauma such as burns, inclaions, and other wounds, connective tissue disorders, catabolic states, testicular-related disorders, and inflammatory, angiogenic and immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of
                                                                                              243
WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour; connective tissue growth factor; cancer; melanoma; arteriosclerosis; leukaemia; lymphoid malignancy; haematopoiesis-related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion; kidney disorder; bone-related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation; testicular-related disorder; anglogenesis; immunological disorder; ss.
                                               CysSerThrThrCysGlyLeuGlyIleAlaThrArgValSerAsnGlnAsnArgPheCys
                                                          Mouse WISP-2 protein complementary nucleotide sequence SEQ ID NO:18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Wnt-1 induced secreted polypeptides, WISP-1,
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Wood WI;
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individuals with neoplastic cell growth or proliferation. The products can be used in the production of transgenic or knock-out animals. Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
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Matches:
Conservative:
Mismatches:
Indels:
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93.63%
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CysArgCysAspAspGlyGlyPheThrCysLeuProLeuCysSerGluAspValArgLeu

GlyAlaGlyProGlyGlyHisGlyAlaValCysLeuLeuAspGluAspAspGlySerCys

919 160 736

556

100

179

TrpValCysAspGlnGlyVal --- ThrProAlaIleGlnArgSerThrAlaGlnGlyHis

CAACTITCTGCCCTTGTCACTCCTGCATCTGCCGATGGCCCCTGTCCAAACTGGAGCACA

GlnLeuSerAlaLeuValThrProAlaSerAlaAspAlaProCysProAsnTrpSerThr

AlaTrpGlyProCysSerThrThrCysGlyLeuGlyIleAlaThrArgValSerAsnGln

196

199 856 219

239

BP

(first entry)

AsnArgPheCysGlnLeuGluIleGlnArgArgLeuCysLeuProArgProCysLeuAla

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101 GluValAsnGlyArgArgTyrLeuAspGlyGluThrPheLysProAsnCysArgValLeu 120
  240 AlaArgSerHisSerSerTrpAsnSerAlaPhe 250
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Products from the present invention can be used to treat WISP-related disorders such as breast, ovarian, and colon cancer or melanoma. The products can be used to treat arteriosclerosis. The products can also be used to treat other diseases e.g. benign and malignant tumours, lenkaemia and lymphoid malignancies, neuronal, glial, astrocytal, bypothalamic and other glandular, macrophagal, epithelial, stromal, and blastocoelic disorders, desmoplasia, fibrotic lesions, kidney disorders, skin disorders such as osteoporosis, trauma such as observed in the catabolic states, testicular-related disorders, and inflammatory, angiogenic and immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The products can be used to induce death in WISP-1, 2 or 3 overexpressing
                                                                                                                                            testicular-related disorder; angiogenesis; immunological disorder; ss
                                                                     WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour connective tissue growth factor; cancer; melanoma; arteriosclerosis; leukaemia; lymphoid malignancy; haematopoiesis-related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion; kidney disorder; bone-related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation;
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                                                                                                                                                                                                                                                                                                                                                       Roy MA, Wood WI
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                                               Mouse WISP-2 protein nucleotide sequence SEQ ID NO:17
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Matches:
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Pennica D,
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Levine AJ,
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Lawrence DA,
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AAX76488;
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WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour; connective tissue growth factor; cancer; melanoma; arteriosclerosis; leukaemia; lymphoid malignancy; haematopoiesis-related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion; kidney disorder; bonner-related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation; testicular-related disorder; immunological disorder; ss. Human WISP-2 protein complementary nucleotide sequence SEQ ID NO:14 Homo sapiens 409921998-A1 06-MAY-1999

MetArgGlySerProLeuIleHisLeuLeuAlaThrSerPheLeuCysLeuLeuSerMet 20

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us-10-010-408-2.p2n.rng

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220

91

211

271

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ProSerTrpAspCysProArgProLysArgIleGlnValProGlyLysCysProGlu 160
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TGCCGCTGCGAGGACGCGGCTTCACCTGCGTGCCGCTGTGCAGGAGGATGTGCGGCTG
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450 GAGGTGAACGCCGCCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCAGCCATCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF-like homologue PRO261 coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 22; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX28435 standard; DNA; 1257
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97US-0059114.
97US-0059117.
97US-0059263.
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97US-0062285.
97US-0062287.
97US-0062816.
97US-0063704.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-229532/19.
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FGF-8 homologue; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-1997
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18-SEP-1997
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17-0CT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                       The present invention describes Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2, AISP-1, 2 and WISP-3 have homology to connective tissue growth factor (CYGF).

Toducts from the present invention can be used to treat WISP-related disorders such as breast, ovarian, and colon cancer or melanoma. The products can be used to treat atteriosclerosis. The products can also be used to treat other diseases e.g. benign and malignant tumnurs, leukaemia and lymphoid malignancies, neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, and blastocelic disorders, desmopolesis-related disorders, tissue-growth disorders, and other wounds, connective tissue disorders, catabolic states, testicular-related disorders, and inflammatory, angiogenic and immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The products can be used to induce death in WISP-1, 2 or 3 overexpressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 GlyAlaGlyProGlyGlyHisGlyAlaValCysLeuLeuAspGluAspAspGlySerCys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluValAsnGlyArgArgTyrLeuAspGlyGluThrPheLysProAsnCysArgValLeu 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyGluSerCysAspHisLeuHisValCysAspProSerGlnGlyLeuValCysGlnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       570 GGGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGGCCTGGTCTGCCAGCCC
                                                                                                                                                                                                                      ო
                                                                                                                                                                                                                    New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and
                                                                                                                                        Hillan K;
                                                                                                                                                        Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 750 BP; 125 A; 242 C; 274 G; 109 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
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Roy MA, W
                                                                                                                                                                                                                                                Disclosure; Page 175-176;.284pp; English.
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                                                                                                                                        Goddard A,
Pennica D,
                                          98US-0081695.
97US-0063704.
98US-0073612.
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1064.00
80.40%
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              98WO-US22991
                                                                                                                                                        Levine AJ,
                                                                                                                                      Cohen RL,
                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                      WPI; 1999-337420/28.
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Best Local Similarity:
Query Match:
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Lawrence DA,
                                                          29-OCT-1997;
03-FEB-1998;
             29-OCT-1998;
                                           14-APR-1998;
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This sequence encodes the EGF-like homologue PRO261.

The invention relates to antibodies (Ab) that bind to any of the polypeptides (I) designated PRO187, PRO533; PRO214; PRO240; PRO211; PRO250; PRO261; PRO260 or EBAF-2. The Ab, or other agents that inhibit tumours; and (II) as diagnostic/prognostic reagents for detection or quantification of (I) in cells or tissues, by standard immunoassays, with overexpression being indicative of cancer. For therapeutic use, the Ab may be condigated to a toxin, chemotherapeutic agent or radioisotope. Genes expressing (I), many of which are growth factor homologues, are overexpressed in some cases of cancer.
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                                                                                                                                                                                                                                                                                                                                                                                     GlyGluSerCysAspHisLeuHisValCysAspProSerGlnGlyLeuValCysGlnPro
                                                                                                                                                                                                                                                                                                                                                                                                           GGGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGGGCCTGGTCTGCTGCCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                               GlyAlaGlyProGlyGlyHisGlyAlaValCysLeuLeuAspGluAspAspGlySerCys
                                                                                                                                                                                                                                                                                                                                                                                                                                          GluValAsnGlyArgArgTyrLeuAspGlyGluThrPheLysProAsnCysArgValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CysArgCysAspAspGlyGlyPheThrCysLeuProLeuCysSerGluAspValArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGGTGTGCGGCCAAGGAGGGGGACTGGGGACCCAGCCCTTCCAGCCCCAAGGACCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 1257 BP; 215 A; 416 C; 385 G; 241 T; 0 other;
                                                                                                                                                             1257
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Matches:
Conservative:
Mismatches:
Indels:
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crims sequence represents a human PRO261 nucleotide sequence. PRO261 is a growth factor. The invention relates to isolated antibodies which bind to cap polypeptide. The "PRO" polypeptides are encoded by genes which are over expressed in the genome of tumour cells. Vectors and host cells comprising the nucleic acid encoding the antibodies and nucleic acids encoding the production of the antibodies. The antibodies and nucleic acid encoding them are used for diagnosing a tumour in a mammal. The antibodies are used for inhibiting the growth of tumour cells and identifying compounds that inhibit a biological or immunological activity of and/or expression of a PRO187, PRO513, PRO514, PRO214, PRO211, PRO210, PRO211, PRO240, PRO211, PRO210, PRO210,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; human; cell growth; proliferation; growth factor; ADEPT; antibody dependent enzyme mediated prodrug therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated antibodies which bind to specific polypeptides used for diagnosis and treatment of neoplastic cell growth and proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390 G; 242 T; 0 other;
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Mismatches:
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AGGGGTCGCAGTCCACAAAACAGTGCCTTC 750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; Fig 13; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       Human PRO261 nucleotide sequence.
                                                                                                                                                                    BP
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98WO-US18824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-271386/23.
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Score:
     130 CTGGGAGTACCCCTGGTGCTGGATGGCTGTGTGCTGCCGGGTATGTGCACGGCGGCTG 189
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 TrpGlyproCysSerThrThrCysGlyLeuGlyIleAlaThrArgValSerAsnGlnAsn
                                                                                                                                                                                 GlyGluSerCysAspHisLeuHisValCysAspProSerGlnGlyLeuValCysGlnPro
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AAS AAS21244-AAS21518 encode for novel human secretory and transmembrane

PRO polypeptides. The PRO polypeptides are useful to detect other

PRO polypeptides, to Auk bloactive molecules to cells expressing

PRO polypeptides, to medulate biological activities of cells expressing

PRO polypeptides, and to detect the presence of mammallan lung, colon,

breast, prostate, rectal, cervical or liver tumours by comparing PRO

prolypeptide expression in a cell sample to that in a control sample.

CC polypeptide expression and expression or differentiation of chondrocytes, the proliferation or differentiation of chondrocytes, the proliferation or cartilage, the proliferation of inner ear utricular supporting cells or

game expression in pergyte cells, the release of proteoglycans from

cartilage, the proliferation of inner ear utricular supporting cells or

game expression in pergyte cells, the release of proteoglycans from

cartilage, the proliferation of endothelial cells some of

the PRO polypeptides may modulate glucose or free fatty acid uptake by

skeletal muscle cells or by adipocytes; or inhibit binding of Arpeptide

to factor VIIA. The PRO polypeptides can be used in assays to identify

molecules involved in binding interactions. The polynocleotides encoding

PRO polypeptides can be used to generate probes, antisense smooding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammallan tumours e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRO polypeptides can be used to generate probes, antisense RNA/
transgenic or knock out animals and can be used in gene therapy
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Tumas D,
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2000WO-US04414.
2000WO-US04914.
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99WO-US31243
99WO-US28564
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99WO-0330095
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2000WO-U$07532
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2000WO-U$13705
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30-MAY-2000; 2000WO-UŠ14941
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ME, Goddard
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Query Match:
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Smith V, Stew
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21-MAR-2000;
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Sequence 1266
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to PRO proteins and coding sequences. The present sequence is the coding sequence for one such PRO protein. It was found that the PRO genes are amplified in the genome of tumour cells. The gene amplification is expected to be associated with the overexpression of the gene product and contributes to tumourigenesis. Therefore, antagonists of PRO proteins are useful for the treatment of benign or malignant tumours, leuksemias, lymphoid malignancies and other disorders such as neuronal, allal, astrocytal, hypothalamic, glandular, epithelial, inflammatory and immunologic disorders.
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                  Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 50; Fig 13; 196pp; English.
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                                                                                                                 99WO-US21090.
99WO-US23089.
99WO-US28214.
99WO-US28313.
                                   99US-0144758.
99US-0145698.
99WO-US20594.
99WO-US30999
                                                                                                99WO-US20944
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Best Local Similarity:
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Wood WI:

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 TGCCGCTGCGAGGACGGCGGCTTCACCTGCCGTGCCGCTGTGCAGCGAGGATGTGCGGCTG 429
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                                                                                                                                                                                                ArgPheCysGlnLeuGluIleGlnArgArgLeuCysLeuProArgProCysLeuAlaAla 240
                                                                                                                                                                                                            Human; anglogenesis-associated protein; PRO; endothelial cell growth; cardiac Mypertropy; cardiavascular disorder; andothelial disorder; anglogenic disorder; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis; crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer; Alzhelmer's disease; Huntington's disease; stroke; drug screening; gene therapy; transgenic animal; ss.
                     161 TrpvalCysAspGlnGlyValThrProAlaileGlnArgSerThrAlaGlnGlyHisGln
                                                                                    LeuSerAlaLeuValThrProAlaSerAlaAspAlaProCysProAsnTrpSerThrAla
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Mark MR, Marsters SA;
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Kuo SS,
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Hillan KJ,
                                                                                                                                                                                                                                                                                                           AAC97451 standard; cDNA; 1266 BP.
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99US-0141037.
99US-0144758.
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Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC
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15-SEP-1999;
05-OCT-1999;
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41 GlnGlyValProLeuValLeuAspGlyCysGlyCysCysLysValCysAlaArgArgLeu

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ValCysAlaGlnLeuCysArgThrProCysThrCysProTrpThrProProGlnCysPro

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US-10-010-408-2 (1-250) x AAC97451 (1-1266)

Length: Matches: Conservative: Mismatches:

4.9e-55 1064.00 80.40% 73.60% 73.89%

Best Local Similarity:

Query Match:

Percent Similarity:

Alignment Scores:

Pred.

Indels:

10 ATGAGAGGCACACCCCCCCCTCCTGGCCTTCTCCCTCTCGCCTCCTCTCAAAG

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The invention relates to novel human angiogenesis-associated proteins designated PRO protein's (AAB53064-B53097), and to nucleic acids encoding PRO protein's The invention also relates to vectors and host cells comprising a PRO nucleid acid, the recombinant production of a PRO protein, and comprising a PRO nucleid acid, the recombinant production of a PRO protein, and comprising a PRO protein, or antegonists of a PRO protein, and compounds which inhibit the expression of a PRO game. The invention additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular, endothalial or angiogenic disorder or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothalial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid, or PRO nucleic acid; and methods of inhibiting or stimulating endothalial componities and protein and methods of inhibiting or stimulating endothalial componities and protein and methods of inhibiting or stimulating endothalial componities and proteins, antibodies against thereof.

PRO nucleic acids, and methods of inhibiting or stimulating endothalial contains and methods of inhibiting or stimulating endothalial contains, antibodies against thereof.

PRO nucleic acids, proferine, antibodies against thereof.

Conditionals and profering any posteins, antibodies against thereof.

Conditionals, and profession of a PRO protein, and accomponity useful in the recombinant production of a production and activities. Crohn's disease, huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, to analyse genetic disorders, and in gene encoding PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids are about severuled acids. The invention of the inpersource represents a cobnection of the inpersource of the propertion of the inperson
                                                                                                                                            New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or angiogenic disorders, "such as atherosclerosis, wounds or cancer -
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Watanabe CK,
                                                                                                                                                                                                                                                                Claim 58; Fig 41; 293pp; English.
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  Paoni NF, Pitti RM,
                                                        2001-090793/10
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                                                                                                                              TrpValCysAspGlnGlyValThrProAlaIleGlnArgSerThrAlaGlnGlyHisGln
                                 GluValAsnGlyArgArgTyrLeuAspGlyGluThrPheLysProAsnCysArgValLeu
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GGGGCAGGACCCGGTGGCCGGGGGCCCTGTGCCCTCTTGGCAGAGGACGACAGCACTGT
                                                         CysArgCysAspAspGlyGlyPheThrCysLeuProLeuCysSerGluAspValArgLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Connective tissue growth factor-3; CTGF-3; human; cancer; arthritis; fibrosis; osteoporosis; diagnosis; therapy; ds
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GluValAsnGlyArgArgTyrLeuAspGlyGluThrPheLysProAsnCysArgValLeu 120
                                                                                          This nucleotide sequence codes for human connective tissue growth factor superfamily. It was discovered in a cDNA library derived from human osteoblasts. The gene has also been identified in cDNA libraries from ovary, testis, heart, lung, skeletal muscle, adrenal medulla, adrenal cortex, thymus, prostate, small intestine and colon. A cDNA clone is deposited as ATCC 97756. Also provided are vectors, host calls and recombinant methods for producing are vectors, host calls and recombinant methods for producing cTGF-3 polypeptides. CTGF-3 nucleic acid sequences or their fragments, e.g. primers or probes, can be used to diagnose diseases where CTGF-3 expression is enhanced, e.g. cancer, arthritis, ibrosis or atherosclerosis, or diseases where expression is decreased such as in osteoporosis. Disorders characterised by decreased or increased levels of CTGF-3 can be treated by administering CTGF-3 polypeptides and anti-CTGF-3 antibodies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CysArgCysAspAspGlyGlyPheThrCysLeuProLeuCysSerGluAspValArgLeu
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TGCCGCTGCGAGGACGGGGTTCACCTGCGTGCCGCTGTGCAGGAGGAGGATGTGCGGCTG
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arthritis, fibrosis
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Mismatches:
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  cancer,
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                                                             English.
  e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.98e-55
1064.00
80.40%
73.60%
73.89%
treatment of
                                                             87pp;
                                                             1A-B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1285
                                                             Claim 2; Fig
                        osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                          respectively
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
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No
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428 160 488

368

188

80

9

40

68

248

180 548 200 608

can be used to induce death in WISP-1, 2 or 3 overexpressing

201 TrpGlyProCysSerThrThrCysGlyLeuGlyIlealaThrargValSerAsnGlnAsn 220	\$\$\$\$\$\$	cells.
221 ArgPheCysGlnLeuGluIleGlnArgArgLeuCysLeuProArgProCysLeuAlaAla 240	Ali Pre Sco	Alignment Scores Pred. No.: Score:
241 ArgSerHisSerSerTrpAsnSerAlaPhe 250 	Per Bes Que: DB:	Percent Similarit Best Local Simila Query Match: DB:
RESULT 13	-SN	US-10-010-408-2
AAX76486 standard; DNA; 1293 BP.	οy	1 Met
AAX76486;	QO	22 ATG
06-AUG-1999 (first entry)	ΟŶ	21 val
Human WISP-2 protein nucleotide sequence SEQ ID NO:13.	qa	82 GTG
WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;	οy	41 Gln
Jeukaemist lymphoid malignancy; haematopoiesis-related disorder; tissue-growth disorder: skin disorder:	<b>q</b> Ω	142 CTG
Kidney disorder; Done-related disorder; osmetyperoris trauma; burn; connective tissue disorder; catabolic state; inflammation;	oy d	61
Homo sabiens.	3 8	707.
~	G Q	262
06-MAY-1999.	٥y	101 Glu
29-OCT-1998; 98WO-US22991.	QQ	111 322 GAG
14-APR-1998; 98US-0081695. 29-0CT-1997; 97US-0063704.	Qy	121
	QΩ	382
(GETH ) GENENTECH INC.	٥y	141
Botstein DA, Cohen RL, Goddard A, Gurney AL, Hillan K; Lawrence DA, Levine AJ, Pennica D, Roy MA, Wood WI;	qa	442
WPI; 1999-337420/28. P-PSDB: AAV17649	Oy do	161
New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3	3 A	181
Example 4; Page 174-175; 284pp; English.	QQ	562 TTT
The present invention describes Wnt-1 induced secreted polypeptides, WISD-1, 2 and 3 The novel wISD not non-tides destructed with a with the novel	Qy	201
and WISP-3 have homology to connective tissue growth factor (CTGF).  Profilets from the present invention can be used to treat without and the control of th	qq	622 TGG
disorders such as breast, ovarian, and colon cancer or melanoma. The products can be used to treat arteriosclerosis. The products can also be	Qy	221
used to treat other diseases e.g. benign and malignant tumours, leukaemia and lymphoid malignancies, neuronal, glial, astrocytal,	QQ	682 CGC
hypothalamic and other glandular, macrophagal, epithelial, stromal, and blastocoelic disorders, haematopolesis related disorders, tissue-growth disperders eth disorders assemblasis.	δ d	241
disorders, bone-related disorders such as osteoporosis, trauma such as burns, incisions, and other wounds, connective tissue disorders, catabolic states, testicular-related disorders, and inflammatory, and immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The products	RES AAH ID XX XX	RESULT 14 AAH28214 ID AAH28214 XX AXA AAH28214

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140
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                                                                                                                                                                                                                     OSETTPASPÇYSProArgProLysArglleGlnValProGlyLysCysCysProGlu 160
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                                                               C; 393 G; 243 T; 0 other;
               1293
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17
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Matches:
Conservative:
Mismatches:
Indels:
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                                                     (1-250) x AAX76486
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232 A; 425
                5.01e-55
1064.00
80.408
73.608
73.898
                           ity:
larity:
BP;
93
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Page 13

20 99 40

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141 ProSerTrpAspCysProArgProLysArgIleGlnValProGlyLysCysCysProGlu 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 TrpValCysAspGlnGlyValThrProAlaIleGlnArgSerThrAlaGlnGlyHisGln 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        667 certreteceaetegagacecagececerergecretecagecerececeaecerec 726
                                                                                                                                  Secreted protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetArgGlySerProLeuIleHisLeuLeuAlaThrSerPheLeuCysLeuLeuSerMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 LeuSerAlaLeuValThrProAlaSerAlaAspAlaProCysProAsnTrpSerThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   547 TITICIGCCTIGICICITCCCTGCCCCCTGGTGCCCCTGCCCAGAATGGAGCACGGCC
                                                     21 ValCysAlaGlnLeuCysArgThrProCysThrCysProTrpThrProProGlnCysPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein encoding cDNA (clone Id HBODE48).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ArgSerHisSerSerTrpAsnSerAlaPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The specification describes a pharmaceutical composition, comprising a growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent, i.e. a protease. The inhibitor agent, i.e. a protease. The inhibitor i.e. a protease, that is upregulated in a damaged tissue such as a wound environment. Growth factors which are included in the composition of the invention are platelet-derived growth factor (PDGF), fibroblast growth factor (FGF), connective tissue derived growth factor (CGF), connectived growth factor (KGF), transforming growth factor (KGF), transforming growth factor (KGF), wascular endothelial growth factor (KGF), wascular endotelial growth factor (KGF), wascular endothelial growth factor (KGF), wascular endothelial growth factor (KGF), wascular endothelial growth
                                                                                                                          platelet-derived growth factor; poge; fibroblast growth factor; FGF; connective tissue derived growth factor; CTGF; chrysalin; VEGF; keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF; transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP; granulocyte macrophage colony stimulating factor; GM-CSF; uPA; vascular endothelial growth factor; urokinase plasminogen activator; dermal ulcer; wound; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition for the treatment of damaged tissue i.e. chronic wounds and dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a //tag= a //product= "connective tissue derived growth factor related protein"
                                                  Connective tissue derived growth factor related protein cDNA
                                                                                                     factor; protein inhibitor; protease; damaged tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mcintosh FS, Occleston NL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 546; 572pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 7..759
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80.40%
73.60%
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Davies MJ, Huggins JP,
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WPI; 2001-418351/44.

P-PSDB; AAB84599

factor

BP;

Sequence 1309

nvention

Alignment Scores:

Pred. No.: Score: Best Local Similarity:

Query Match

Percent Similarity

(PFIZ ) PFIZER LTD (PFIZ ) PFIZER INC

WO200149309-A2

Homo sapiens

21-DEC-2000; 29-DEC-1999; 486

246 100

8

186

9

120 366

306

546 200 909 220 240

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The invention provides novel human secreted proteins and polynucleotides encoding them. The secreted proteins can be expressed by standard recombinant methodology. The secreted proteins and polynucleotides are used to prevent, treat or ameliorate a medical condition in e.g. humans, also be used in diagnosting a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme treated include autoimmune diseases e.g. rheumatoid arthritis, there is treated include autoimmune diseases e.g. rheumatoid arthritis, or eraptoraliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infections caused by bacteria, viruses and fungi and coular disorders e.g. corneal infection. The polypeptides can also be used as used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, chemotaxis. The polypeptides can also be used as a food additive or represents a human secreted protein encoding cDNA.
                                                                                                                                                                                    Birse CE, Soppet DR, Olsen HS;
Shi Y, Choi GH, Fiscella M;
                                                                                                                                                                                                                                                                                                                                            17 isolated nucleic acid molecules encoding human secreted proteins, used to preventing, treating or ameliorating a medical condition \, -
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 427-428; 482pp; English.
                                                                                                                                                                                    Baker KP,
Duan DR,
                                                                                                                                                                               Rosen CA, Komatsoulis GA, 1
Moore PA, Wei P, Ebner R,
Ni J, Ruben SM, Barash SC;
                                          31-JAN-2000; 2000US-0179065.
04-FEB-2000; 2000US-0180628.
12-SEP-2000; 2000US-0231968.
                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
17:JAN-2001; 2001WO-US01431.
                                                                                                                                                                                                                                                                       WPI; 2001-476220/51.
P-PSDB; AAB85542.
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Sequence 1337 BP; 257 A; 427 C; 396 G; 252 T; 5 other;

5.19e-55 Length: 1337 1064.00 Matches: 184 80.40% Conservative: 17 73.60% Mismatches: 49 73.89% Indels: 0	US-10-010-408-2 (1-250) x AAH46952 (1-1337)	oren]	ATGAGAGGACACGAGAGACCCACCTGCGTTTCTCCCTCTCTGCTCTCTCT	ValCysAlaGlnLeuCysArgThrProCysThrCysProTrpThrProProGlnCysPro 40	GTGCGTACCCAGCTGTGCCGACACCATGTACTGCCCCTGGCCACCTCCCCGATGCCCG 166	GlnGlyvalProLeuValLeuAspGlyCysGlyCysCysLysValCysAlaArgArgLeu 60	167 CTGGGAGTACCCCTGGTGGCTGCTGCTGCTGCCGGGTATGTGCTGGCGGCTG 226	61y6luSerCysAspHisLeuHisValCysAspProSerGlnGlyLeuValCysGlnPro 80	GGGGAGCCCTGCGAACTAACTCTGCGACGCCAGCCAGGGCTGGTCTGCCAGCCC 286	GlyAlaGlyProGlyGlyHisGlyAlaValCySLeuLeuAspGluAspAspGlySerCys 100	GGGCAGGACCCGGTGGMCGGGGGCCCCTGTCTCGCAGAGGACGACGACGACGTGT 346
	2 (1-250) x A	MetArgGlySerF	ATGAGAGGCACACC	ValCysAlaGlnI	STGCGTACCCAGO	SlnGlyValProi	CTGGGAGTACCC	3lyGluSerCysA	GGGAGCCCTGCG	3lyAlaGlyProG	SGGCAGGACCCG
Alignment Scores: Pred. No.: Score: Score: Bercent Similarity: Best Local Similarity: Query Match:	-10-010-408-2	1	47 8	21 \	107	41 0	167	61 6	227	81 6	287
Al: Pre Scc Per Per Der DB:	us.	δ	qq	ογ	g	ò	Q	ογ	qq	ογ	QΩ

Qy 1	101	GluValAsnGlyArgArgTyr	GluValAsnGlyArgArgTyrLeuAspGlyGluThrPheLySProAsnCysArgValLeu 120
Dp 3	347	GAGGTGAACGGCCGCCTGTAT	rcggaagggagacttcagccccactgcagcatccgc 406
Qy 1	121		CysArgCysAspAspGlyGlyPheThrCysLeuProLeuCysSerGluAspValArgLeu 140
Db 4	407	TGCCGCTGCGAGGACGCGCGC	TTCACCTGCGTGCCGCTGTGCAGGATGTGCGGCTG 466
Qy 1	141		9ProLysArglleGlnValProGlyLysCysCysProGlu 160
Db 4	467	CCCAGCTGGGACTGCCCCCAC	CCCAGCTGGGACTGCCCCACCCCAGGGGGTCGAGGTCCTGGGCAAGTGCTGCCCTGAG 526
Oy 1	161		TrpValCysAspGMnGlyValThrProAlaileGlnArgSerThrAlaGlnGlyHisGln 180
Dp 2	527	TGGGTGTGCGGCCAAGGAGG	GGACTGGGGACCCAGCCCTTCCAGCCCAAGGACCCCAG 586
Qy 1	181	LeuSerAlaLeuValThrPro	LeuSerAlaLeuvalThrProAlaSerAlaAspAlaProCysProAsnTrpSerThrAla 200
Dp 2	587		CTGCCCCCTGGTGTCCCCTGCCAATGGAGCACGGCC 646
Qy 2	201		TrpGlyProCysSerThrThrCysGlyLeuGlyIleAlaThrArgValSerAsnGlnAsn 220
op qa	647	TGGGGACCCTGCTGGACCACC	TGTGGGCTGGGCATGCCGGGTGTCCAACCAGAAC 706
0y 2	221		ArgPheCysGlnLeuGluIleGlnArgArgLeuCysLeuProArgProCysLeuAlaAla 240
Db 7	707	CGCTTCTGCCGACTGGAGACC	CAGCGCCGCCTGTCCAGGCCCTGCCCACCCTCC 766
Oy 2	141	ArgSerHisSerSerTrpAsn	Seralaphe 250
Db 7	19	767 AGGGTCGCAGTCGACAAACAGTGCCTTC	AGTGCCTTC 796
Search comp Job time :	1et 242	Search completed: August 1, 2003, Job time : 242 secs	2003, 03:37:41
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Command line parameters:

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-Q-/cgn2_1/USPTO_spool/US10010408/runat_25072003_101856_17954/app_query.fasta_1.391
-DB-ISSUED_PATENTS_NA -OFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCXT=0 -UNITS-bits -STARX=1 - END=-1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFWI-pto -NORM-ext -HEAPSIZE=500 -WINLEN-0 -MAXLEN-2000000000
-USER-US10010408_@CGN_1_1_40_@runat_25072003_101856_17954 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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GENERAL INFORMATION:
APPLICANT: Cohen, Robert
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audre
APPLICANT: Hillan, Kennet
APPLICANT: Lawrence, Davi
APPLICANT: Levine, Arnold
APPLICANT: Pennica, Diane
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Gurney, Austin L.
Hillan, Kenneth J.
Lawrence, David A.
Levine, Arnold J.
Pennica, Diane
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Cohen, Robert
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ER APPLICATION NUMBER: US 60/063,704
ER FILING DATE: 1997-10-29
ER APPLICATION NUMBER: US 60/073,612
ER FILING DATE: 1998-02-04
ER APPLICATION NUMBER: US 60/081,695
ER FILING DATE: 1998-04-14
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AsnArgPheCysGlnLeuGluIleGlnArgArgLeuCysLeuProArgProCysLeuAla
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Sequence 13, APF-
Sequence 13, APF-
No. 6387657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
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APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P1176R2
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ORGANISM: Homo
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                                               GluValAsnGlyArgArgTyrLeuAspGlyGluThrPheLysProAsnCysArgValLeu
                                                                                                                GlyAlaGlyProGlyGlyHisGlyAlaValCysLeuLeuAspGluAspAspGlySerCys
                                                                                                                                                                               GlyGluSerCysAspHisLeuHisValCysAspProSerGlnGlyLeuValCysGlnPro
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GENERAL INFORMATION:
APPLICANT: Botstein, David A.
APPLICANT: Cohen, Robert
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Rood, William I.
FITTLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
FABRITED ADDITICATION NUMBER: US 60/063,704
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                                                                                US-10-010-408-2 (1-250)
                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                             ; TYPE: DNA; ORGANISM: Homo sapiens US-09-182-145-14
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EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-04-14
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APPLICANT: Botstein, David A.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Levine, Arnold J.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACI
FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT APPLICATION NUMBER: US 60/063,704
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER APPLICATION NUMBER: US 60/081,695
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  RESULT 6
US-09-182-145-39
; Sequence 39, Ap
; Patent No. 6387
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; SEQ ID NO 38
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Home
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CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/09/182,145B
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LOCATION: 1-841
OTHER INFORMATION: Seq
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TYPE: DNA
ORGANISM: Artificial sequence
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Hillan, Kenneth J.
Lawrence, David A.
                                                                                            GluValAsnGlyArgTyrLeuAspGlyGluThrPheLysProAsnCysArgValLeu
                                                                                                                                          GlyAlaGlyProGlyGlyHisGlyAlaValCysLeuLeuAspGluAspAspGlySerCys
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Wood, William I.
ProSerTrpAspCysProArgProLysArgIleGlnValProGlyLysCysCysProGlu
                                               CysArgCysAspAspGlyGlyPheThrCysLeuProLeuCysSerGluAspValArgLeu
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Sequence 1, Application Patent No. 5408040
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  FEATURE:
NAME/KEY:
LOCATION:
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                                                                           TOPOLOGY: line MOLECULE TYPE: C
                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D.
REGISTRATION NUMBER: 31,67
REFERENCE/DOCKET NUMBER: P
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APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE
                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 619-455-5100
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                   LENGTH: 2075 base pairs TYPE: nucleic acid STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
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T: 4225 Executive Square, Suite 1400
La Jolla
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RESULT 8
US-08-386-680-1
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 COMPUTER READABLE
                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                             APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISS
NUMBER OF SEQUENCES: 2
                                              CITY:
STATE:
                  COUNTRY: US
ZIP: 92037
                                                          ADDRESSEE: Spensley Horn Jubas
STREET: 4225 Executive Square,
CITY: La Jolla
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DB:
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Best Local Similarity:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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LENGTH: 2075 base pairs
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PRIOR APPLICATION DATA:
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STRANDEDNESS: single
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                                                  PheThrCysLeuProLeuCysSerGluAspValArgLeuProSerTrpAspCysProArg
                                                                                             CGCAGCGGAGAGTCCTTCCAGAGCAGCTGCAAGTACCAGTGCACGTGCCTGGACGGGGCG
                                                                                                                                                                                 GlyAlaValCysLeuLeuAspGluAspAspGlySerCysGluValAsnGlyArgArgTyr
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                                 GTGGGCTGCATGCCCCTGTGCAGCATGGACGTTCGTCTGCCCAGCCCTGACTGCCCCTTC
                                                                                                                          LeuAspGlyGluThrPheLysProAsnCysArgValLeuCysArgCysAspAspGlyGly
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US-08-459-717-
   Percent Similarity:
Best Local Similarity:
                                                                Alignment Scores:
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TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 1:
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PRIOR APPLICATION NUMBER: US 07/752,427
APPLICATION NUMBER: 30-Aug 1991
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John
REGISTRATION NUMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 619-455-5100
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CORRESPONDENCE ADDRESS:
                                                                                                                                           FEATURE:
                                                                                                                                                                                       TOPOLOGY: 1
MOLECULE TYPE:
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OPERATING SYSTEM:
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version
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DB:
                                                                                                                                                                                                                                                  Sequence 1, Application US/08712302 Patent No. 5783187
                                                                                                                                                                                                                                    GENERAL INFORMATION:
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati.
OPERATING SYSTEM: PC-DOS.
                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     APPLICANT: Grotendorst, Gary R. APPLICANT: Bradham Jr., Douglas M., TITLE OF INVENTION: CONNECTIVE TISSUE
                                                                           COUNTRY:
                                                                                             STATE:
                                                                                                             CITY:
                                                                                                                           STREET:
                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                           745
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                                                                                                                                                                       OF SEQUENCES:
                                                                                             La Jolla
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PC-DOS/MS-DOS
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Suite 1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PD TELECOMMUNICATION INFORMATION: TELEPHONE: 619-455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,680
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US/08/167,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: DB60R32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 11-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                                                GTGGGCTGCATGCCCCTGTGCAGCATGGACGTTCGTCTGCCCAGCCCTGACTGCCCCTTC
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ProLysArgIleGlnValProGlyLysCysCysProGluTrpValCysAspGlnGlyVal 167
                                                                                                                                                                                  ATCGGCGTGTGCACCGCC---AAAGATGGTGCTCCCTGCATCTTCGGTGGTACGGTGTAC
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               Percent Similarity:
Best Local Similari
                                                  Score:
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                                                                                Alignment Scores
                                                                                                                  US-08-880-031-1
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APPLICANT: Grotendorst, Gary R.

APPLICANT: Bradham Jr., Douglas M.,

APPLICANT: Bradham Jr., Douglas M.,

TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                            TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Relicurrent APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                 FEATURE:
                                                                                                                                                                                IMMEDIATE SOURCE:
CLONE: DB60R32
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CITY: La J
STATE: CA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 92037
                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Application 5916756
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5 Executive Square, Suite 1400
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                                 Length:
Matches:
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                                                                                                                                                                                                                                                                               Sequence 1, Application US/09097179 Patent No. 6149916
                                                                                                                           GENERAL INFORMATION:

APPLICANT: Grotendorst, Gary R.

APPLICANT: Bradham Jr., Douglas M.,

TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Spensley Horn Jubas & Lubitz

STREET: 425 Executive Square, Suite 1400

CITY: La Jolla
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                   CITY:
STATE:
                                                                                    COUNTRY: US
ZIP: 92037
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 PatentIn Release #1.0, Version
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Best Local Similarity:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
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NAME: Wetherell, Jr. Ph.D.
REGISTRATION NUMBER: 31,67
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PRIOR APPLICATION DATA:
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LOCATION:
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                                                             LeuAspGlyGluThrPheLysProAsnCysArgValLeuCysArgCysAspAspGlyGly 127
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEPAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 1:
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FEATURE:
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APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH
                                                                      NO:::
                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                 NAME/KEY:
LOCATION:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
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SYSTEM: PC-DOS/MS-DOS
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DB:
                                                                                                                                                                                                                                       Sequence 7, Application US/09142569
Patent No. 6413735
GENERAL INFORMATION:
APPLICANT: Lau, Lester F.
COUNTY FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                          TITLE OF INVENTION: Extracellular Matrix Signalling Molecules NUMBER OF SEQUENCES: 17
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                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: United
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                                                                                                                                                               STREET: 6300 Sears Tower,
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DB:
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
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FILING DATE: 02-Apr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                 ThrProAlaIleGlnArgSerThrAlaGlnGlyHisGlnLeuSerAlaLeu----
                                                                                                           GTGGGCTGCATGCCCCTGTGCAGCATGGACGTTCGTCTGCCCAGCCCTGACTGCCCCTTC
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                                                                                                                                                                                                                                                         ATCGGCGTGTGCACCGCC - - - AAAGATGGTGCTCCCTGCATCTTCGGTGGTACGGTGTAC
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OTHER INFORMATION: "CTGF cDNA coding sequence"
                                        CCGAGGAGGGTCAAGCTGCCCGGGAAATGCTGCGAGGAGTGGGTGTGACGAG-----
                                                                                                                                                                PheThrCysLeuProLeuCysSerGluAspValArgLeuProSerTrpAspCysProArg
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REGISTRATION NUMBER: 3
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--ValThrProAlaSerAlaAspAlaProCysProAsnTrpSerThrAla
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                                                                                                                                                                  Query Match:
                                                                                                                                                                                     Best Local Similarity:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 30-MAY
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                                                          GCCTTCGTGGTCCTCGCCCTCTGCAGCCGGCCGGCCGTCGGCCAGAACTGCAGCGGG
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CTGF
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VENTION: CONNECTIVE TISSUE GROWTH
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AspGlyCysGlyCysCysLysValCysAlaArgArgLeuGlyGluSerCysAspHisLeu

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uCysLeuBroArgProCysLeuAla 239	221 ArgPheCysGlnLeuGluIleGlnArgArgLeuCysLeuProArgProCysLeuAla 239	221	Ş
CATCTCCACCCGGGTTACCAATGACAAC 804	TGGAGCGCCTGTTCCAAGACCTGTGGGATGGG	745	ğ
yIleAlaThrArgValSerAsnGlnAsn 220	TrpGlyProCysSerThrThrCysGlyLeuGlyIleAlaThrArgValSerAsnGlnAsn	201	Ą
AGCCAACTGCCTGGTCCAGACCACAGAG 744		685	8
pAlaProGysProAsnTrpSerThrAla 200	;ValThrProAlaSerAlaAspAlaProGysProAsnTrpSerThrAla 200	185	Ą
GCCTGCCGTCGCGGCTTACCGACTGGAA 684		634	မွ
yHisGlnEeuSerAlaLeu 184	ThrProAlaIleGlnArgSerThrAlaGlnGlyHisGlnEeuSerAlaLeu 184	168	ă
CGAGGAGTGGGTGTGACGAG 633	CCGAGGAGGTCAAGCTGCCCGGGAAATGCTGCGAGGAGTGGGTGTGTGACGAG 633	580	ğ
sProGluTrpValCysAspGlnGlyVal 167		148	ž
TCGTCTG@CCAGCCCTGACTGCCCCTTC 579	520 GTGGGCTGCATGCCCCTGTGCAGCATGGACGTTCGTCTGGCCAGCCCTGACTGCCCCTTC 579	520	岁
lArgLeuProSerTrpAspCysProArg 147	PheThrCysLeuProLeuCysSerGluAspVal	128	Ϋ́
GTACCAGTGCACGTGCCTGGACGGGGCG 519	460 CGCAGCGGAGAGTCCTTCCAGAGCAGCTGCAAGTACCAGTGCACGTGCCTGGACGGGGC 519	460	용
gValLeu@ysArgCysAspAspGlyGly 127	LeuAspGlyGluThrPheLysProAsnCysArc	108	¥
TCCCTGCATCTTCGGTGGTACGGTGTAC 459	ATCGGCGTGTGCACCGCCAAAGATGGTGCTCCCTGCATCTTCGGTGGTACGGTGTAC 459	403	퓻
ySerCys@luValAsnGlyArgArgTyr 107		88	¥
TGACTTCGGCTCCCCGGCCAACCGCAAG 402	GACCCCTGCGACCCGCACAAGGGCCTCTTCTGT	343	ğ
sGlnProĠlyAlaGlyProGlyGlyHis 87	HisValCysAspProSerGlnGlyLeuValCysGlnProGlyAlaGlyProGlyGlyHis 87	68	¥
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Search completed: August 1, 2003, 04:22:58 Job time : 59 secs

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Title:
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-DB-Published_Applications_NA -QFMT=fastap -SUFETX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST=45 -DCCALIGN=200 -THR_SCORE=-pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER-US10010408_@CGN_1_157_@runat_25072003_101856_17969
-NCPU=6 -TCPU=3 -NO_MMAP -LARGEQUERY -NCEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                        : /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
    /cgn2_6/ptodata/2/pubpna/USO8_NEW, PUB.seq:*
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    /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
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                           Description
Sequence 3, Appli
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US-10-010-408-3
                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10010408 Publication No. US20020165185A1
                                                                                                                                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: John J. Castellot, Jr.
TITLE OF INVENTION: No. US20020165185A1el Heparin-Induced CCN-Like Molecules
and Uses Therefor
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1308.
             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,408
FILING DATE: 07-Dec-2001
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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CITY: Boston
STATE: Massachusetts
CLASSIFICATION: <Unknown>
                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                        ADDRESSEE: LAHIVE & COCKFIELD,
                                                                                                                                                                                                                                                                                                                                                                                                                                 28 State Street
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US-10-1146-726-319
US-10-146-727-319
US-10-146-727-319
US-10-146-727-319
US-10-146-727-319
US-10-123-390-4319
US-10-123-904-319
US-10-127-825A-319
US-10-124-127-825A-319
US-10-124-125-319
US-10-140-474-319
US-10-141-141-319
US-10-141-141-319
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SEQUENCE CHARACTERISTICS:
LENGTH: 753 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 1..750
SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)27-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: cDNA
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                                  GlyGluSerCysAspHisLeuHisValCysAspProSetGlnGlyLeuValCysGlnPro
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                                                                                CCCAGCTGGGACTGCCCACGCCCCAAGAGAATACAGGTĞCCAGGAAAGTGCTGCCCCGAG
                                                                                           ProSerTrpAspCysProArgProLysArgIleGlnValProGlyLysCysCysProGlu
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APPLICATION NUMBER: 09/044,273
FILING DATE: March 19, 1998
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
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STRANDEDNESS: single
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Conservative:
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Query Match:
US-10-010-408-2 (1-250)
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Publication No. US20020165185A1
GENERAL INFORMATION:
APPLICANT: John J. Castellot,
                                                                                                                                                                                                                                                                                                                    TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                             No . .
                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 249..1001
SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/044,273
FILING DATE: March 19, 1998
APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NO.
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TrpGlyProCysSerThrThrCysGlyLeuGlyIleAlaThrArgValSerAsnGlnAsn
                                                                                                                                                                                                                                                                                                                                                                                                NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: LAHIVE & COCKFIELD, STREET: 28 State Street
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                                                                                                                                                                                           Sequence 12, Application US/10010408 Publication No. US20020165185A1 GENERAL INFORMATION:
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                        APPLICANT: John J. Castellot, Jr.
TITLE OF INVENTION: No. US20020165185Alel Heparin-Induced CCN-Like Molecules
and Uses Therefor
                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE
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COUNTRY: USA
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                                                                                         CITY: Boston
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NAME: AMY E. MANDIRAGOURAS
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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                                                                                         AspCysProArgProLysArgIleGlnValProGlyLysCysCysProGluTrpValCys
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TYPE: nucleic acid
STRANDEDNESS: single
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FILING DATE: March 19, 1998
APPLICATION NUMBER: «Unknown»
FILING DATE: «Unknown»
  LeuValThrProAlaSerAlaAspAlaProCysProAsnTrpSerThrAlaTrpGlyPro
                                        AspGlnGlyValThrProAlaIleGlnArgSerThrAlaGlnGlyHisGlnLeuSerAla
                                                                             GACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGCCCCGAGTGGGTATGT
                                                                                                                             GATGACGGTGGCCTGCCTGCCGCTGTGCAGGATGTGCGGCTGCCCAGCTGG
                                                                                                                                          AspAspGlyGlyPheThrCysLeuProLeuCysSerGluAspValArgLeuProSerTrp
                                                                                                                                                                               GGCCGCAGGTACCTGGATGGAGAGACCTTTAAACCCCAATTGCAGGGTCCTGTGCCGCTGT
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; ORGANISM: MUS
US-10-112-267-17
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APPLICANT: Cohen, Robert
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: AND ICATION WISP POLYPEPTIDES AND NUCLEIC AC:
FILE REFERENCE: P1176R2
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US-10-112-267-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/112,267
CURRENT FILLING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION PILING DATE: LEARLIER APPLICATION NUMBER: EARLIER APPLICATION NUMBER: EARLIER APPLICATION FILING DATE: EARLIER APPLICATION NUMBER: EA
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DATE: 1998-02-04
APPLICATION NUMBER: US 60/081,695
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                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/112,267

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US,
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US,
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Lewine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUMBER OF THE REFERENCE: P1176R2
                                           ; TYPE: DNA
; ORGANISM: Mus
US-10-112-267-18
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US-10-112-267-18/c
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                                                                                           SEQ ID NO 18
LENGTH: 1734
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Publication No. US20030068678Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Botstein, APPLICANT: Cohen, RAPPLICANT: Goddard,
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Sequence 319, Application US/10137866
Publication No. US20030129689A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini Maureen
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
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Score:
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Matches:
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C151
CURRENT APPLICATION UMBER: US/10/137,866
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-08-16
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059120
PRIOR APPLICATION NUMBER: 60/059121
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OR FILING DATE: 1997-09-18
OR APPLICATION NUMBER: 60/059352
OR FILING DATE: 1997-09-19
OR APPLICATION NUMBER: 60/05958
OR FILING DATE: 1997-09-19
OR APPLICATION NUMBER: 60/059836
OR FILING DATE: 1997-09-24
OR APPLICATION NUMBER: 60/062250
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/06285
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/06287
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/06281
OR APPLICATION NUMBER: 60/062814
OR APPLICATION NUMBER: 60/062816
OR APPLICATION NUMBER: 60/063045
                                                                                                                                                                                                                   OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063082
OR FILING DATE: 1997-10-31
OR APPLICATION NUMBER: 60/063127
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063327
OR FILING DATE: 1997-10-27
OR FILING DATE: 1997-10-27
OR APPLICATION NUMBER: 60/063329
OR APPLICATION NUMBER: 60/063329
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Godowski, Paul
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E: 1997-10-28
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1997-11-24

LING DATE: 1997-11-24

LOR APPLICATION NUMBER: 60/06921

TOR FILING DATE: 1997-12-11

PR REPLICATION NUMBER: 60/06921

R RILING DATE: 1997-12-11

DR FILING DATE: 1997-12-11
DR APPLICATION NUMBER: 60/06
WR FILING DATE: 1997-12-11
DR APPLICATION NUMBER: 60/06
DR FILING DATE: 1997-12-16
DR APPLICATION NUMBER: 60/07

NUMBER: 60/069334 : 1997-12-11

60/072320 60/069694 APPLICATION NUMBER: 60/066453

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OR APPLICATION NUMBER: 7

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FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/06453
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APPLICATION NUMBER: 60/066511

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60/065186 60/064809

APPLICATION

NUMBER: 60/066364

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DR FILING DATE: 1998-01-23
DR APPLICATION NUMBER: 60/073612
DR FILING DATE: 1998-02-04
DR APPLICATION NUMBER: 60/074086
DR FILING DATE: 1998-02-09
DR APPLICATION NUMBER: 60/077791
DR FILING DATE: 1998-03-12
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DR FILING DATE: 1998-03-20
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DR FILING DATE: 1998-03-25
DR APPLICATION NUMBER: 60/079294
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DR APPLICATION NUMBER: 60/079728
DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/08103
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DR APPLICATION NUMBER: 60/080165
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DR FILING DATE: 1998-04-15

DR APPLICATION NUMBER: 60/081818

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DR FILING DATE: 1998-04-24

DR APPLICATION NUMBER: 60/083322

DR FILING DATE: 1998-04-28

DR APPLICATION NUMBER: 60/083545

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NUMBER: 60/084637 1998-05-07

NUMBER: 60: 1998-05-1

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                                                                                                     SEQ
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                                                                                                                                                        APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C308
                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/146,726
CURRENT FILING DATE: 2002-05-15
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Filvaroff, Ellen
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                   GENERAL INFORMATION:
APPLICANT: Baker, Kev
APPLICANT: Beresini
APPLICANT: Deforge,
APPLICANT: Desnoyer;
APPLICANT: Filvarof,
APPLICANT: Gao, Wei-r,
APPLICANT: Gao, Wei-r,
APPLICANT: Goddard,
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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                                           Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
                                                                            DeForge, Laura
                                                                                        Beresini, Maureen
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US-10-146-727-319
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C312
CURRENT APPLICATION NUMBER: US/10/146,727
CURRENT FILING DATE: 2002-05-15
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 319
LENGTH: 1266
TYPE: DNA
COMMENT OF SECTION
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                                                 LeuSerAlaLeuValThrProAlaSerAlaAspAlaPr@CysProAsnTrpSerThrAla
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Smith, Victoria
Stewart, Timothy /
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Best Local Similarity:
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US-10-146-788-319
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LENGTH: 1266
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C322
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Filvaroff, Ellen
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                                                                                                 Prior Application removed
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 319
LENGTH: 1266
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C397
                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/152,380 CURRENT FILING DATE: 2002-05-21 Prior Application removed - See Palm or F
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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                                           Gerritsen, Mary E
                                                      Gao, Wei-Qiang
                                                                Desnoyers, Luc
Filvaroff, Ellen
                                                                                       DeForge, Laura
                                                                                                  Beresini, Maureen
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LENGTH: 1266
TYPE: DNA
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C412
CURRENT APPLICATION NUMBER: US/10/153,934
CURRENT FILING DATE: 2002-05-22
Prior Application removed - See file Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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                                                               LeuSerAlaLeuValThrProAlaSerAlaAspAlaPtoCysProAsnTrpSerThrAla
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Wood, William
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PRIOR FILING DATE: 1997-09-17
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TITLE OF INVENTION:
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DR APPLICATION NUMBER: 60/059836
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APPLICATION NUMBER: 60/063082
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OR APPLICATION NUMBER: 60/064809
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OR APPLICATION NUMBER: 60/065186
OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/065846
OR FILING DATE: 1997-11-17
OR APPLICATION NUMBER: 60/066364
OR FILING DATE: 1997-11-21
OR APPLICATION NUMBER: 60/066453
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OR APPLICATION NUMBER: 60/069212
OR APPLICATION NUMBER: 60/069278
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OR APPLICATION NUMBER: 60/06934
OR FILING DATE: 1997-12-11
OR APPLICATION NUMBER: 60/069694
OR FILING DATE: 1997-12-16
OR APPLICATION NUMBER: 60/072320
OR FILING DATE: 1998-01-20
OR FILING DATE: 1998-02-09
OR APPLICATION NUMBER: 60/074086
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OR APPLICATION NUMBER: 60/079294
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/079294
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079728
OR APPLICATION NUMBER: 60/08120

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DR FILING DATE: 1998-04-14
DR APPLICATION NUMBER: 60/081817
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Smith, Victoria
Stewart, Timothy .
Tumas, Daniel
                                                               Gerritsen, Mary E.
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Filvaroff, Ellen
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 319
LENGTH: 1266
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APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 319
LENGTH: 1266
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                GluValAsnGlyArgArgTyrLeuAspGlyGluThrPheLysProAsnCysArgValLeu
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  GAGGTGAACGGCCGCCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCAGCATCCGC 369
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                                                                                                                                                      ; SEQ ID NO 319
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: HOMM
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                                                                                                                                                                                                                                      APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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Search completed: August 1, Job time : 237 secs

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-DB=EST -OFMT=fastap -SUFFIX=P2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXY=0
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10010408_GCGN_1_1_1906_GTRUNAT=0 -MAXLEN=200000000
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-MODEL=frame+_p2n.model
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## SUMMARIES

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## ALIGNMENTS

RESULT 1
BM805088
LOCUS
DEFINITION
AGENCOURT\_6490429 NIH\_MGC\_125 Homo sapiens cDNA clone IMAGE:5725937

ACCESSION
BM805088
VERSION
KEYWORDS
ORGANISM
CORGANISM
EUCHORS
AUTHORS
REFERENCE
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

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Tissue Procurement: Invitrogen
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Contact: Ro
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Location/Qualifiers
                              ProSerTrpAspCysProArgProLysArgIleGlnValProGlyLysCysCysProGlu
                                                                                  CysArgCysAspAspGlyGlyPheThrCysLeuProLeuCysSerGluAspValArgLeu
                                                                                                                                         GluValAsnGlyArgArgTyrLeuAspGlyGluThrPheLysProAsnCysArgValLeu
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_125"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-*Organ: Ovary (pool of 3); Vector: pcMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1:3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Email: cgapbs-r@
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/clone="IMAGE:5805819"
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cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2045 row: k column: 04
High quality sequence stop: 752.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 979)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
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/lab_host="DHIOB (phage resistant)"
/note="Organ: breast; Vector: pOTB7; Site_1: EcoRI;
/note="Organ: breast; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II gr. (Life Technologies).
Note: this is a NIH_MGC Library."
Note: this is a NIH_MGC Library."
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                Contact: Robert Strausberg,
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Plate: LLAM11450 row: j column: 11
High quality sequence stop: 865.
Location/Qualifiers
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                                                                                                  CTGCGAGGACGGCGTCCACCTGCGTGCCGCTGTGCAGCGAGGATGTGCGGCTGCCCAG
                                                                                                                 gCysAspAspGlyGlyPheThrCysLeuProLeuCysSerGluAspValArgLeuProSe
                                                                                                                                                     CCCTGCGACCAACTCCACGTCTGCGACGCCAGCCA-GGCCTGGTCTGCCAGCCCGGGGCA
                                                                                                                                                                                                                                                                                         SerCysAspHisLeuHisValCysAspProSerGlnGlyLeuValCysGlnProGlyAla 82
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                                                                                                                                                                                                                                                                                                                                                                                        ACCCAGCTGTGCCCGACACCATGTACCTGCCCCTGGCCACCTCCCCGATGCCCGCTGGGA
|CysAspGlnGlyValThrProAlaIleGlnArgSerThrAlaGlnGlyHisGlnLeuSe
                                           CTGGGACTGCCCCACCCCAGGAGGGTCGAGGTCCTGGGCAAGTGCTGCCCTGAGTGGGT
                                                          rTrpAspCysProArgProLysArgIleGlnValProGlyLysCysCysProGluTrpVa 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-Torgan: pooled brain, lung, testis; vector: pckV-SpORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

3 10 c 288 g 154 t
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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BM043988
BM043988.1 GI:16773255
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelomammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo (bases 1 to 750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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/db_xref="taxon:9606"
/clone="IMAGE:5446794"
/clone_lib="NIH_MGC_40"
/tissue_type="carcinoma.cell libe"
/tissue_type="carcinoma.cel
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BM921531
Tissue Programment: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/
National institutes of Health, I
Unpublished (1999)
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                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                        Mammalia; Eutheria; 1 (bases 1 to 1006)
                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                              Email:
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Sutheria; Primates; Catarrhini; Hominidae;
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Plate: LLAM12788 row
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CTTGTCTCTCCCTGCCCCTGGTGTCCCCTGCCCAGAATGGAGCACGNGCCTGGGGACC
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Location/Qualifiers
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a 368 c 317 g 169 t 4 others
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/clone_lib="NIH_MGC_115"
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/db_xref="taxon:9606"
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1 (bases 1 to 651)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                 /clone="IMAGE:5258159"
/clone_lib="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Ozgan: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Ozgan: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Ozgan: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Cotantly cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGAG(G), Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MCC Library. | "
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/db_xref="taxon:9606"
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                                                   cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2047 row: k column: 19
High quality sequence stop: 517.
Location/Qualifiers
                                                                                                                                                                                              Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia: Eutheria: Primates: Catarrhini; Hominidae: 1 (bases 1 to 1073)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections 1 (100)
                                                                                                                                                                                                                                                                                      5', mRNA sequence
BQ073722
BQ073722.1 GI:199
                                                                                                                                                                                                                                                                                                            BQ073722
AGENCOURT_7046577
5', mRNA sequence
                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                          Contact: Robert Strausberg,
                                                                                                                                                                                       Unpublished (1999)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5806602"
/clone_lib="NIH_MGC_101"
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NIH_MGC_101
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                                                                                               Leu-GlyIleAla---ThrArgValSerAsnGlnAsnArgPheCysGlnLeu-GluIleG
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US-10-010-408-2 (1-250) x BQ073722
                    GlyGluThrPheLysProAsnCysArgValLeuCysArgCysAspAspGlyGlyPheThr
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/lab_host="DH10B (phage-resistant)".
/note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5: adaptor:
GGCACGAGG). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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cDNA Library Arrayed by: The I.M.A.G.
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 GlyAlaValCysLeuLeuAspGluAspAspGlySerCysGluValAsnGlyArgArgTyr
                                                          HisValCysAspProSerGlnGlyLeuValCysGlnProGlyAlaGlyProGlyGlyHis
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/lab_host="PH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EccRI; cDNA made by oligo-dT priming.
Directionally cloned into EccRI/XhoI sites using the
following 5' adaptor: GGCACGAGG(). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MCC_Library. | "
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/db_xref="taxon:9606"
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BI457367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI457367 916 bp mRNA linear bal 41-ro 603185689F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5258398
                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI457367.1
EST.
                                                                                                                                                                                                                           http://image.llnl.gov
Plate: LLCM1870 row: a column:
                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                               CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:5288398"
/clone=Lib="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DHHOB (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
                                                                                                                                                                                      ocation/Qualifiers
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Euteleostomi; Homo.

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Collection (MGC)

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603072631F1 NIH_MGC_119
    mRNA sequence
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a 305 c 304 g 170 t 1 others
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Indels:
Gaps:
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AUTHORS
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Clone distribution: MCC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11408 row: n column: 07
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
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1 (bases 1 to 888)
                                                                                                             HisValCysAspProSerGlnGlyLeuValCysGlnProGlyAlaGlyProGlyGlyHis
LeuAspGlyGluThrPheLysProAsnCysArgValLeuCysArgCysAspAspGlyGly
                                                                 GlyAlaValCysLeuLeuAspGluAspAspGlySerCysGluValAsnGlyArgArgTyr
                                                                                                                                                                                             AspGlyCysGlyCysCysLysValCysAlaArgArgLeuGlyGluSerCysAspHisLeu
                                                  GGGGCCCTGTGCCTCTTGGCAGAGGACGACAGCAGCTGTGAGGTGAACGGCCGCCTGTAT
                                                                                                                                                                                                                                           CACCTCCTGGCTTC-TCCCTCCTCTGCCTCCTCAAAGGTGCGTACCCAGCTGTGCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           this is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5164614"
/clone_lib="NIH_MGC_119"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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                                                                                                                                                                                                                                                 quality sequence stop:
                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5169065"
/clone_lbb="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note=*organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: ECORV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C Gruber (Invitrogen). Research Genetics tracking code 013. Note:
                                                                                                                                                                                                                                 Location/Qualifiers
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1 (bases 1 to 790)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
Contact: Robert Strausberg, Ph.D.
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/lab_host="DBIOB (phage-resitane)"
/note="organ: prostate; vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACGAGGG. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5452480"
/clone_lib="NIH_MGC_40"
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AGENCOURT_8931684 NIH_MGC_40
5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.gov
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                                              /tissue_type="carcinoma, cell line"
/lab_host="DBHOB (phage resistant)"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NH_MGC Library."
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/db_xref="taxon:9606"
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                      UW2109
GlaxoSmithKline
709 SwedeLand Road, P.O. Box 15
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-l@gsk.com
Seq primer: T7
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Lark,M.W.
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 620)

Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Hominidae; Connor,J.R., Badger,A.M., Lee,J.C., Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C.,
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HNC57-1-D9.R
                                                                                                            Osteoarthr. Cartil.
21482651
                                                                                                                    Identification and initial characterization sequenced tags (ESTs) each from adult human osteoarthritic cartilage cDNA libraries Osteoarthr. Cartil. 9 (7), 641-653 (2001)
                                                                                                                                                                                                                                     Homo
                                                                                                  Contact: Sanjay Kumar
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AGENCOURT 6492297 N
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name and the state of Health, Mational Institutes of Health, Munublished (1999)
                                Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

1 (Dases 1 to 1166)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgGlySerProLeuIleHisLeuLeuAlaThrSerPheLeuCysLeuLeuSerMetVal
                                                                                                                                                                                                                                                                                                                                    CGTACCCAGCTGTGCCCGACACCATGTACCTGCCCCTGGCCACCTCCCCGATGCCCGCTG
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                                                                                                                                                                                                  GTGTGCGGCCAAGGGGGGGACTGGGGACCCAGCCCCTTCCAGCCCAAGGA
                                                                                                                                                                                                                                               AGCTGGGACTGCCCCCACCCCAGGAGGGTCGAGGTCCTGGGCAAGTGCTGCCCTGAGTGG
                                                                                                                                                                                                                                                                                         CGCTGCGAGGACGGCGTCCACCTGCCGTGCCGCTGTGCAGCGAGGATGTGCGGCTGCCC
                                                                                                                                                                                                                                                                                                      ArgCysAspAspGlyGlyPheThrCysLeuProLeuCysSerGluAspValArgLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                            GAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGCCAGGGCCTGGTCTGCCAGCCCGGG
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="HNC (Human Normal C:
/clone_lib="HNC (Human Normal C:
/tlssue_type="cartilage"
/lab_host="E.coli DH10 B"
/note="vector: pSPORT I: Site_1
Directional"
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Matches:
Conservative:
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5 Homo
                        Mammalian
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sapiens
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                        Gene
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133
31
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                                                                                                                                              linear EST 20-FEB-2002 CDNA clone IMAGE:5589134
                        Collection
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                                                                  Euteleostomi;
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326 81 266 61 206

566 161 506 141 446 121 386 41

Oy 21 ValCysAlaGinLe	Pred. No.: 785. Score: 785. Percent Similarity: 73.5 Best Local Similarity: 66.6 Best Watch: 54.5 Query Match: 13 DB: 13 DB: 13 DB: 14.5000 x Bh	COMMENT CONTROL CONTRO	
ValCysAlaGlnLeuCysArgThrProCysThrCysPagoTrpThrProProGlnCysPro 40	5e-54 Length: 1166 15.00 Matches: 149 15.54 Conservative: 15 1828 Mismatches: 43 1.828 Mismatches: 46 166 170 Gaps: 46 180543799 (1-1166)	Email: Compart Strausberg, Ph.D.  Email: Capabbs - Remail. Inh gov Tissue Procurement: Invitrogen cDNA Library Preparation: Life Technologies, Inc. cCNA Library Preparation: Life Technologies, Inc. cCNA Library Inc. cOrporation Clone Inc. consortium/ELNL at: http://image.llnl.gov plate: LLAM12361 row: f column: 15 High quality sequence stop: 547. Location/Qualifiers //Location/Qualifiers //Location/Qualifiers //Location/Qualifiers //Clone="THAGE:.5589134" //Clone="THAGE:.5589134" //Clone="THAGE:.5589134" //Clone=lib="NHH_MGC_125" //Lab_host="DHIOB" //Lab_	

Db	Qy	Db	Qy	Db	Qy	Db
859 TGGGC 863	210 euGly 211	799 CTGCCCCAAAATGGGAGCAACGGGCCTGGGGGGACCCTTGCTCCAACACCCTGTGGGGCC 858	193 oCys-ProAsnTrpSerThrAlaTrpGlyProCysSerThrThrCysGlyL 210	739 ACCCCAAGGACCCCAGNNTTTCTGGGCCTTGTCTCTTCCCCTGGCCCCTGGNGGTCCCC 798	LeuSerAlaLeuValThrProAlaSerAlaAs	

Search completed: August 1, 2003, 04:47:29 Job time: 1466 secs

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Products from the present invention can be used to treat Wilsy-related
C disorders such as breast, ovarian, and colon cancer or melanoma. The
C products can be used to treat arteriosclerosis. The products can also be
C used to treat other diseases e.g. benign and malignant tumours,
CC leukaemia and lymphoid malignancies, neuronal, glial, astrocytal,
CC hypothalamic and other glandular, macrophagal, epithelial, stromal, and
CD blastocoelic disorders, haematopoiesis-related disorders, kidney
CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney
CC disorders, bone-related disorders such as osteoporosis, trauma such as
CC burns, incisions, and other wounds, connective tissue disorders,
CC catabolic states, testicular-related disorders, and inflammatory,
CC angiogenic and immunologic disorders including arteriosclerosis. The
CC products can also be used for detection and diagnosis especially of
CC individuals with neoplastic cell growth or proliferation. The products
CC can be used in the production of transgenic or knock-out animals.

Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
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29-OCT-1997;
03-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes Wnt-1 induced secreted polypeptides. WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, Wish and WISP-3 have homology to connective tissue growth factor (CTGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 246; 284pp; English.
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Lawrence DA,
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                                                                                                                                                                                                                                                                                                                                                                     y Match
      123
                                                            61
                                                                                                                                                                            Similarity
CDDGGFTCLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGV-TPAIQRSTAQGHQL
                                                   SCDHLHVCDPSQGLVCQPGAGPSGRGAVCLFEEDDGSCEVNGRRYLDGETFKPNCRVLCR 120
                                                                                         SCDHLHVCDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                     249
                                                                                                                                                                                                                                                                                                            Conservative
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97US-0063704.
98US-0073612.
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Pennica D,
                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                         Score 1298.5;
Pred. No. 5.8
                                                                                                                                                                                                                                                                                                            Mismatches
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Roy MA,
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                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                 The present invention describes Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-3 have homology to connective tissue growth factor (CTGF). Products from the present invention can be used to treat WISP-related disorders such as breast, ovarian, and colon cancer or melanoma. The products can be used to treat arteriosclerosis. The products can also be used to treat other diseases e.g. benign and malignant tumours, leukaemia and lymphoid malignancies, neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, and blastocoelic disorders, haematopolesis-related disorders, kidney disorders, skin disorders, desmoplasia, fibrotic lesions, kidney disorders, bone-related disorders such as osteoporosis, trauma such as burns, incisions, and other wounds, connective tissue disorders, testicular-related disorders, and inflammatory, catabolic states, testicular-related disorders, and inflammatory.
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29-OCT-1997;
03-FEB-1998;
                              products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The production be used in the production of transgenic or knock-out animals.

Antibodies can be used to induce death in WISP-1, 2 or 3 overexpres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 247;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
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א AJ,
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Pennica D,
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Roy MA,
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                                     2 or 3 overexpressing
                                                                                                  products
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New isolated Wnt-1 induced secreted polypeptides, WISP-1,

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Best Local S
Matches 226
                                                                                                                          connective tissue growth factor; cancer; melanomä; arteriosclerosis; leukaemia; lymphoid malignancy; haematopolesis-related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion; kidney disorder; bone-related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation;
                                                                                                                                                                                                                                                                                                      WNT-1 induced secreted protein; WISP-1; WISP-2;
                                                                                                                                                                                                                                                                                                                                                                              Mouse WISP-2 protein SEQ ID NO:78.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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Pred. No. 1e-90;
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                                                                                                                                                                                                                                                                                                         WISP-3; CTGF; tumour;
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29-OCT-1997;
03-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-3 have homology to connective tissue growth factor (CTGF). Products from the present invention can be used to treat WISP-related disorders such as breast, ovarian, and colon cancer or melanoma. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 245-246; 284pp; English
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                   LSALVTPASADAPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQRRLCLPRPCLAA
                                                                                                                                                                                                  ESCDHLHVCDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLC
   RSHSSWNSAF 250
                                                                                                                                            RCDDGGFTCLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGV-TPAIQRSTAQGHQ
                                                                                                                                                                               ESCDHLHVCDPSQGLVCQPGAGPSGRGAVCLFEEDDGSCEVNGRRYLDGETFKPNCRVLC
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Levine AJ,
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RESULT 2
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                                                                                          Castellot JJ
                                                                                                                                            19-MAR-1998;
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                                                                                                                                                                                                                                                                          cardiovascular
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DB; AAZ07521.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250;
         acid sequences encoding rat heparin-induced CCN-like protein, methods to identify modulators or in diagnostic applications
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Pred. No. 1.4e-100;
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cell proliferation; fibrotic disorder
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RESULT 3
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Best Local S
Matches 227
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29-OCT-1997;
03-FEB-1998;
     WPI; 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour connective tissue growth factor; cancer; melanoma; arteriosclerosis; leukaemia; lymphoid malignancy; haematopoiesis-related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion; kidney disorder; bone-related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides a rat heparin-induced CCN-like protein (HICP) protein. Agents that stimulate or inhibit HICP protein activity or expression, antisense HICP nucleic acid molecules and HICP antibodies, can be used to modulate cell-associated activity. HICP modulators can be used to treat disorders characterized by aberrant HICP protein activity or expression. Probes capable of hybridizing to HICP mRNA or antibodies specific for HICP can be used to treat disorders, such as a cardiovascular or fibrotic disorder, characterized by aberrant cell proliferation. The present sequence represents the rat HICP mature polypeptide.
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DB; AAX76488.
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                                                                                                                                             1308.5
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Copyright (c) 1993 - 2003 Compügen Ltd.
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## ALIGNMENTS

RESULT 1
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ID AAY2 WPI; 1999-562060/47. N-PSDB; AAZ07516, AAZ07517. Castellot JJ; 18-MAR-1999; 23-SEP-1999 W09947556-A2 Rattus sp. Heparin-induced CCN-like protein; HICP; cell-associated activity; rat; cardiovascular disorder; aberrant cell proliferation; fibrotic disorder. Rat HICP polypeptide 26-NOV-1999 AAY27434; AAY27434 standard; Protein; 250 (TUFT ) TUFTS 19-MAR-1998; (first entry) COLLEGE. 98US-0044273 99WO-US05999 B

Nucleic acid sequences encoding rat heparin-induced CCN-like protein, used in methods to identify modulators or in diagnostic applications

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29-OCT-1997;
03-FEB-1998;
The present invention describes Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-3 have homology to connective tissue growth factor (CTGF). Products from the present invention can be used to treat WISP-related
                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour connective tissue growth factor; cancer; melanoma; arteriosclerosis; leukaemia; lymphoid malignancy; haematopoiesis-related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion; kidney disorder; bone-related disorder; osteoporosis; trauma; burn; kidney disorder; bone-related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation;
                                                                                                            Disclosure;
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Levine AJ,
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97US-0063704.
98US-0073612.
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AAY17684
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XX AAY1
XX O6-A
DT O6-A
DX MOUS
XX WNT
KW CONN
KW CONN
KW Liss
KW Kidn
KW CONN
KW LEST
XX WO99
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29-OCT-1997;
03-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       products can be used to treat arteriosclerosis. The products can used to treat other diseases e.g. benign and malignant tumours, leukaemia and lymphoid malignancies, neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stroma blastocoelic disorders, haematopoissis-related disorders, tissuedisorders, skin disorders, desmoplasia, fibrotic lesions, kidney disorders, bone-related disorders such as osteoporosis, trauma such as osteoporosis, trauma such as osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                burns, incisions, and other wounds, connective tissue disorders, catabolic states, testicular related disorders, and inflammatory, any anyiogenic and immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The products can be used in the production of transgenic or knock-out animals.

Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
                                                                                                                                                                                                               WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour; connective tissue growth factor; cancer; melanoma; arteriosclerosis; leukaemia; lymphoid malignancy; haematopoiesis-related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion; kidney disorder; bone-related disorder; osteoporosis; trauma; burn;
                                                                                                                                                                                                                                                                                                                                          06-AUG-1999
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                                                                                            06-MAY-1999
                                                                                                                         WO9921998-A1
                                                                                                                                                                                    testicular-related
                                                                                                                                                                                                   connective tissue disorder; catabolic state;
                                                                                                                                                                                                                                                                                                            Mouse
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98US-0081695.
97US-0063704.
98US-0073612.
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Pred. No. 1.9e
8; Mismatches
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RESULT 9
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Best Local S
Matches 222
connective leukaemia;
                                              06-AUG-1999
                                                                           AAY17685 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WISP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Botstein
                               Mouse
                                                             AAY17685;
                                                                                                                                                                                                                                                                                                   Sequence
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               induced secreted protein; WISP-1; WISP-2;
                                                                                                                 241
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                                                                                                                                                            185
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                               WISP-2
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                                                                                                                                                    VTPASADAPCPNWSTAWGPCSTTCGLGIATRVSNQNRF@QLEIQRRLCLPRPCLAARSHS
                                                                                                                                                                                    GGFTCLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDOGV-TPAIQRSTAQGHQLSAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                               t invention describes Wnt-1 induced secreted polypeptides,
and 3. The novel WISP polypeptides, designated WISP-1, WIS
have homology to connective tissue growth factor (CTGF).
tissue growth factor; lymphoid malignancy;
                                                                                                                                                                                                                                                                                                   246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 249;
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wnt-1 induced secreted
                              protein SEQ ID
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                                            entry)
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90.2%;
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Pennica D,
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Pred.
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haematopoiesis-melated
                                                                                                                                                                                                                                                                    ed. No. 6.5
Mismatches
       cancer;
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No. 6.5e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides,
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Roy Ma
      WISP-2; WISP-3; CTGF; tumour;
melanoma; arteriosclerosis;
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ood WI;
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                                                                                                                                                                                                                                                                                   Length
disorder;
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QΥ 밁 80

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WNSAF

GFTCLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGV-TPAIQRSTAQGHQLSALV

GFTCLPLCSEDVRLPSWDCPRPRRIQVPGRCCPEWVCDQAVMQPAIQPSSAQGHQLSALV

LHVCDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDDG IHLLAISFLCILSMVYSQLCPAPCACPWTPPQCPPGVPLVLDGCGCCRVCARRLGESCDH | IHLLATSFLCLLSMYCAQLCRTPCTCPWTPPQCPQGVPLVLDGCGCCKVCARRLGESCDH

126

185 120

245 180 LHVCDPSQGLVCQPGAGPSGRGAVCLFEEDDGSCEVNGRRYLDGETFKPNCRVLCRCDDG

20 д Qy

7

Matches Query Match Best Local

221;

Conservative

8

Similarity

88.9%; 90.2%;

Score 1280.5; DB Pred. No. 1.3e-88; Mismatches

DB 20; 15;

245; 1;

Indels Length

Gaps

66

60

Sequence

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61 67

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14-APR-1998;
29-OCT-1997;
03-FEB-1998;
                                                                                                                                                                                                                          disorders such as breast, ovarian, and colon cancer or melanoma. The products can be used to treat arteriosclerosis. The products can also used to treat other diseases e.g. benign and malignant tumours, leukaemia and lymphoid malignancies, neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, blastocoelic disorders, haematopolesis related disorders, tissue-grow disorders, skin disorders, desmoplasia, fibrotic lesions, kidney of disorders, bone-related disorders such as osteoporosis, trauma such a missorders, bone-related disorders such as osteoporosis, trauma such a missorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                        burns, incisions, and other wounds, connective tissue disorders, catabolic states, testicular-related disorders, and inflammatory, angiogenic and immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The products can be used in the production of transgenic or knock-out animals.

Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue-growth disorder; skin disorder; desmoplasia; fibro kidney disorder; bone-related disorder; osteoporosis; tracconnective tissue disorder; catabolic state; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes Wht-1 induced secreted polypeptides, WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-and WISP-3 have homology to connective tissue growth factor (CTGF) products from the present invention can be used to treat WISP-related discrete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Wnt-1 induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lawrence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           testicular-related disorder; angiogenesis; immunological disorder
cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0081695.
97US-0063704.
98US-0073612.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
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Roy MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 desmoplasia; fibrotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL,
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WNSAF

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disorders such as breast, ovarian, and colon cancer or melanoma. The products can be used to treat arteriosclerosis. The products can also be used to treat other diseases e.g. benign and malignant tumours, leukaemia and lymphoid malignancies, neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, and colon colored to disorders, haematopoiesis-related disorders, tissue-growth coloreders, skin disorders, desmoplasia, fibrotic lesions, kidney coloreders, skin disorders such as osteoporosis, trauma such as turns, incisions, and other wounds, connective tissue disorders, catabolic states, testicular-related disorders, and inflammatory, catabolic states, testicular-related disorders, and inflammatory, candiogenic and immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of conditionals with neoplastic cell growth or proliferation. The products can be used in the production of transgenic or knock out animals.
                    Query Match
Best Local :
   Matches
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29-OCT-1997;
03-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue-growth disorder; skin aisurue, www.r-----kidney disorder; bone-related disorder; osteoporosis; trauma; burn; kidney disorder; bone-related disorder; catabolic state; inflammation; connective tissue disorder; catabolic state; imminological disorder.
                                                                                                                                                                                                                                                                                                                                                        The present invention describes Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-3 have homology to connective tissue growth factor (CTGF).

Products from the present invention can be used to treat WISP-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour connective tissue growth factor; cancer; melanoma; arteriosclerosis; leukaemia; lymphoid malignancy; haematopoiesis-related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion;
                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Botstein
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                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DA,
                                                                   244
                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 250-251; 284pp;
   Conservative
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Levine AJ,
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97US-0063704.
98US-0073612.
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                88.6%;
90.2%;
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Pred. No. 2.66
8; Mismatches
                                 Score
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                  1276.5; DB
No. 2.6e-88;
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Roy MA,
                                 DB 20;
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ood WI;
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HLLATSFLCLLSMVCAQLCRTPCTCPWTPPQCPQGVPLVLDGCGCCKVCARRLGESCDHL

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disorders, skin disorders, desmoplasia, fidisorders, bone-related disorders such as

fibrotic lesions,

disorders kidney

as

and other

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RESULT 11
AAY17687
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29-OCT-1997;
03-FEB-1998;
The present invention describes Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-3 have homology to connective tissue growth factor (CTGF). Products from the present invention can be used to treat WISP-related disorders such as breast, ovarian, and colon cancer or melanoma. The products can be used to treat arteriosclerosis. The products can also be used to treat other diseases e.g. benign and malignant tumours, leukaemia and lymphoid malignancies, neuronal, gilal, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, and blastocoelic disorders, hadmatopolesis-related disorders, tissue-growth
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                                                                                                                                                                                                                                                           Page 251-252;
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Levine AJ,
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97US-0063704.
98US-0073612.
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Pennica D,
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Roy Ma
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Disclosure;

Page 252-253; 284pp; English.

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29-OCT-1997;
03-FEB-1998;
                                         Botstein
Lawrence
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                                                                                                                                                                                                                                    WNT-1 induced secreted protein; WISP-1; WISP-2; MISP-3; CTGF; tumour; connective tissue growth factor; cancer; melanome; arteriosclerosis; leukaemia; lymphoid malignancy; haematopolesis-related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion; kidney disorder; bone-related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation;
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 Wnt-1 induced
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Levine
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90.1%;
                                        Goddard A,
Pennica D,
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secreted
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                                                                                                                                                                                                                              angiogenesis;
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Pred. No. 1e-87;
8; Mismatches
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polypeptides, WISP-1,
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Best Local S
Matches 218
                                                                          WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour; connective tissue growth factor; cancer; melanoma; arteriosclerosis; leukaemia; lymphoid malignancy; haematopolesis related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion; kidney disorder; bone-related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation; testicular-related disorder; angiogenesis; immunological disorder.
                                              Mus sp
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Pred. No. 2e-87;
8; Mismatches
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Pred. No. 4e-87;
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Best Local S
Matches 216
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Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
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Lawrence DA,
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29-OCT-1997;
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                                                                 SQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDDGGFTCLP
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                                                                                              Sequence
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W⊚od WI;
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APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Levine, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, Wilsam I.
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APPLICANTON WIMBER: US/09/182,145B
CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER APPLICATION DATE: 1998-02-04
EARLIER APPLICATION DATE: 1998-04-14
NUMBER: OF SEQ ID NOS: 156
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                                                                                                                                                                     GESCHILHVCDPSQGLVCQPGAGPSGRGAVCLFEEDDGSCEVNGRRYLDGETFKPNCRVL
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                                              CRCDDGGFTCLPLCSEDVRLPSWDCPRPRRIQVPGRCCPEWVCDQAVMQPAIQPSSAQGH
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US-09-182-145-59
US-09-182-145-61
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Pred. No. 1.1e
9; Mismatches
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SAME

Gaps

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Result

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1308 1303 1298 1299 1291 1284 1280 1276 1268 1268 1268 1267 1257 1257

1243 1234 1232 1232 1228

Database

Maximum Minimum Total number Searched:

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RESULT 3
US-09-182-145-79
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; GENERAL INFORMATION:
APPLICANT: Botstein, David;
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey;
APPLICANT: Gurney, Austin
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; ORGANISM: Homo sapiens
US-09-182-145-78
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APPLICANT: Gurney, Austin L:
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
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Best Local Similarity 90.0
Matches 225; Conservative
                                                                                                                                         Sequence 79, Application US/09182145B Patent No. 6387657
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SEQ ID NO 78
LENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/182,145B CURRENT FILING DATE: 1998-10-29 EARLIER APPLICATION NUMBER: US 60/063,704 EARLIER FILING DATE: 1997-10-29 EARLIER APPLICATION NUMBER: US 60/073,612 EARLIER FILING DATE: 1998-02-04 EARLIER APPLICATION NUMBER: US 60/081,695 EARLIER ETTING NUMBER: US 60/081,69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P1176R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nce 78, Appli
nt No. 6387657
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  Gurney, Austin L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-182-145-80
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APPLICANT: Botstein, David
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
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SEQ ID NO 79
LENGTH: 249
TYPE: PRT
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Best Local Similarity
Matches 224; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
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                            EARLIER
EARLIER
                                                                                                 CURRENT APPLICATION NUMBER: US/09/182,145;
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
                                                                                                                                                                                                                    APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
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APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P1176R2
                                                                                   EARLIER
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No. 6387657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 SHGSWNSAF 249
                                                   APPLICATION NUMBER: US 60/073,612 FILING DATE: 1998-02-04
                                                                                                                                                             APPLICATION NUMBER: US/09/182,145B
FILING DATE: 1998-10-29
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                               APPLICATION
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  DATE:
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                               NUMBER: US 60/081,695
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Pred. No. 7.86
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.8e-105;
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APPLICANT: BOLISTEIN, David A.
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Roy, Margaret Ann
APPLICANT: WOOd, William I.
CURRENT: INTERNATION: WIMSP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US 60/09/182,145B
CURRENT APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1998-10-29
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-04-14

NUMBER OF SEQ ID NOS: 156
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; SEQ ID NO 80
; LENGTH: 248
; TYPE: PRT
; ORGANISM: HOMO 9
US-09-182-145-80
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US-09-182-145-81
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                                                                                                                                  ; ORGANISM: Homo sapiens US-09-182-145-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 223
                                                                                                                                                                       SEQ ID NO 81
LENGTH: 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 81, Application US/09182145B Patent No. 6387657
                                                                              Matches
                                                                                                      Query Match
                                                                                                                                                            TYPE: PRT
                                                                   Local 223;
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nes 223;
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                                                                                        Similarity
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                                                                                       89.7%;
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                                                                            Score 1291.5; DB 4;
Pred. No. 3.1e-104;
8; Mismatches 15;
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Pred. No. 2.6
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NUMBER OF SEQ ID NOS: 156
SEQ ID NO 82
LENGTH: 246
TYPE: PRT
ORGANISM: Homo sapiens
US-09-182-145-82
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APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Lawrence, David A.
APPLICANT: Lewine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAM
FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
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                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                       Query Match .
Best Local Similarity
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Patent No. 6387657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1998-04-14
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                                                                                                                                                                                                           66 HLHVCDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDD 125
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                                                                                                                                                                                           HLHVCDPSQGLVCQPGAGPSGRGAVCLFEEDDGSCEVNGRRYLDGETFKPNCRVLCRCDD 120
                            SWNSAF 250
                                                            GGFTCLPLCSEDVRLPSWDCPRPRRIQVPGRCCPEWVCDQAVMQPAIQPSSAQGHQLSAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVTPASADGPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQRRLCLSRPCLASRSH
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                                                                                                                                                                                                                                                                                                                                     89.2%;
90.2%;
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Pred. No. 1.3e-103;
B; Mismatches 15;
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US-09-182-145-84
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LENGTH: 245
TYPE: PRT
ORGANISM: Homo sapiens
US-09-182-145-83
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CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-04-14
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 221;
                                                                         APPLICANT:
                                                                                                       APPLICANT: Botstein, David
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Roy, Margaret Ann
APPLICANT: WOOd, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEY ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
                                 APPLICANT:
                                                             APPLICANT:
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mes 221; Conservative
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                                           : Gurney, Austin L.
: Hillan, Kenneth J.
: Lawrence, David A.
: Levine, Arnold J.
: Pennica, Diane
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ROY, Margaret Ann
Wood, William I.
NVENTION: WISP POLYPEPTIDES
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Pred. No. 2.8e
8; Mismatches
   AND
 NUCLEIC ACIDS
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   ENCODING
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; SEQ ID NO 84
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-182-145-85
                                                   NUMBER OF SEQ :
SEQ ID NO 85
LENGTH: 243
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Best Local S
Matches 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                               TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER FILING DATE: 1997-10-29
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/073,612
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CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/081,695
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                                                                                                                                                                                                                                                                                                                APPLICANT: Roy, Margaret Ann APPLICANT: Wood, William I.
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                                                                                                                   EARLIER FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Botstein,
              ORGANISM: Homo sapiens
                                  TYPE: PRT
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Hillan, Kenneth J.
Lawrence, David A.
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                                                                                                                                                                                                                                                                                                                                                       Levine, Arnold J. Pennica, Diane
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                                                                                                                   1998-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             David
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Pred. No. 6.1e
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les 15;
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180

120

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APPLICANT: Botstein, David A.
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-04-14
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; ORGANISM: Homo sapiens
US-09-182-145-86
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Patent No. 6387657
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Best Local Similarity
Matches 218; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                     Q ID NO 86
LENGTH: 242
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90.1%;
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Pred. No. 3e-
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APPLICANT: Cohen, Robert
APPLICANT: Cohen, Robert
APPLICANT: Coddard, Andrey
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lewine, Arnold J.
APPLICANT: Lewine, Arnold J.
APPLICANT: Lewine, Arnold J.
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-04-14
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US-09-182-145-89
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US-09-182-145-87
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Sequence 89, Application US/09182145B Patent NO. 6387657
GENERAL INFORMATION:
APPLICANT: Botstein, David A.
APPLICANT: Cohen, Robert
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SEQ ID NO 87
LENGTH: 241
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Best Local Similarity 90.0%;
Matches 217; Conservative
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Pred. No. 1.5e-101;
8; Mismatches 15;
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240 249

180

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NUMBER OF SEQ ID NOS: 156
SEQ ID NO 89
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-09-182-145-89
                        APPLICANT: BOSTEEIN, David A.
APPLICANT: Godber, Robert
APPLICANT: Godber, Robert
APPLICANT: Godberd, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, David A.
APPLICANT: Pennica, Diane
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACT
FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-04-14
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US-09-182-145-88
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Best Local Similarity
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APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P1176R2
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: Hillan, Kenneth J.
: Lawrence, David A.
: Levine, Arnold J.
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ilarity 90.4%;
Conservative
              ID NOS:
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Pred. No. 2.6e
8; Mismatches
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; LENGTH: 238
; TYPE: PRT
; ORGANISM: Homo s
US-09-182-145-90
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FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
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Best Local S
Matches 216
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APPLICANT:
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TYPE: PR
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NO. 6387657
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Wood, William I.
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Hillan, Kenneth J.
Lawrence, David A.
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Pred. No. 2.6e
8; Mismatches
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Pred. No. 5.86
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CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER PHILING DATE: 1997-10-29
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 91
LENGTH: 237
TYPE: PRT
ORGANISM: Homo sapiens
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Search completed: July 25, Job time : 30 secs
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Best Local Similarity 90.3%;
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APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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Gurney, Austin L.
Hillan, Kenneth J.
Lawrence, David A.
Levine, Arnold J.
Pennica, Diane
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               2003, 12:38:36
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Perfect score:
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/cgn2_6/ptodata/2/pubpaa/USO9B_PUBCOMB.pep:*
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US-10-112-267-79
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US-10-112-267-82
US-10-112-267-83
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320,	Sequence 320, App	320,	320,	320,	æ	320,	æ	320,	•	320,	•	320,	320,	Sequence 320, App	320	320	e 69,	53,	Sequence 19, Appl	Sequence 98, Appl	99,	97,	96,	95,	e 94,	e 93,	e 92,	e 91,	Sequence 90, Appl

## ALIGNMENTS

RESULT 1 US-10-010-408-2

Sequence 2, Application US/10010408

publication No. US20020165185A1

GENERAL INFORMATION:

APPLICANT: John J. Castellot, Jr.

INTEL OF INVENTION: No. US20020165185A1e1 Heparin-Induced CCN-Like Molecules

INTEL OF INVENTION: No. US20020165185A1e1 Heparin-Induced CCN-Like Molecules

INTEL SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSE: LAHIVE 6 COCKFIELD, LLP

STREE: 28 State Street

CITY: Boston

STATE: MASSACHUSETLS

COUNTRY: USA

21P: 02109

COUNTRY: USA

21P: 02109

COUNTRY: USA

21P: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM: C-OOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/10/010,408

FILING DATE: OT-Dec-2001

CLASSIFICATION NUMBER: US/10/010,408

FILING DATE: MATCH 19, 1998

APPLICATION NUMBER: US/10/010,408

FILING DATE: CONKNOWN>

PRIOR APPLICATION NUMBER: US/10/010,408

FILING DATE: CONKNOWN>

APPLICATION NUMBER: US/10/010,408

FILING DATE: US/10/010,408

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Publication No. US20020165185A1
GENERAL INFORMATION:
APPLICANT: JOHN J. Castellot, Jr.
TITLE OF INVENTION: No. US20020165185A1e1
and Uses Therefor
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Best Local Similarity
Matches 250; Conserv
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                          PRIOR APPLICATION NUMBER: 09/044,273
APPLICATION NUMBER: 09/044,273
FILING DATE: March 19, 1998
APPLICATION NUMBER: «Unknown>
FILING DATE: «Unknown>
ATTORNEY,AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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1 RSHSSWNSAF 250
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                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/010,408 FILING DATE: 07-Dec-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSALVTPASADAPCPNWSTAWGPCSTTCGLGIATRVSNONRFCQLEIQRRLCLPRPCLAA 240
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LENGTH: 250 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 28 State Street
                                                  TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: LAHIVE & COCKFIELD, LLP
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ilarity 100.0%;
Conservative (
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Pred. No. 6.9e-143;
Mismatches (0;
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ
US-10-010-408-13
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                                                                                                                                                                                                      ; ORGANISM: Mus musculus US-10-112-267-20
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                                                                                                                                  Query Match
Best Local S
Matches 226
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LENGTH: 251
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Publication No.
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PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
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CURRENT FILING DATE: 2002-03-27
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Hillan, Kenneth J.
Lawrence, David A.
Levine, Arnold J.
Pennica, Diane
Pennica, Diane
               GESCDHLHVCDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVL
GESCDHLHVCDPSQGLVCQPGAGPSGRGAVCLFEEDDGSCEVNGRRYLDGETFKPNCRVL
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Wood, William I.
                                                                  MRGNPLIHLLAISFLCILSMVYSQLCPAPCACPWTPPQCPPGVPLVLDGCGCCRVCARRL
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Pred. No. 6.8e-102;
9; Mismatches 15;
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ACIDS

ENCODING

US/09/182,145B

DB 15;

Indels Length

1;

Gaps

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24 QLCRTPCTCPWTPPQCPQGVPLVLDGCGCCKVCARRLGESCDHLHVCDPSQGLVCQPGAG
                                                                                                    DCPRPKRIQVPGKCCPEWVCDQGVTPAIQRSTAQGHQLSALVTPASADAPCPNWSTAWGP
                                                                                                                                                                  PGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDDGGFTCLPLCSEDVRLPSW
CSTTCGLGIATRVSNQNRFCQLEIQRRLCLPRPCLAARSHSSWNSAF 227
                    CSTTCGLGIATRVSNQNRFCQLEIQRRLCLPRPCLAARSHSSWNSAF 250
                                                                                DCPRPKRIQVPGKCCPEWVCDQGVTPAIQRSTAQGHQLSALVTPASADAPCPNWSTAWGP
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US-10-112-267-78
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Best Local S
Matches 225
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CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 78
LENGTH: 250
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APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: P1176R2
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Gurney, Austin L.
Hillan, Kenneth J.
Lawrence, David A.
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Pennica, Diane
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APPLICANT: WOOD, WILLIAM I.
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/10/112,267
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
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APPLICANT:
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Best Local Similarity 90.0%;
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SEQ ID NO 79
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APPLICANT:
APPLICANT:
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                                                                                                                                  APPLICANT: Botstein, APPLICANT: Cohen, Ro
APPLICANT: Goddard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 24
TYPE: PRT
ORGANISM:
                                      APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                           181
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Gurney, Austin L.
Hillan, Kenneth J.
Lawrence, David A.
Levine, Arnold J.
Pennica, Diane
Roy, Margaret Ann
Wood, William I.
Gurney, Austin L.
Hillan, Kenneth J.
Lawrence, David A.
Levine, Arnold J.
Pennica, Diane
Roy, Margaret Ann
Wood, William I.
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                                                                                                                                    Goddard, Audrey
                                                                                                                                                      Cohen, Robert
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                                                                                                                                                                        David A.
                                                                                                                                                                                                                                                                                                                                249
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                                           CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
PRIOR PILING DATE: EARLIER FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704.
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
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PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US
PRIOR FILING DATE: EARLIER FILING DATE: 1997-105-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US
PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
                                                                                                                                                                                                               FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/10/112,267
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                       APPLICANT: WOOD, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC
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TYPE: PRT
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CURRENT FILING DATE: 2002-03-27
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No of
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Hillan, Kenneth J.
Lawrence, David A.
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Roy, Margaret Ann
Wood, William I.
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Pred. No. 1.5e-100;
9; Mismatches 15;
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10-29
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                                                                                                                                                                         NUMBER OF SEQ
SEQ ID NO 82
LENGTH: 246
TYPE: PRT
                                                                                      Query Match
Best Local
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Best Local
                                                                       Matches
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PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-02-04
PRIOR PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
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CURRENT FILING DATE: 2002-03-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
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                                                                                      Similarity
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                     LIHLLATSFLCLLSMVCAQLCRTPCTCPWTPPQCPQGVPLVLDGCGCCKVCARRLGESCD
LIHLLAISFLCILSMVYSQLCPAPCACPWTPPQCPPGVPLVLDGCGCCRVCARRLGESCD
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Lawrence, David A.
Levine, Arnold J.
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                                                                      Conservative
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90.2%;
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90.3%;
                                                                  Score 1284.5; DB 15
Pred. No. 6.7e-100;
8; Mismatches 15;
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Pred. No. 1.8e-100;
"" matches 15;
                                                                                                                                                                                                                                               DATE: 1998-04-14
                                                                                                      DB 15;
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HLHVCDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDD

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-112-267-83
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US-10-112-267-83
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SEQ ID NO 83
LENGTH: 245
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Publication No. US20030068678A1
                                                                                                                                                                                                                                                                                                                                            Matches
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CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: EARLIER DATE: 1997-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
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APPLICANT:
APPLICANT:
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APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
FILE REFERENCE: P1176R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Botstein, David A.
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
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                               246
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                                                                                                                                                                                                 LHYCDPSQGLYCQPGAGPGGHGAYCLLDEDDGSCEVNGRRYLDGETFKPNCRYLCRCDDG
                               WNSAF 250
                                                                                                                              VTPASADAPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQRRLCLPRPCLAARSHS
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                                                                                   TPASADAPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQRRLCLPRPCLAARSHSS
                                                                                                                                                                                                                                                                      IHLLATSFLCELSMYCAQLCRTPCTCPWTPPQCPQGVPLVLDGCGCCKVCARRLGESCDH
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                                                                 TPASADGPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQRRLCLSRPCLASRSHGS
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Hillan, Kenneth J.
Lawrence, David A.
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Pennica, Diane
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                                                                                                                                                                                                                                                                                                                                                        88.9%;
                                                                                                                                                                                                                                                                                                                                      Score 1280.5; DB 15;
Pred. No. 1.4e-99;
8; Mismatches 15; II
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-112-267-84
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US-10-112-267-85
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US-10-112-267-84
: Sequence 84, Application US/10112267
: Publication No. US20030068678A1
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APPLICANT: Botstein, I
APPLICANT: Cohen, Rol
APPLICANT: Goddard, I
APPLICANT: Gurney, AU
APPLICANT: Hillan, Ku
APPLICANT: Lawrence,
APPLICANT: Levine, Au
APPLICANT: Levine, Au
                                          APPLICANT: Botstein, E
APPLICANT: Cohen, Rob
APPLICANT: Goddard, A
APPLICANT: Gurney, Au
                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 84
LENGTH: 244
                                                                                                                                 Sequence 85, Application US/10112267 Publication No. US20030068678A1
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR ETLING DATE: EARLIER FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
NUMBER: OF SEQ ID NOS: 156
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               APPLICANT:
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Gurney, Austin L.
Hillan, Kenneth J.
Lawrence, David A.
                                                                                                                                                                                                                                                                                                      NSAF
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                                                                                                                                                                                                                                                                                                                                                                                               FTCLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGV-TPAIQRSTAQGHQLSALVT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                            NSAF
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Wood, William I.
                                                                               Cohen, Robert
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Hillan, Kenneth J.
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Arnold
                                                                                               David A.
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90.2%;
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Sequence 86, Application US/10112267
Publication No. US20030068678A1
GENERAL INFORMATION:
APPLICANT: Botstein, David A.
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
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Best Local Similarity
Matches 219; Conserv
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SEQ ID NO 85
TITLE OF INVENTION: WISD POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAMI FILE REFERENCE: P1176R2

CURRENT APPLICATION NUMBER: US/10/112,267

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B

PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704

PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
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CURRENT APPLICATION NUMBER: US/10/112,267
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
PRIOR PILING DATE: EARLIER FILING DATE: 1998-02-04-04
PRIOR PILING DATE: EARLIER FILING DATE: 1998-04-14
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
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                                                                                                                                                                                                                                                                   Levine, Arnold J.
Pennica, Diane
Roy, Margaret Ann
Wood, William I.
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Roy, Margaret !
Wood, William :
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Pred. No. 1.4
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NUMBER OF SEQ ID NOS: 156
SEQ ID NO 86
LENGTH: 242
TYPE: PRT
Query Match
Best Local Similarity
Matches 217; Conserv
                                                                                                                      PRIOR FILING DATE: EARLIER FILING
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 87
LENGTH: 241
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Best Local Similarity
Matches 218; Conserv
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                                                                                                         LENGTH: 24
TYPE: PRT
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CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: WISP POLYPEPTIDES AND FILE REFERENCE: P1176R2
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Wood, William I.
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                      87.5%;
90.0%;
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90.1%;
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     Score 1260.5; DB 15
Pred. No. 6.7e-98;
8; Mismatches 15;
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Pred. No. 3.1
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APPLICANT: BOCSTEIN;
APPLICANT: Cohen, Rc
APPLICANT: Goddard,
APPLICANT: Gurney,
APPLICANT: Hillan, R
APPLICANT: Hawrence,
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Publication No. US20030068678A1
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CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B

PRIOR PILING DATE: EARLIER FILING DATE: 1998-10-29

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704

PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-02-04

PRIOR PILING DATE: EARLIER FILING DATE: 1998-04-14

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/081,695

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
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APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P1176R2
                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 156
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TYPE: PRT
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al Similarity 90.4%;
216; Conservative
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Hillan, Kenneth J.
Lawrence, David A.
Levine, Arnold J.
Pennica, Diane
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             APCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQRRLCLPRPCLAARSHSSWNSAF 250
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FILE GEFERNCE: P1176R2

FILE REFERNCE: P1176R2

CURRENT APPLICATION NUMBER: US/10/112,267

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/(PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: EARLIER APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/(PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US/(PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US/(P
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; TYPE: PRT
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US-10-112-267-88
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US-10-112-267-88
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APPLICANT: Cohen, Rol
APPLICANT: Goddard,
APPLICANT: Gurney, A
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Best Local
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APPLICANT:
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APPLICANT:
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LCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGV-TPAIQRSTAQGHQLSALVTPASAD 191
                                                                                                                                                                                                                                                                                                                  SQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDDGGFTCLP 132
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Hillan, Kenneth J.
Lawrence, David A.
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Pennica, Diane
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90.4%;
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Pred. No. 1.2e-97;
8; Mismatches 14; 1
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Search completed: July 25, 2003, 12:39:05 Job time: 24 secs

ും താരുന്നു. ഇത് എന്നുവായ എല്ലാനു ആയോഗ്യാന് ഇതുന്നു. ഈ വാധാന് വിവര് വിവര് വിവര് വിവര് വിവര് വിവര് വിവര് വിവര് വ • •

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                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M92934; GB:M36965; GB:S56201; NID:g180923; PIDN:AAA91279.1; PIR;Oemar, B.S.; Werner, A.; Yang, Z.; Garnier, J.M.; Gentz, R.; Luescher, T.F. submitted to the EMBL Data Library, April 1994
A;Description: Differential cloning and expression of human connective tissue growth A;Reference number: S44205
A;Accession: S44205
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A40551
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A; Residues: 1-349 < BRA>
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Result No.

Database

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Maximum Minimum

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Searched:

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## ALIGNMENTS

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RESULT 2 A40578 beta IG-M2 C;Species: C;Date: 06 C;Accessic R;Brunner,	Qу	Qy Db	Qу	Qy	Query Match Best Local : Matches 11:	A; Status: prelimina A; Molecule type: mR A; Residues: 1-349 < A; Cross-references:
RESULT 2 A40578 beta IG-M2 protein precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 01-Dec-2000 C;Accession: A40578; A53228 R;Brunner, A.; Chinn, J.; Neubauer, M.; Purchio, A.F.	185VTPASADAPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQRRLCLPRPCLA 239	128 FTCLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGVTPAIQRSTAQGHQLSAL 184   :	68 HVCDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDDGG 127     :	13 SFLCILSMVCAQLCRTPCTCPWTP-PQCPQGVPLVLDGCGCCKVCARRLGESCDHL 67	Query Match 39.2%; Score 564; DB 2; Length 349; Best Local Similarity 46.9%; Pred. No. 2.1e-35; Matches 112; Conservative 28; Mismatches 81; Indels 18; Gaps	A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-349 <oem> A;Cross-references: EMBL:X78947; NID:g474933; PID:g474934</oem>

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C;Accession. C;Accession of a R;Joliot, V; Martinerie, C; Dambrine, C;, Martinerie, C; Dambrine, C;, Martinerie, C; Dambrine, C;, Martinerie, C; Dambrine, C;, Dambrine, C
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A; Residues: 1-160, 'K', 162-348
A; Cross-references: GB:M70641;
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A;Title: Identification of a gene family regulated by transforming growth factor-beta.

A;Reference number: A40578; MUID:91229699; PMID:2029337
                                                                                                                                                                                                                                                                                                                                                                                        A; Gene:
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A; Residues: 1-351 <JOL>
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                                                                                                                                                                                                                                                                                                         Similarity
PNCRVLCRCDDGGFTCLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQ-----
                                                                                                            VCARRLGESCDHLHVCDPSQGLVCQPGAGPGGHGAVCLLDEBDGSCEVNGRRYLDGETFK 114
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                                                                         VCARQRGESCSPLLPCDESGGLYCDRGPEDGGGAGICMVLEGD-NCVFDGMIYRNGETFQ
                                                                                                                                                                             QGLPVLLL----LLLLLRPCEVSGREAACPRPCGGRCPAEPPRCAPGVPAVLDGCGCCL
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                                                                                                                                                                                                             R.Martinerie, C.; Huff, V.; Joubert, I.; Badzioch, M.; Saunde Oncogene 9, 2729-2732, 1994
A;Title: Structural analysis of the human nov proto-oncogene A;Reference number: 138069; MUID:94336229; PMID:7520150
A;Accession: I38069
A;Status: preliminary; translated from GB/EMBL/DDBJ
             A;Gene: novH
A;Introns: 28/3; 104/1; 188/1; 259/3
A;Introns: 28/3; 104/1; 188/1; 259/3
C;Superfamily: thrombospondin type 1 repeat homology
F;203-250/Domain: thrombospondin type 1 repeat homology <THR1>
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C;Genetics:
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A; Residues: 1-357 <R
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                                                                                                                                                                             <RES>
                                                                                                                                                   EMBL: X78351; NID: g587422; PIDN: CAA55146.1; PID: g825696
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RESULT 4
A41428
CEF-10 protein precursor - chicken
CEF-10 protein gallus (chicken)
C:Species: Gallus gallus (chicken)
C:Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change
C:Accession: A41428
                                            gene novH protein - human
C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-375 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Simmons, D.L.; Levy, D.B.; Yannoni, Y.; Erikson, R.L.
Proc. Natl. Acad. Sci. U.S.A. 86, 1178-1182, 1989
A;Title: Identification of a phorbol ester-repressible v-src-inducible
A;Reference number: A41428; MUID:89145206; PMID:2537491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:J04496; NID:g211435; PIDN:AAA48661.1; PID:g211436
                                                                                                                                                                                                                                                                                                                             190 LTRNNELIAIVKGGLKMLPVFGSEPQSRAFENPKCIVQTTSWSQCSKTCGTGISTRVTND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 CLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 CDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDDGGFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAAALLCLARLALGSPCPAVCQCPAAAPQCAPGVGLVPDGCGCCKVCAKQLNEDCSRTQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPAIQRSTAQGHQLSALVTPASADAPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEI
                                                                                                                                                                                                                             NPDCKLIKETRICEVRPC
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                              -CPNWSTAWGPCSTTCGLGIATRVSNQ
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Saunders,
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QY 121 CRCDDGGFTCLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQ 165	Qy 61 GESCDHLHVCDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVL 120 A	Qy       1 MRGSPLIHLLATSFLCLLSMVCAQLCRTPCTCPWTPPQCPQGVPLVLDGCGCCKVCARRL 60         P	Query Match  34.8%; Score 500.5; DB 2; Length 379;  Best Local Similarity 35.6%; Pred. No. 1.4e-30;  Matches 96; Conservative 35; Mismatches 106; Indels 33; Gaps 2;	61 21/3; 93/1; 208/1; 279/3 1y: von Willebrand factor type C repeat homology main: von Willebrand factor type C repeat homology <vwc></vwc>	nces: EMBL:x56790; NID:g50632; PIDN:CAA40109.1; PID:g50633 thors did not translate the codon for residue 108 thors translated the codon GAT for residue 337 as Gln	d from GB/EMBL/DDBJ A RESS	A;Title: Promoter function and structure of the growth factor-inducible immediate early f;Reference number: 148319; MUID:91288203; PMID:2062642	e 33/ as Gin	references: GB:M32490; NID:g192909; PIDN:AAA37512.1; PID:g309206		, a growth factor-inducible immediate-early gene.		G:Date: 28-Sep-1990 #sequence revision 18-Nov-1992 #text change 05-Nov-1999	מינים	640 6 640	Qy 237 C 237	194ILGVEVSUSSVNCIEDTIEWINCSKSCGMGFSTRVINNNRQCEMLKQTRLCMVRP 248	177 QGHQLSALVTPASADAPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQRRLCLPRP 236	134 RDGQIGCVPRCQLDVLLPEPNCPAPRKVEVPGECCEKWICGPDEEDSLGGLTLAAYRPEA 193	DDGGFTCLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGVTPAIQRSTA 176	GVIYRSGEKFQPSCKFQCTC 133	QY 64 CDHLHVCDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRC 123	Db 22 LLHLLGQVAATQRCPPQCPGRCPATPTTCAPGVRAVLDGCSCCLVCARQRGES 74	ATSFLCLLSMVCAQLCRTPCTCPWTPPQCPQGVPLVLDGCGCCKVCARRLGES 63
A; Residue: 560-1172 <la2> A; Cross-references: GB:M81339 A; Experimental source: fibroblast</la2>	A;Title: Thrombospondin II: partial cDNA A;Reference number: A42173; MUID:9221796; A;Accession: A42173	A; Residues: 1-1172 <lab> A; Cross-references: GB:L12350; NID:g30750 R; LABell, T.L.; Milewicz, D.J.; Disteche, Genomics 12, 421-429, 1992</lab>	A;Title: Sequence and characterization of A;Reference number: A47379; MUID:94010892 A;Accession: A47379 mRNA	, L & J & F	RESULT 8 thrombospondin 2 precursor - human	Db 1284ALCDPISGHCSCQPGWRGKKCNI	1239	QY 125 DGGFTCLPLCSEDVRLPSWDCPRPKR:	1184 EGLWGSNCMKHCLCMHGGE	Db 1124 CRCPAGWTGPDCQTSCPLGRHGEGCR	30	Similarity 26.3%; 9; Conservative 18	ns: ///1;	ics: CESP:Y64G10A.f	A; Cross-references: EMBL:AL110498; NID:e: A; Experimental source: clone Y64G10A	A;Status: preliminary; translated from GE A;Molecule type: DNA A;Molecule type: DNA	A; Reference number: Z20336 A; Accession: T27283	ough, ed to	<pre>C;Date: 15-Oct-1999 #sequence_revision 15 C;Accession: T27283</pre>	hypothetical protein Y64G10A.f - Caenorha C; Species: Caenorhabditis elegans	RESULT 7	6 1	QY 208 CGLGIATRVSNQNRFCQLEIQRRLCLL	TRT

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CLPRPC 237
| |||
CEVRPC 270
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                                                                                                                                   of the complete human thrombospondin 2 cDNA: p 92; PMID:8406456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCEVNGRRYLDGET-----FKPNCRVLCRCD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 161; DB 2; Length 1620;
No. 0.00015;
.smatches 93; Indels 54; Gaps 11;
A sequence, chromosome location, and expressio 61; PMID:1559694
                                              505; PIDN:AAA03703.1; PID:g307506 e, C.M.; Byers, P.H.
                                                                                                                                                                                                                       03-Aug-1995 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                            NRPCLKGYFGRHCSQSCRC 1323
                                                                                                                                                                                                                                                                                                                                                                             STTCGLGIATRVSNQNRFC 223
                                                                                                                                                                                                                                                                                                                                                                                                                 KSCVSGHYGAKCEETCECENG----- 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                             RIQVPG----KCCPEWVCDQGVTPAIQRSTAQGHQ 180
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A; Note:
C; Keywor
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F:552-691/Domain: EGF homology cour/
F:928-930/Region: cell attachment (R-G-D) motif
F:151,316,330,457,584,710,1069/Binding site: carbohyd‡ate (Asn) (cell f:157-226/Disulfide bonds: #status predicted
F:167-226/Disulfide bonds: interchain #status predicted
F:266,270/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                           R:Gao, Z.; Garbers, D.L.
J. Biol. Chem. 273, 3415-3421, 1998
A:Title: Species diversity in the structure
A:Reference number: Z22080; MUID:98123114; p
A:Accession: T42215
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                                                        A; Map position:
C; Function:
                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-5376 <G
A; Cross-references: E
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C; Superfamily:
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                                   A; Description: functions in
                                                                                                 A; Gene:
                                                                                                                                                                                                 A;Status: preliminary;
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Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                    Alternate names: sperm-specific membrane protein; Species: Mus musculus (house mouse); Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
                                                                                                                    Genetics:
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                  found exclusively
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cell adhesion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGGWSHWSPWSSCSVTCGVGNITRIRLCNSPVP---QMGGKNC------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VCAQLCRTPCTCPWTPPQCPQGVPLVLDGCGCCKVCARR#GESCDHLHVCDPSQG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----KGSGRETKACQGAPCPIDGRWSPWSPWSACTVTCAGGIRERTRVCNSPEPQYGGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              participates in cell migration and adhesion, and in platelet aggregation thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; v.a.-hydroxyaaparagine; calcium binding; cell adhesion; glycoprotein; trime
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                                                                                                                                                            <GA0>
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                                                                                                                                       EMBL: U97068;
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                multiple cell adhesion n the apical region of t
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                                                                                                                                   NID: g3327420;
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Pred. No. 0
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PMID:9452468
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the sperm head
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MEGF 6

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A; Title: Identification of high-molecular-weight A; Reference number: 214126; MUID:98360089; PMID:9A; Accession: T13954
                                                                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
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C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-May-2000
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 A;Cross-references: EMI
A;Experimental source:
                                  A; Molecule type: mRNA
A; Residues: 1-1574 <NAK>
                                                                                                                                         R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, Genomics 51, 27-34, 1998
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Immunogenetics 49, 773-786,
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A; Residues: 1-1036 < PAN>
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                                                                  A;Status: preliminary; translated
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Best Local
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                                                                                                                                                                                                                                                                                                                                                      Q-GVTPAIQRSTAQGHQLSALVTPASADAPCPNWSTAWGPCSTTCGLGIATRVSNQNRF
                                                                                                                                                                                                                                                                                                                                                                                      DRCIPLDHCQDRHCPDGMAYDECGSGCGPFSCDNLPSYICPRICR---AGCFCPEGLVKD
                                                                                                                                                                                                                                                                                                                                                                                                                         FTCLPL-----CSEDV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FDECGSGCGP------ASCE----NLPRDICPRICRAGCFCPEGLVKDQDGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLHLKASSFLDNCVTDMCSFQGLQQKLCARMSAMTATCQDAGYPVKPWREPQFC----PL
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EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; ce: strain Sprague-Dawley; brain
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z18253; MUID:99328904; F
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27.5%;
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Pred. No. 0.0075;
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Pred. No. 0.0
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PMID:9693030
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.023;
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                  PID: 93449294
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A;Molecule type: mRNA
A;Residues: 1-2321 <001>
A;Residues: 1-2321 <001>
A;Residues: C: Ducros, A.; Vahedi, K.; Chabriat, H.; Mouton, P.;
R;Joutel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabriat, H.; Mouton, P.;
X, M.M.; Weissenbach, J.; Bach, J.F.; Bousser, M.G.; Tournier-Lasserve, E.
Nature 383, 707-710, 1996
A;Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causin A;Reference number: S71825; MUID:97032728; PMID:8878478
A;Accession: S71825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 24-Jul-1998 #sequence_revision
C;Accession: S78549; S71825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
S78549
                                 F;1838-1870/Domain: ankyrin repeat homology F;1871-1903/Domain: ankyrin repeat homology F;1905-1937/Domain: ankyrin repeat homology F;1938-1970/Domain: ankyrin repeat homology F;1971-2003/Domain: ankyrin repeat homology
                                                                                                                                                                                              F;123-155/Domain:
F;162-194/Domain:
                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 67-113;138-194;268-333,'G',335-346;536-613;716-765;1240-1279;1815-1888
A;Cross-references: EMBL:U97669
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A; Accession: S78549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                  F;318-349/Domain:
                                                                                                                                                                                                                                              A; Description: may be involved in pathogenesis of CADASIL, C; Superfamily: notch protein; ankyrin repeat homology; EGF
                                                                                                                                                                                                                                                                               A; Map position: 19p13.1
C; Function:
                                                                                                                                                                                                                                                                                                             A; Gene: notch3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Joutel, A.; Tournier-Lasserve, E. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                notch3 protein -
                                                                                                                  F;928-959/Domain:
                                                                                                                                  F;853-884/Domain:
                                                                                                                                                                               F; 240-271/Domain:
                                                                                                                                                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown
                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  559 CPPDTFGKNCSSPCTCQNGGTCDPVLGACRCPPGVSGAHCEDGCPKGFYGKHCRKKCHCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRGSPLIHLLATSFLCL-----LSMVCAQLCRT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACEHGAS ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CKAGFQGERCQAECESGFFGPGCRHRCTCQP-GVACDPVSGE----CRTQCPPGYQGEDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRGE---HTLTEKFYCLDHSFGHDCSLTCDD-CRNGGTCFPGQDGCDCPEGWTGIICNET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCGLGIATRVSNQNRFCQLEIQRRLCLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQECPVGTFGVNCSGSCSCVGAPCHRVTGECLCPPGKTGEDCGADCPEGRWGLGCQEICP 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKCCPEWVCDQGVTPAIQRSTAQGHQLS--ALVTP-----ASADAPCPNWSTAWGPCST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NRGRCHRLYGACLCDPGLYGRFCHLACPPWAFGPGCSEDCLCEQSHTRSC--NPKDGSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGESCDHLH---VCDPSQ-----GLVCQPGA-GPG------GHGAVCLLDEDDGSCE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----VNGRR----YLDGETFKPNCRVLCRCDDGGFTCLPLCSEDVRLPSWDCPRPKRIQVP
                                                                                                                                                                                                                                            notch protein; ankyrin repeat homology;
                                                                                                              EGF homology <EGF>
EGF homology <EGX3>
EGF homology <EGF3>
EGF homology <EGX4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.4%;
24.1%;
    9.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -CNPETGTCLCLP 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 136; DB 2; Pred. No. 0.011;
    Score 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 April 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GCCKVCARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-Jul-1998 #text_change 08-Sep-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234
                                                   <AN2>
<AN3>
<AN4>
                                                                                                   <AN1>
                                    <AN5>
    DB
   2
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    Length 2321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----PCTCP--WT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                            causing a homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                           type
                                                                                                                                                                                                                                                                                                                                                                                                                                      causing
                                                                                                                                                                                                                                                             of stroke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alamowito
                                                                                                                                                                                                                                                                                                                                                           POC?
                                                                                                                                                                                                                                                             and
granulin precursor [validated] - human N;Alternate names: epithelin N;Contains: granulin A; granulin B; gra C;Species: Homo sapiens (man) C;Date: 30-Sep-1992 #sequence_revision
                                                                                 RESULT 14
GYHU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
T26972
                                                                                                                                                                                                                                                                                                                                           맑
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP:Y47H9C.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: T26972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Harris,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QY
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         964
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                                                                                                                                                                                                                                                                                                                                                                                                          61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLCLPRPCL
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A:Map position: 1
A:Introns: 50/2; 84/2; 150/1; 238/3; 342/3; 797/1; 851/1; 947/2; 1017/1; 1083/1
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: clone Y47H9C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-1111 <WIL>
A; Cross-references: EMBL; ALO32657; PIDN: CAA21739.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, A; Reference number: Z20293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein Y47H9C.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te:C;Accession: T26972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              796 CSCPQGWQGPRCQQDVDECAGPAPCGPHGICTNLAGSFSCTCHGGYTGPSCDQDINDCDP
                                                                                                                                                                                                                                                                                                             22 CAQLCRT------PCTCP--WTPPQCPQGVPLVLDGCGCCKVCARRLGESCDHL 67
                                         --WYCDQGYTPAIQRSTAQGHQLSALYTPASA----DAPCPNWSTAWGPCSTTC
                                                                                                                                                                                      TGECTCPAGLQGANCDIGCPEGSYGPGCKL----HCKCVNGK--CDKETGE-----CT
                                                                                                                                                                                                                                                                                  CAHQCQCNQRGVGCDGADGKCQCDRGWTGHRCEHHCPADTFGANCEKRCKCPKGIGCDPI 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NPCLNGGSCQDGVGSFSCSCLPGFAGPRCARDVDECLSNPCGPGTCTDHVASF-----
FGFLCQETVTPSPCASTDPKNGVCLSCPPGSSGIHCEHNCPAGSYGDG-CQQVC
                                                                                                                                     H---VCDPS-QGLVCQPGAGPGGHGAVCLLDEDDGSCE-VNGRRYLDGETFKPNCRVLCR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S---QGLVCQPGAG------PGGHGAVCLLDEDD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCP--WTPPQC-----
                                                                                            CQPGFFGSDCSTTCSKGKYGESCELSCPCSDASCSKQTGKCLCPLGTKGVSCDQKCDPNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIQRSTAQGHQLSALVTPASADAPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQR 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TCTCPPGYGGFHCEQDLPDCS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNCRVLCRCDD--GGFTC---LPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGVTP 169
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----NSFSCLCRPGYTGAHCQH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238
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                                                                                                                                                                                                                                                                                                                                                                                             9.2%;
26.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 132.5; DB Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                October
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1998
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                            93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSPDB:GN00019; CESP:Y47H9C.4
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112;
                                                                                                                                                                                                                                                                                                                                                                            61;
                                           208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGF
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B; granulin C;

03-May-1996 #text\_change 08-Dec-2000

granulin D; granulin

E; granulin

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F;18-593/Product: granulin #status predicted <MAT>
F;18-593/Product: progranulin #status predicted <PRO>
F;18-44/Product: paragranulin #status experimental <PGR>
F;8-44/Product: granulin G #status predicted <GRC>
F;123-179/Product: granulin F #status predicted <GRC>
F;123-179/Product: granulin B #status experimental <GRB>
F;206-261/Product: granulin A #status experimental <GRA>
F;201-336/Product: granulin A #status experimental <GRA>
F;364-417/Product: granulin C #status experimental <GRC>
F;442-496/Product: granulin D #status predicted <GRD>
F;518-573/Product: granulin E #status predicted <GRD>
F;518-573/Product: granulin E #status predicted <GRD>
                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:136006; OMIM:138945
A;Map position: 17pter-17qter
A;Introns: 46/3; 88/3; 117/1; 154/3; 200/1;
C;Superfamily: granulin
C;Keywords: glycoprotein; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 281-283,'X',285-289,'S',291-295 <KAR>
A;Experimental source: urine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Bhandari, V.; Palfree, R.G.E.; Bateman, A.
Proc. Natl. Acad. Sci. U.S.A. 89, 1715-1719, 1992
A;Title: Isolation and sequence of the granulin precursor
A;Reference number: A38118; MUID:92179253; PMID:1542665
A;Accession: A38118
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A:Title: Structure and chromosomal location of the human
A:Reference number: JC1284; MUID:93038704; PMID:1417868
A:Accession: JC1284
                                                                                                                                                                                                                                                                                          C; Keywords: glycoprotein; tandem repeat F;1-17/Domain: signal sequence #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: GDB: GRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Characterisation of UGP and its relationship with beta-core A; Reference number: A56873; MUID:93229246; PMID:8471426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kardana, A.; Bagshawe, K.D.;
Br. J. Cancer 67, 686-692, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 364-367, 'X', 369-385, 'H', 387-396 <BA3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-406,'R',408-433,'G',435-453,'G',455-459,'Q',461-546,'A',548-566,'R',568-59
A;Cross-references: GB:M75161; NID:g183612; PIDN:AAA58617.1; PID:g183613
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A; Residues: 1-406, 'R',
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A;Title: The epithelin precursor encodes two proteins with A;Reference number: A38128; MUID:92317004; PMID:1618805
A;Accession: A38128
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R; Plowman, G.D.;
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A;Cross-references: GB:X62320; NID:g31192; PIDN:CAA44196.1;
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;Bhandari, V.;
368/Binding
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267, 13073-13078,
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class of peptide from leukocytes
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78, 1992
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Search completed: July

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C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal C;Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple hel F;37-96/Domain: von Willebrand factor type C repeat homology <WC>F;1263-1492/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                                                                                                                                                                                                                                                                                                                                                                                                     collagen alpha 1'(II) chain precursor - African cla C; Species: Xenopus laevis (African clawed frog) C; Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 C; Accession: A40333
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A; Residues: 1-1492 <SUA>
A; Cross-references: GB: M63596
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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          GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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CTGF_HOUSE
CTGF_HOUSE
CTGF_RAT
CTGF_ROUSE
NOV_CHICK
CTGF_PIG
NOV_COTJA
NOV_NOUSE
NOV_HUMAN
NOV_RAT
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NOV_XENTA
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018739 bos taurus
p29279 homo sapien
0921e9 rattus norv
p29268 mus musculu
p28686 gallus gall
p19336 gallus gall
019113 sus scrofa
p42642 coturnix co
064299 mus musculu
p48745 homo sapien
09225 rattus norv
p51609 xenopus lae
Q9es72 rattus norv
p18406 mus musculu
p48742 homo sapien
p35442 homo sapien
p35442 homo sapien
p37999 oryctolagus
Q9ng30 homo sapien
Q92832 homo sapien
Q92832 homo sapien
Q92832 homo sapien
Q94167 bos taurus
Q9m47 homo sapien
p14162 homo sapien
p28799 h granulins
p98167 bos taurus
Q81581 mus musculu
p28481 mus musculu
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p35440 gallus gall
Q9y493 homo sapien
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8.5	8.5	8.5	8.6	8.6	8.6	8.6	8.7	8.7	8.8	8.8	8.8
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FBN2_HUMAN	TENA_HUMAN	NTC3_RAT	SERR_DROME	CA13_CHICK	MUCL_RAT	NEL1_RAT	ATS9_HUMAN	GRN_RAT	NTC4_MOUSE	CA13_HUMAN	NTC1_MOUSE
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	P24821 homo sapien										

## ALIGNMENTS

DR DDR DDR DDR DDR DDR DDR DDR DDR DDR	88888888	X X X X X X X X X X X X X X X X X X X	RESULT CTGL_R ID CC AC Q AC Q DT 2 DT 2 DT 2 DT 2 OT C
EMBL; AF259981; AAF69011.1; InterPro; IPR000867; Insl_gro_fac_pr. InterPro; IPR000867; Insl_gro_fac_pr. InterPro; IPR001007; VWF_C. Pfam; PF00109; tsp_1; 1. Pfam; PF00090; tsp_1; 1. Pfam; PF00090; vwc; 1. SMART; SM00121; IB; 1. SMART; SM00121; IB; 1. SMART; SM00214; VWC; 1. PROSITE; PS00222; IGF_BINDING; 1. PROSITE; PS01208; VWFC_1; 1. PROSITE; PS01208; VWFC_1; 1. PROSITE; PS01208; VWFC_2; 1. Signal. 1 23 POTENTIAL.	entry is copyright. It is produced through a liss Institute of Bioinformatics and the EMBL oinformatics Institute. There are no restrict ofit institutions as long as its content is is statement is not removed. Usage by and f es a license agreement (See http://www.isb-sib to license@isb-sib.ch).	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLINE-98414629; PubMed-9742130;  Zhang R.; Averboukh L., Zhu W., Zhang H., Jo H., Dempsey P.J.,  COffey R.J., Pardee A.B., Liang P.;  "Identification of rCop-1, a new member of the CCN protein family, as a negative regulator for cell transformation.";  MOL Cell. Biol. 18:6131-6141(1998).  -!- FUNCTION: May play an important role in modulating bone turnover.  Promotes the adhesion of osteoblast cells and inhibits the binding of fibrinogen to integrin receptors. In addition, inhibits osteocalcin production (By similarity).  -!- SUBCELJULAR LOCATION: Secreted (Probable).  -!- SIMILARITY: Contains 1 IGFBP domain.  -!- SIMILARITY: Contains 1 TSP type-1 domain.	LT 1 RATCRATCRATCRATCRATCRATCRATCRATCOUNTY 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 28-FEB-2003 (Rel. 41, Last annotation update) 28-FEB-2003 (Rel. 41, Last annotation update) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last sequence update) 29-FEB-2003 (Rel. 41, Last sequence update) 20-FEB-2003 (Rel. 41, Last sequence update) 20-FEB-2003 (Rel. 41, Cast annotation update) 20-FEB-2003 (Rel. 41, Last annotation update) 20-FEB-2003 (Rel. 41, Last annotation update) 20-FEB-2003 (Rel. 41, Cast annotation update) 20-FEB-2003 (Rel. 41, C

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                                                      MEDINE-99287915; PubMed-10358067;
MEDINE-99287915; PubMed-10358067;
Kumar S., Hand A.T., Connor J.R., Dodds R.A., Ryam P.J., Trill J.J.,
Fisher S.M., Nuttall M.E., Lipshutz D.B., Zou C., Hwang S.M.,
Votta B.J., James I.E., Rieman D.J., Gowen M., Lee J.C.;
"Identification and cloning of a connective tissue growth factor-like CDNA from human osteoblasts encoding a novel regulator of osteoblast
                                                                                                                                                                                                   TISSUE-Mammary gland;
MEDLINE-99061933; PubMed-9843955;
Pennica D., Swanson T.A., Welsh J.W., Roy M.A., Lawrence D
Brush J., Taneyhill L.A., Deuel B., Lew M., Watanabe C., C
Melham M.F., Finley G.G., Quirke P., Goddard A.D., Hillan
Gurney A.L., Botstein D., Levine A.J.;
"WISP genes are members of the connective tissue growth fa
                                                                                                                                                                                                                                                                                                                                                           CTGL_MOUSE STANDARD: PRT; 251 AA. 092064; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Connective tissue growth factor-like protein (WNTI inducible signaling pathway protein 2) WISP2 OR CTGFL.
                                                 cDNA from human functions.";
                                                                                                                                                                  that are up-regulated in wnt-1-transformed cells an expressed in human colon tumors."; proc. Natl. Acad. Sci. U.S.A. 95:14717-14722(1998).
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                       Biol.
FUNCTION: May play an important role in modulating bone tun
Promotes the adhesion of osteoblast cells and inhibits the
of fibrinogen to integrin receptors. In addition, inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chem. 274:17123-17131(1999).
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194
196
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164
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96.8%;
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IGEBP.
VWFC.
TSP TYPE-1.
N-LINKED (GLCNAC. ...) (POMF):
9A147074626BCA47 CRC64;
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Pred. No. 2.3e
2; Mismatches
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                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
.3e-98;
                                                                                                                                                                                           tissue d
                                                                                                                                                                                                                                                                                                                                                                       precursor (WISP-2).
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and abe
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R.L.,
             binding
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CTGL_HUMAN
ID CTGL_H
AC 076076
DT 28-FEB
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DE Connec
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Matches
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          CTGL_HUMAN
076076;
28-FEB-2003
28-FEB-2003
15-SEP-2003
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DOMAIN
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal.
SIGNAL
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SMART;
SMART;
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or send a
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InterPro;
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EMBL;
MGD; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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SUBCELLULAR
SIMILARITY:
SIMILARITY:
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L; AF126063; AA
; MGI:1328326;
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n; PF00090; tsp.1; 1.
n; PF00093; vwc; 1.
RT; SM00121; IB; 1.
RT; SM00209; TSP1; 1.
RT; SM00204; VWC; 1.
SITE; PS00222; IGF_BINDING; 1
SITE; PS00222; TSP1; 1.
SITE; PS0092; TSP1; 1.
SITE; PS0184; VWFC_2; 1.
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pro; IPR000884; TSP1.
pro; IPR001007; VWF_C.
pr00219; IGFBP; 1.
pr00090; tsp_1; 1.
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                                                                                                                                                                                                                                                                                                  1 MRGSPLIHLLATSFLCLLSMVCAQLCRTPCTCPWTPPQCPQGVPLVLDGCGCCKVCARRL
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                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                 CRCDDGGFTCLFLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGV-TPAIQRSTAQGH
                                                                                                                          ARSHSSWNSAF
                                                                                                                                                       GESCDHLHVCDPSQGLVCQPGAGPSGRGAVCLFEEDDGSCEVNGRRYLDGETFKPNCRVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                        MRGNPLIHLLAISFLCILSMVYSQLCPAPCACPWTPPQCPPGVPLVLDGCGCCRVCARRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                email to license@isb-sib.ch).
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98
195
197
251 AA;
(Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation updat
rissue growth factor-like protei
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in production (By similarity).
AR LOCATION: Secreted (Probable).
Y: Contains 1 IGFBP domain.
Y: Contains 1 VWFC domain.
Y: Contains 1 TSP type-1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; AAC96320.1; -.; AAD18058.1; -.
26; Wisp2.
                                                         STANDARD;
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164
239
197
27095 1
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251
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CONNECTIVE TISSUE GROWTH FA
PROTEIN.
IGFBP.
VWFC.
TSP TYPE-1.
N-LINKED (GLCNAC. . .) (POT
N-LINKED (GLCNAC. . .) (POT
                                                                                                                                                                                                                                                                                                                                   9;
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); Mismatches
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  precursor
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  (CTGF-L)
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RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Deloukas P., Matthews L.H., Ashurst J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.E., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Blrd C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Blrd C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Rice C.M., Ross M.T., Scott C.E., Sebra H.K., Shownkeen R., Sims S.,
RA Rice C.M., Ross M.T., Scott C.E., Sebra H.K., Shownkeen R.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Wilnehead S.L., Whittaker P., Williey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Roders J.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interacts
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pennica D., Swanson T.A., Welsh J.W., Roy M.A., Lawrence D.A., i Brush J., Tameyhill L.A., Deuel B., Lew M., Watanabe C., Cohen i Melham M.F., Finley G.G., Quirke P., Goddard A.D., Hillan K.J., Gurney A.L., Botstein D., Levine A.J.;

"MISP genes are members of the connective tissue growth factor that are upp-regulated in wnt-1-transformed cells and aberrantly expressed in human colon tumors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99287915; PubMed=10358067; Kumar S., Hand A.T., Connor J.R., Dodds R.A., Ryan P.J. Fisher S.M., Nuttall M.E., Lipshutz D.B., Zou C., Hwang Votta B.J., James I.E., Rieman D.J., Gowen M., Lee J.C. "Identification and cloning of a connective tissue grow cDNA from human osteoblasts encoding a novel regulator functions.":
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I.; Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21638749; PubMed=11780052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99061933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rowles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         new member of the connective tissue growth factors with the breast cancer associated mucin MUC1."; d (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                               sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sci. U.S.A. 95:14717-14722(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=9843955;
                                                                                                                                                                                                                                                                                               comparative
                                                                                                                                                                                                                                                                                               analysis
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                                                                                                                                                                                                                                                                                               of
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
AB Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
AR Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Mazny D.M., Sodergren E.D., Dickson M.C.,
AN Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
AN Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
AN Whiting M., Madan A., Touchman J.W., Green E.D., Dickson M.C.,
AN Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
AN Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
AN Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Mazra M.A.,
"Genezation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                          Pfam; PF00219; IGFBP; 1
Pfam; PF00090; tsp_1; 1
Pfam; PF00093; vwc; 1.
SMART; SM00121; IB; 1.
SMART; SM00209; TSP1; 1.
SMART; SM00214; VWC; 1.
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                                                                 SEQUENCE
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                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteocalcin production.
SUBCELULIAR LOCATION: Secreted (Probable)
TISSUE SPECIFICITY: Expressed in primary
ovary, testes, and heart.
SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 1 TSP type-1 domain.
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Promotes the adhesion of osteoblast cells and inhibits the
of fibringen to integrin receptors. In addition, inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; AF083500; AAC70350.1;
AF074604; AAC25794.1;
; AF100780; AAC95322.1;
; AL139352; CAB94788.1;
; BC017782; AAH17782.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss institute of Bioinformatics and the EMBL outstation - EDUTOPEAN BIOINFORMATICS INSTITUTE THERE are NO restrictions on its by non-profit institutions as long as its content is in no way
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                                                               250 AA;
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98
194
 Conservative
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                                                                                                                                                                                            VWFC_2;
                                                                                                                                                                                                             VWEC_
                                                                                                                                                                                                                             TSP1;
                                                                                                                                                                                                                                             IGF_BINDING;
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 Score 1064; I
Pred. No. 9.2e
.7; Mismatches
                                                                                                                            POTENTIAL. CONNECTIVE PROTEIN.
                                                                                              VWFC.
                                                                                TSP TYPE-1.
                                                                                                             IGFBP.
                                                                 C499837EF42FEEAC
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, Carninci P., Mullahy S.J.,
Abramson R.D., Mullahy S.J.,
                .2e-74;
                                   DB
     49;
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                                                                 CRC64;
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L., Scheetz T.E.,
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Mammalia; Eutheria; C
Bovidae; Bovinae; Bos
NCBI_TaxID=9913;
                                                                                                                                                                                                            15-JUL-1998
28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGF_BOVIN
018739; Q90
                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage, by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
EMBL; AF000137; AAB66596.1; -.
EMBL; AF309555; AAG30290.1; -.
InterPro; IPR006208; Cys_Knot_C.
InterPro; IPR006207; Cys_Knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
                                                                                                                                                                                                                                                                                                                      Liliensiek B., Lin Z., Fotsis T., Schimanski M., Bierhaus A.,
Kanitz M., Kauffmann G., Schweigerer L., Ziegler R., Nawroth
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      Connective tissue
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                                                                                                                              SYNTHESIS (BY SIMILARITY).

SUBUNIT: MONOMER (BY SIMILARITY).

SUBCELLULAR LOCATION: FOUND IN THE EXTRACELLULAR MATRIX AND AS A SOLUBLE FORM (BY SIMILARITY).

SIMILARITY: Contains 1 IGFBP domain.

SIMILARITY: Contains 1 VWFC domain.

SIMILARITY: Contains 1 TSP type-1 domain.

SIMILARITY: Contains 1 TSP type-1 domain.
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InterPro; IPR001007; Vys
Pfam; PF000007; Cys_knot
Pfam; PF000219; IGFBP; 1
Pfam; PF00099; tsp_1; 1
Pfam; PF00093; vc; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
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SMART; SM00214; VWC; 1
 Eukaryota; Metazoa;
Mammalia; Eutheria;
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                   Homo sapiens (Human).
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; IPRO01007; VWF_C.
00007; Cys_knot; 1.
00219; IGFBP; 1.
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CTGE_HUMAN STANDARD; PRT; 349 AA. P29279; Q96QX2; 01-DEC-1992 (Rel. 24, Created) 01-DEC-1992 (Rel. 24, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Connective tissue growth factor precursor (Hyr specific protein 24). CTGF OR HCS24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; PS01185; CTCK_1; 1.
2; PS01225; CTCK_2; 1.
3; PS00222; IGF_BINDING; :
4; PS50092; TSP1; 1.
5; PS01208; VWFC_1; 1.
6; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                            DTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNAFCRLEKQSRLCMVRPCEA
                                                                                                                                                                                                                                                                                                                                              FTCLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGVTPAIQRSTAQGHQLSAL---
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33 100
101 167
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37924 MW;
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               Chordata;
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IN REF. 1).
CV -> YI (IN REF. 1).
CV -> Y (IN REF. 1).
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Pred.
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CONNECTIVE TISSUE GROWTH FACTOR
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Craniata; V
Catarrhini;
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               Vertebrata;
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.3e-36;
   Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81;
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                 Euteleostomi;
                                                                                     chondrocyte-
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SEQUENCE FROM N.A.
TISSUB-Umbilical vein endothelial ce
MEDLINE-93187114; PubMed-1293144;
Igarashi A., Bradham D.M., Okochi H.
"Connective tissue growth factor.";
J. Dermatol. 19:642-643(1992).
                                                                                                                                                                                                This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                       chondrocytes in culture.";
Endocrinology 141:264-273(2000).
-i-FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRETED
-i-FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRETED
VASCULAR ENDOTHELIAL CELLS. PROMOTES PROLIFERATION AND
DIFFERENTIATION OF CHONDROCYTES. MEDIATES CELL ADHESION AN
ENHANCES FIBROBLAST GROWTH FACTOR-INDUCED DNA SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Chondrocytes;
MEDLINE-20080284; PubMed-10614647;
Nakanishi T., Nishida T., Shimo T., Kobayashi K.,
Tamatani T., Tezuka K., Takigawa M.;
"Effects of CTGF/Hcs24, a product of a hypertroph.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             numen connective tissue growth factor is atherosclerotic lesions."; Circulation 95:831-839(1997).
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MEDLINE-97207446; PubMed=9054739;

Oemar B.S., Werner A., Garnier J.M., Do

Marz W., Rupp J., Pech M., Luescher T.F.

"Human connective tissue growth factor i
                              Genew;
                                                          EMBL; M92934; AAA91279.1; -
EMBL; X78947; CAA55544.1; -
EMBL; AL354866; CAC44023.1;
                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specific gene, on the proliferation and
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"Connective tissue growth factor: a cysteine-rich mitogen secreted human vascular endothelial cells is related to the SRC-induced immediate early gene product CEF-10.";
J. Cell Biol. 114:1285-1294(1991).
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[3]
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Note-No experimental confirmation available,
SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                 European Bioinformatics Institute.
GO:0005578; C:extracellular matrix; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: FOUND IN SOLUBLE FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                     Name=Long;
                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative
                                             A40551;
                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                 V; HGNC:2500;
121009; -.
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Pfam; PF00090; tvc; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00209; TSP1; 1
SMART; SM00214; VWC; 1.
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PROSITE; PS91208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
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GO:0005520; F:insulin-like growth factor bindi
GO:0008151; P:cell growth and/or maintenance;
GO:0008544; P:epidermal differentiation; TAS.
GO:0009611; P:response to wounding; TAS.
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PS00222;
PS50092;
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                                                                                                                                                                                      DTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEA
                                                                                                                              FTCLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGVTPAIQRSTAQGHQLSAL----
                                                                                                                                                     DPCDPHKGLFCDFGSPANRKIGVCTA-KDGAPCIFGGTVYRSGESFQSSCKYQCTCLDGA 130
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IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1.
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CTCK_2; 1.
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46.9%;
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Pred. No. 6.
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CTGF\_RAT STAN
Q9R1E9; Q9WVS1;
28-FEB-2003 (Rel. 4
28-FEB-2003 (Rel. 4
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Rattus norvegicus (Rat).
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Eukaryota; Futheria; Rodentia;
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PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20145935; PubMed-10679821; Xu J., Smock S.L., Safadi F.F., Rosenzweig A.B., Marks S.C. Jr., Owen T.A., Popoff S.N.; "Cloning the full-length cDNA for rat connective implications for skeletal development."; J. Cell. Biochem. 77:103-115(2000).
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SUBCELLULAR LOCATION: Secreted.

SUBCELLULAR LOCATION: Secreted.

SIMILARITY: Contains 1 TGFBP domain.

SIMILARITY: Contains 1 TSP type-1 domain.

SIMILARITY: Contains 1 TSP type-1 domain.
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pF00093; vwc; 1.
psw00041; CT; 1.
sw00011; IB; 1.
sw00209; TSP1; 1
sw00214; vwc; 1.
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PS01225; CTCK_2; 1.
PS00222; IGF_BINDING; 1
PS00227; TSP1; 1.
PS01208; VWFC_1; 1.
PS01208; VWFC_2; 1.
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IPR006207; Cys_knot_C.
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IPR000884; TSP1
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Sciurognathi; Muridae; Murinae; Rattus.
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A Klausner R.D., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,
A Klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
A Altschul S.E., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A List Chenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A List Chenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Blosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Hillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Cenneration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-91229699; PubMed-2029337;

Brunner A., Chinn J., Neubauer M.G., Purchi
"Identification of a gene family regulated factor beta.";

factor beta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P29268; Q922U0;
01-DEC-1992 (Rel. 24, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Connective tissue growth factor precursor (FI (Hypertrophic chondrocyte-specific protein 24 CTGF OR FISP12 OR FISP-12 OR HCS24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=91363290; PubMed=1888698;
RYSECK R.-P., Macdonald-Bravo.H.,
                   "Generation and initial analysis
              human and
                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                      DNA Cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCVPLCSMDVRLPSPDCPFPRRVKLPGKCCEEWVCDEP----KDRTVVGPALAAYRLED
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                mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mapping, and expression of fisp-12, a growth ene encoding a secreted cysteine-rich protein. Differ. 2:225-233(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                     10:293-300(1991).
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                cDNA sequences
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Rodentia;
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45
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Pred.
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Sciurognathi;
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No. 6.
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thi; Muridae; Murinae; Mus
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n 24).
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protein.";
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MGD; MGI:
GO; GO:00
GO; GO:001
GO; GO:001
GO; GO:000
GO; GO:000
GO; GO:000
GO; GO:000
GO; GO:000
                                                                     Pfam; PF00090; tsp_1; 1.
Pfam; PF00099; vwc; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM001209; TSP1; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01125; CTCK_2; 1.
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EMBL; M70642;
EMBL; M80263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Babic A.M., Chen C.C., Lau L.F.;

"Fispl2/mouse connective tissue growth factor mediates endothelial
cell adhesion and migration through integrin alphavbeta3, promotes
endothelial cell survival, and induces angiogenesis in vivo.";
Mol. Cell. Biol. 19:2958-2966(1999).

-i- FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRETED BY
VASCULAR ENDOTHELIAL CELLS. PROMOTES PROLIFERATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION, AND SUPPLIANCE PUBMED-91327410; PubMed-9184077; MEDLINE-97327410; PubMed-9184077; Kireeva M.L., Latinkic B.V., Kolesnikova T.V., Chen C.C., Yar Abler A.S., Lau L.F.; Cyr61 and Fispl2 are both ECM-associated signaling molecule; Cyr61 and Fispl2 are both ECM-associated signaling molecule; Cyr61 and Fispl2 are both ECM-associated signaling molecule;
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FUNCTION,
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                             InterPro; IPR006208; Cys_knot.
InterPro; IPR008207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000884; TSP1.
InterPro; IPR001007; VWF_C.
Pfam; PF00007; Cys_knot; 1.
Pfam; PF00219; IGFBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99182484; PubMed=10082563; Babic A.M., Chen C.C., Lau L.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IR; A40578; A40578.

IGD; MGI:95537; Ctgf.

G0:0005578; C:extracellular matrix; IDA.

G0:00005278; F:heparin binding activity; IDA.

G0:00005178; F:integrin binding activity; IDA.

G0:00005178; F:integrin binding activity; IIDA.

G0:00001525; P:angiogenesis; IDA.

G0:00016477; P:cell migration; IDA.

G0:00001647; P:cell migration; IDA.

G0:0000543; P:FGF receptor signaling pathwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: TESTIS, SPLEEN, KIDNEY, LUNG, HEART, AND HRAIN (LOWEST LEVEL IN TESTIS AND HIGHEST IN LUNG).
INDUCTION: By growth factors.
SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYNTHESIS (BY.SIMILARITY).
SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: FOUND IN TH
SOLUBLE FORM.
TISSUE SPECIFICITY: TESTIS, SPLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO:0007229; P:integrin-mediated GO:0001503; P:ossification; IMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M80263; AA; BC006783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                     PS01225; CTCK_2; 1.
PS00222; IGF_BINDING;
PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Res.
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AAA73135.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ossification;
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signaling patl
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Best Local
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01-DEC-1992
28-FEB-2003
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Cell adhe
SIGNAL
                   nephroblasiomas.";

Mol. Cell. Biol. 12:10-21(1992).

Mol. Cell. Biol. 12:10-21(1992).

Mol. Cell. Biol. 12:10-21(1992).

Mol. Cell. Biol. 12:10-21(1992).

FUNCTION: IMBEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL GROWTH REGULATION. ITS OVEREXPRESSION IS ASSOCIATED WITH TUMORIGENESIS AND EXPRESSION OF A N. TERMINAL-TRUNCATED VERSION OF NOV GENE IN CHICKEN EMBRYONIC FIBROBLASTS (CEF) IS SUFFICIEN TO INDUCE THE TRANSFORMATION OF CEF IN VITRO.

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: BRAIN AND HEART, AND AT A LOWER LEVEL IN MUSCLE AND INTESTINE, IN THE EMBRYO. LUNG AND LESS SO IN BRAIN SPLEEN, IN ADULT CHICKEN.

-!- DEVELOPMENTAL STAGE: MAVI-INDUCED NEW HORDERS EXPRESS A HICKEY AND ADULT CHICKEN.
                                                                                                                                                                                                     STRAIN-Brown leghorn;
MEDLINE-92107157; PubMed-1309586;
Joliot V., Martinerie C., Dambrin
                                                                                                                                                                    Crochet J., Perbal B.;
"Proviral rearrangements and overexpression of (nov) in myeloblastosis-associated virus type
                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
Archosauria; Aves; Neogn
                                                                                                                                                                                                                                                                                                                                VON
                                                                                                                                                                                                                                                                                                                                            VOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                            P28686;
                                                                                                                                                                                                                                                                                                                                                                                                      NOV_CHICK
                                                                                                                                                                                                                                                                                                                                           protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HVCDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDDGG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSMVCAQLCRTP------CTC-PWTPPQCPQGVPLVLDGCGCCKVCARRLGESCDHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPCDPHKGLFCDFGSPANRKIGVCTA-KDGAPCVFGGSVYRSGESFQSSCKYQCTCLDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50184;
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OF NOV GENE KIDNEY.
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(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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. 24, Last sequence upo
. 41, Last annotation ursor (Nephroblastoma (
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                                                                                                                                                                                                                                                                                          ; Chordata; Craniata; Vertebrata; Euteleostomi; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthesis;
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45.6%;
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           TRANSCRIPTION
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TSP TYPE-1.
CTCK.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 550.5;
Pred. No. 6.9e
26; Mismatches
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                        EXPRESS A HIGH
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Best Local S
Matches 109
                                                                                                                                                                                                                                                                                                                                  Pfam; PF00007; Cys_knot; 1.
Pfam; PF000219; IGFBB; 1.
Pfam; PF00093; tvc; 1.
Pfam; PF00093; vwc; 1.
SMART; SM00121; IB; 1.
SMART; SM00121; IB; 1.
SMART; SM00121; VWc; 1.
SMART; SM00214; VWc; 1.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01255; CTCK_2; 1.
PROSITE; PS01255; CTCK_2; 1.
PROSITE; PS01203; VWFC_1; 1.
PROSITE; PS01203; VWFC_1; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS01208; VWFC_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR;
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SIMILARITY:
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                                                                                     115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an email to license@isb-sib.ch).
                 QRRLCLPRPC
                                        TPAIQRSTAQGHQLSALVTPASADAPCPNWSTAWGPCSTT@GLGIATRVSNQNRFCQLEI
                                                                             PNCRVLCRCDDGGFTCLPLCSEDVRLPSWDCPRPKRIQVPG
                                                                                                      VCARQRGESCSPLLPCDESGGLYCDRGPEDGGGAGICMVI
                                                                                                                VCARRLGESCDHLHVCDPSQGLVCQPGAGPGGHGAVCLLD
                                                                                                                                         QGLPVLLL-----LLLLLRPCEVSGREAACPRPCGGRCPA
                                                                                                                                                       RGSPLIHLLATSFLCLLSMVC----AQLCRTPC--TCPWI
QTRLCMMRPC
                                  AMAAYRQEA---TLGIDVSDSSAN--CIEQTTEWSACSKSGGMGFSTRVTNRNQQCEMVK
                                                                    PSCKYQCTCRDGQ1GCLPRCNLGLLLPGPDCPFPRK1EVPGECCEKWVCDPRDEVLLGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR005208; Cys_knot.
IPR005207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1.
IPR000884; TSP1.
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Contains
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1 VWFC domain.
1 TSP type-1 domain.
1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                             ¥.
                                                                                                                                                                          34;
                                                                                                                                                                        Score 541.5;
Pred. No. 3.3e
34; Mismatches
                                                                                                                                                                                                                  TSP TYPE-1.
CTCK.
BY SIMILARIJ
                                                                                                                                                                                                                                                                                         IGFBP.
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ام ع. ع.
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                                                                                                                                                                                            DB 1;
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                                                                                                    EPPRCAPGVPAVLDGCGCCL
                                                                                                                                                                          Indels
                                                                                                                                                                                         Length
                                                                                                                                                         PPQCPQGVPLVLDGCGCCK
                                                                                     CCPEWVCDQ-----
                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                            351;
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                                                                                     -GV
                                 235
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CE10_CHICK
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE-89145206; PubMed-2537491;

Simmons D.L., Levy D.B., Yannoni Y., Erikson R.L.;

Simmons D.L., Levy D.B., Yannoni Y., Erikson R.L.;

"Identification of a phorbol ester-repressible v-sr.

Proc. Natl. Acad. Sci. U.S.A. 86:1178-1182(1989).

-!- FUNCTION: PROBABLE SECRETED REGULATORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CEF-10 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Contains 1 IGFBP domain.

SIMILARITY: Contains 1 VWFC domain.

SIMILARITY: Contains 1 TSP type-1 domain.

SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Secreted INDUCTION: BY V-SRC.
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                                                                                                                                                                                                               ; TSP1; 1.
; VWFC_1; 1.
; VWFC_2; 1.
nding; Signal.
                                                                       375
164
268
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Neognathae; Galliformes; Phasianidae; Phasianinae;
             37.6%;
                                                         MW;
 35,
                                                                    TSP TYPE-1.
CTCK.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
             Score 541; DB 1;
Pred. No. 3.9e-34;
                                                                                                                                                                       CEF-10 PROTEIN VWFC.
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                                                         95F28553BE35D5AE CRC64;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Probable).
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019113;
15-JUL-1998
15-JUL-1998
                                 InterPro;
InterPro;
InterPro;
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InterPro;
                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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the European Bioinformatics Institute and the European Bioinformatics Institutions as 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Uterus;
MEDLINE-97390475; PubMed-9242708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Purification and characterization of novel heparin-binding grofactors in uterine secretory fluids. Identification as heparingegulated Mr 10,000 forms of connective tissue growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Connective tissue
                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harding P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: MONOMER (By similarity).

SUBCELLULAR MONOMER (BY SIMILARITY).

SUBCELLULAR LOCATION: FOUND IN THE EXTRACELLULAR MATRIX AND AS A SOLUBLE FORM (BY SIMILARITY) domain.

SIMILARITY: Contains 1 IGFBP domain.

SIMILARITY: Contains 1 VWFC domain.

SIMILARITY: Contains 1 TSP type-1 domain.

SIMILARITY: Contains 1 TSP type-1 domain.

SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGN. Chem. 272:20275-20282(1997).
FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRETED FUNCTION: MAJOR CONNECTIVE TISSUE PROMOTES PROLIFERATION AND VASCULAR ENDOTHELIAL CELLS. PROMOTES PROLIFERATION AND DIFFERENTIATION OF CHONDROCYTES (BY SIMILARITY). MEDIATES ADHESION AND ENHANCES FIBROBLAST GROWTH FACTOR-INDUCED DNA CRUMENTES FOR THE PROBLEM OF THE PROPERTY OF THE PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYNTHESIS (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190
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                                                                                                                                                                                                                   U83916; AAC48756.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAAALLCLARLALGSPCPAVCQCPAAAPQCAPGVGLVPDGCGCCKVCAKQLNEDCSRTQP
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                                                            IPR006208; Cys_knot.
IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
IPR000884; TSp1.
                                     IPR001007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 41, Last annotation update)
tissue growth factor precursor.
Cys_knot;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                 VWF_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00090; tsp_1; 1
Pfam; PF00093; vwc; 1
SMART; SM00041; CT; 1;
SMART; SM00121; IB; 1
SMART; SM00209; TSP1; 1
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                COTJA
                                                                                                                                                                                           01-NOV-1995
01-NOV-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID DISULFID DISULFID DISULFID SEQUENCE:
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.

1. FUNCTION: IMMEDIATE EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL GROWTH REGULATION (BY SIMILARITY).

1. SUBCELLULAR LOCATION: Secreted (By similarity).

1. SIMILARITY: Contains 1 IGFBP domain.

1. SIMILARITY: Contains 1 VMFC domain.

1. SIMILARITY: Contains 1 TSP type-1 domain.

1. SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
Pfam;
Pfam;
                                                                                    Weiskirchen
                                                                                                                                        Eukaryota; Metazoa
Archosauria; Aves;
                                                                                                                                                   NOV.

Coturnix coturnix japonica (Japanese quail).
                                                                                                                                                                               NOV protein
                                                                                                                                                                                                                                    NOV_COTJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                              SEQUENCE FROM N.A.
                                                                                                                   NCBI_TaxID=93934;
                                                                                                                                                                                                                           P42642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adhesion;
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                                                                                                                                                                                                                                                                                                                                                                                                                  12 AFVILLALCSRPASGODCSGQCQCAAGKRRACPAGVSLVLDGCGCCRLCAKQLGELCTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00222; IGF_BINDING;
PS50092; TSP1; 1.
PS01208; VWFC_1; 1.
PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS01185; CTCK_1;
PS01225; CTCK_2;
                                                                                                                                                                                                                                                                                                                                                                                             HVCDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDDGG
                                                                                                                                                                                                                                                                                        DTFGPDPTMMRANCLVQTTEWSACSKTCGMGISTRVTNDNAFCRLEKQSRLCMVRPCEA
                                                                                                                                                                                                                                                                                                            ----VTPASADAPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQRRLCLPRPCLA
                                                                                                                                                                                                                                                                                                                                  VGCVPLCSMDVRLPSPDCPFPRRVKLPGKCCEEWVCDEP-----KDHTVVGPALAAYRLE
                                                                                                                                                                                                                                                                                                                                                   FTCLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGVTPAIQRSTAQGHQLSAL---
                                                                                                                                                                                                                                                                                                                                                                         DPCDPHKGLFCDFGSPANRKIGVCTA-KDGAPCVFGGTVYRSGESFQSSCKYQCTCLDGA
                                                                                                                                                                                        (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                  precursor
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                                                                                     Bister K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VWFC.
TSP TYPE-1.
TSP TYPE-1.
CTCK.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
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); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                     PRT;
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ام
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..5e-33;
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Best Local S
Matches 101
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Pfam; PF00099; tsp_1; 1.
Pfam; PF00099; vwc; 1.
SMART; SM00041; CT; 1.
SMART; SM00021; IB; 1.
SMART; SM00121; VWC; 1.
SMART; SM00121; VWC; 1.
SMART; SM00214; VWC; 1.
SMART; SM00214; CTCK_1; 1.
PROSITE; PS01185; CTCK_2; 1.
PROSITE; PS00225; CTCK_2; 1.
PROSITE; PS00225; IGF_BINDING; 1
PROSITE; PS0022; TSP1; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS01208; VWFC_2; 1.
            NOV_MOUSE
Q64299;
Q1-NOV-1997
Q1-NOV-1997
15-SEP-2003
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   protein
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01; Conservative
                                                                                                                                                                                                                                                  CPRPCGGRCPAEPPRCAPGVPAVLDGCGCCLVCARQRG
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                                                                                                                 QTTEWSACSRSCGMGFSTRVTNRNQQCEMVKQTRLCMMRPC
                                                                                                                                                                                                        DGGGTGICMVLEGD-NCVFDGMIYRNGETFQPSCKYQ
                                                                                                                                                                                                                     PGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLC
                                                                                                                            DCPFPRKIEVPGECCEKWVCEPRDEVLLGGFAMAAYRC
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IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1_
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  (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 42, Last annotation updat
homolog precursor (NovH) (Nephr
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                                                           STANDARD;
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45.7%;
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CTCK.
BY SIMILARITY.
OF CHICKED (GLCNAC.)
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VWFC.
TSP TYPE-1.
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Pred.
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                                                          PRT;
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(See http://www.isb-sib.
               update)
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   overexpressed
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257; CAA...
.1:109185; NOV.
.1:109185; NOV.
.7:109185; NOV.
.7:109185; NOV.
.7:10906208; Cys_knot_C.
.2:Pro; IPRO06208; Tspl.
.2:Pro; IPRO0667; Insl_gro_fac_pr.
.2:Pro; IPRO08084; Tspl.
.4:Pro; IPRO01097; VWF_C.
.4:Pro; IPRO01097; Cys_knot; 1.
.5:Pro; IPRO01097; Cys_knot; 1.
.5:Pro; Pro00097; Cys_knot; 1.
.5:Pfam; PF000097; Cys_knot; 1.
.7:Pfam; PF00099; tspl; 1.
.8:MART; SM00041; CT; 1.
.8:MART; SM00041; CT; 1.
.8:MART; SM00029; Tspl; 1.
.8:MART; SM00029; Tspl; 1.
.8:MART; SM00214; VWC; 1.
.8:MART; SM00214; VWC; 1.
.8:MART; SM00214; CT; 1.
.8:MART; SM00214; CT; 1.
.9:TTE; PS01185; CTCK_1; 1.
.9:TTE; PS01185; CTCK_2; 1.
.9:TTE; PS01185; CTCK_2; 1.
.9:TTE; PS01185; CTCK_2; 1.
  Growth fa
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                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See
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I SIMILARITY: Contains 1 VWFC domain.
I SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 C-terminal cystine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY GROWTH REGULATION (BY SIMILARITY).
-1- SUBUNIT: Interacts with FBLM1 (By similar SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nephrogenesis.";
Oncogene 12:1479-1492(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Snaith M.R., Natarajan D., Taylor L.B., Choi C.P., Perbal B., Schofield P.N., Boulter C.A.; "Genomic structure and chromosomal mapping of the Genomics 38:425-428(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-129/Sv; and ICR; TISSUE-Brain;
MEDLINE-97131523; PubMed-8975721;
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"Regulation of nov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96204003; PubMed=8622864; Martinerie C., Chevalier G., Raus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6
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Mammalia; Eutheria;
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NOV.
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                                                                                                                                         E; PS01225; CTCK_1; 1.
3; PS00222; IGE_BINDING; 1
9; PS00022; TSP1: 1
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                                                                                                                        PS50092; TSP1; 1.
PS01208; VWFC_1;
PS50184; VWFC_2;
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   (Mouse)
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Rodentia;
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WT1: a potential role for
IGFBP.
VWEC.
TSP TYPE-1.
TSP TYPE-1.
CTCK.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                        POTENTIAL.
NOV PROTEI
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Best Local
           MEDLINE-22388257; PubMed-12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin Gam., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McCwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                       Jiang D., "Cloning, Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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9:2729-2732(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                 N.A.
                                                                                                                                                                                                                                                                                             N.A.
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                                                                                                                                                                                                                                                                                                                                                                                   L1 W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334
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277
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42.5%;
  D.M.,
                                                                                                                                                                                                                                                                                                                                  and expression of human nov gene."; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Joubert I.,
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Sodergren
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Pred. No. 2.7e
%% Mismatches
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N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
; OBECEBCFC67829DE CRC64;
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Catarrhini;
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i; Hominidae;
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nes 87;
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  Gay L.J., Hul
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EMBL; X78351; CAA55146.1; JOINED. EMBL; X78352; CAA55146.1; JOINED. TWBL; X78353; CAA55146.1; JOINED. EMBL; X78354; CAA55146.1; JOINED. EMBL; X78354; CAA65403.1; -... EMBL; X9584; CAA65403.1; -... EMBL; BC015028; AAH15028.1; -...
                                                                                                                                                                               Pfam; PF00007; Cys_knot; 1
Pfam; PF000019; IGFBP; 1.
Pfam; PF00090; tsp_1; 1.
Pfam; PF00090; twc; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00121; TSP1; 1.
SMART; SM00214; VWC; 1.
SMART; SM00214; VWC; 1.
DOMAIN
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DISULFID
                                                                                                     PROSITE;
PROSITE;
PROSITE;
PROSITE;
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                                                                                                                                                                                                                                                                                      InterPro;
InterPro;
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"The C-terminal domain of the regulatory protein
promote interaction with fibulin IC: a clue for a
cell-adhesion signaling.";
Proc. Natl. Acad. Sci. U.S.A. 96:869-874(1999).
-i- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO F
GROWTH REGULATION (BY SIMILARITY).
                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                         MIM;
                                                                                                                                                                                                                                                                                                                                                                                 PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blakesiey R.W., Touchman J.W., Green E.D., Dickson M.C., Rodiniquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full human and mouse cDNA sequences.", proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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SIMILARITY: Contains 1 IGFBP domain.

SIMILARITY: Contains 1 VWFC domain.

SIMILARITY: Contains 1 TSP type-1 domain.

SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Interacts with SUBCELLULAR LOCATION: SO TISSUE SPECIFICITY: INCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European
                                                                                                                                                                                                                                                                                                                                                                                 138069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation surpean Bioinformatics Institute. There are no restrictions on its Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                  HGNC:7885; NOV.
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                                                                                                    PS50092;
PS01208;
PS50184;
                                                                                                                                                        PS01185;
PS01225;
                                                                                                                                             PS00222;
                                                                                                                                                                                                                                                                                                    IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helton E., Ketteman
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                                                                                                                                                                                                                                                                                                                                          IPR006208; Cys_knot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  equires a license agreement (S email to license@isb-sib.ch).
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                                                                                         Signal
                                                                                                     VWFC_1;
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                                                                                                                               IGF_BINDING;
TSP1; 1.
                                                                                                                                                        CTCK_1; 1.
CTCK_2; 1.
 357
107
174
250
338
301
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POTENTIAL.

NOV PROTEIN I

IGFBP.

VWFC.

TSP TYPE-1.

CTCK.

BY SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXPRESSION
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                                                                 HOMOLOG
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o Y., Bouffard
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NOVH is sufficient
a role of NOVH in
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SIMILARITY.

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RESULT NO. 10 P. 1
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Best Local
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                                                             protein.

Interacts with FBLN1 (By similarity)

SUBURIT: Interacts with FBLN1 (By similarity)

SUBURITARION: Secreted.

ITSUE SPECIFICITY: Ubiquitous.

SIMILARITY: Contains 1 IGFBP domain.

SIMILARITY: Contains 1 VWFC domain.

SIMILARITY: Contains 1 TSP type-1 domain.

SIMILARITY: Contains 1 C-terminal cystine knowlike (CTCK) domain.
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CARBOHYD
CONFLICT
SEQUENCE
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28-FEB-2003
15-SEP-2003
                             the
                                                                                                                                                                                                                                                           that
                                                                                                                                                                                                                                                                    Liu C., Liu X.J., Crowe P.D., Keln
Ling N., De Souza E.B., Maki R.A.;
"Nephroblastoma overexpressed gene
                                                                                                                                                                                                                                                                                                               STRAIN=Sprague-Dawley;
MEDLINE=20035752; PubMed=10570975;
                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-10116;
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                                                                                                                                                                                              it induces protein tyrosine phosphorylation.";
le 238:471-478(1999).
PRUNCTION: Can act as a growth factor for some specific receptor that leads to the phosphorylation.
      3 SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
on notifit institutions as long as its content is in
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(Rel. 41, Last sequence up
(Rel. 42, Last annotation
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
OF CHCNAC...) (
N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
N-K (IN REF. 3).
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Pred. No. 1.7e-32;
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                    Kelner G.S.,
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RESULT
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Best Local
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InterPro; IPR000867; I
InterPro; IPR000884; T
InterPro; IPR001007; V
Pfam; PF00007; Cys_kno
Pfam; PF000219; IGFBP;
                                                 NOV_XENLA
P51609;
01-OCT-1996
01-OCT-1996
28-FEB-2003
NOV protein
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CARBOHYD
SEQUENCE
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InterPro;
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DOMAIN
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SIGNAL
 Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; M
                                          VOV
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                           Xenopus laevis (African clawed frog)
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; PF00093; vwc; 1.
T; SM00041; CT; 1.
T; SM00121; IB; 1.
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SM00214;
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; PS01225; CTCK_2; 1.
; PS00222; IGF_BINDING; PS50022; TSP1; 1.
; PS01208; VWFC_1; 1.
; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor;
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                                                                                                                                                                                                                                                      PLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVC---DQG-----VTPAIQRSTAQGHQLSA
                                                                                                                                                                                                                                                                                            QSSGLYCDRSADPNNETGICMVPEGD-NCVFDGVIYRNGEKFEPNCQYHCTCRDGQIGCV
                                                                                                                                                                                                                                                                                                                     PSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDDGGFTCL
                                                                                                                                                                                       ----DSSINCIEQTTEWSACSKSCGMGLSTRVTNRNLQCEMVKQTRLCMVRPC
                                                                                                                                                                                                              LVTPASADAPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQRRLCLPRPC
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                                                  (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
homolog precursor (Xnov).
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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: IGFBP; 1.
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TSP1; 1
VWC; 1.
                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                21
351
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not; 1.
Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cys_knot_C.
Insl_gro_fac_pr.
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CTCK.

GTCK.
BY SIMILARITY.
O-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . . .) (POTENTIAL).
MW; 02619707DE7C1BFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
NOV PROTEI
IGFBP.
VWFC.
                Craniata;
                                                                                                                       PRT;
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                Vertebrata; Euteleostomi;
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.8e-32;
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  Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                   , 98
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Pipidae;
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Best Local
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SMART; SM00209; TSP1; 1.
SMART; SM00209; TSP1; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01185; CTCK_
PROSITE; PS01225; CTCK_
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DOMAIN
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SIGNAL
CHAIN
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the chicken nov gene."
Gene 171:243-248(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ring Z., King M.L.;
"Isolation and characterization of xnov, a Xenopus laevis ortholog of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
WEDLINE=96257227; PubMed=8666280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A GROWTH REGULATION (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation een the Swiss Institute of Bioinformatics and the EMBL outstation on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00090;
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                                                                                                                                                                                                                                                                                                                                         factor;
                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                   PS50092; TSP1; 1.
PS01208; VWFC_1; 1.
PS50184; VWFC_2; 1.
TCLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGVTPAIQRSTAQGHQLSALVTPA 188
                                                 VCDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDDGGF
                                                                                                  LATSFLCLLSMVCAQLCRTPC-TCPWTPPQCPQGVPLVLDGCGCCKVCARRLGESCDHLH
                                  PCQEDKGLYCEFNADPRMETGTCMALEGN-SCVFDGVVYRNRESFQPSCKYHCTCLNGHI 123
                                                                                  LALCFILLIQQVASQKCPSQCDQCPEEPPSCAPSVLLILDGCGCCPVCARQEGESCSHLN
                                                                                                                                                                                                                                                                                                                                                                                       PS00222; IGF_BINDING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    PS01225; CTCK
                                                                                                                                                                                                                                                                                                                                                                                                               PS01185; CTCK_1; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-profit institutions as long
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IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001007; VWF_C.
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21
93
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                                                                                                                                   Conservative
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0; tsp_1; 1.
1; vwc; 1.
                                                                                                                                                                                                                                                                                                                                        Signal
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                                                                                                                                                                                 38070 MW;
                                                                                                                                              35.6%;
                                                                                                                                 42;
                                                                                                                               Score 512; DB 1; Le
Pred. No. 5.5e-32;
Pred. No. 5.5e-32;
                                                                                                                                                                              BY SIMILARITY.
N-LINKED (GLCNAC. . .) (PO:
                                                                                                                                                                                                                                                                              VWFC.
TSP TYPE-1.
                                                                                                                                                                                                                                                                    CICK.
                                                                                                                                                                                                                                                                                                                POTENTIAL.
NOV PROTEIN HOMOLOG.
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                                                                                                                                                     Length 343;
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                                                                                                                                                                                            (POTENTIAL).
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GCVPRCNLDLLLPGPDCPFPRRVKVPGECCEKWVCDSKEEMAIGGFAMAAYRPEATLGID 183
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Search completed: July 25, 2003, 12:35:30 Job time: 25 secs

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Perfect score:
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
       1302.5
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_human:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_ptage:*
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Gapop 10.0 , Gapext 0.5
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       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compu
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sp_bacteria:*
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sp_mhc:*
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       Q9PT80
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O8cic8 mus musculu
O9pt80 notophthalm
O98tq8 gallus gall
O42607 xenopus lae
O8ca67 mus musculu
O98tx5 xenopus lae
O97765 sus scrofa
O99pp0 rattus norv
O54775 mus musculu
O9wtm9 rattus norv
O95388 homo sapien
O9ps6 gallus gall
O9ps6 gallus gall
O9ps6 gallus gall
O9ps6 homo sapien
O9id7 homo sapien
O9uid7 homo sapien
O9uid7 nomo sapien
                                                                                                                                                                                                                                                                                                                                                                                                  Description
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ID Q8CI
AC Q8CI
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9.7	9.7	9.7	9.7	9.7	9.7	9.7	10.0	10.0	10.3	10.3	10.4	10.5	10.7	10.7	10.7	10.7	10.9	11.0	11.0	11.2	11.2	11.2	13.9	14.6		7	20.2	0
507	425	938	483	482	426	406	1246	685	947	1028	2327	1048	1034	1004	1034	747	4123	5146	1637	969	626	1664	77	470	374	230	280	100
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Q8MS81	002661	Q8CIA2	Q8K0Q1	Q9CVG8	Q8VEA6	Q925I3	075095	Q9TTS5	Q8BKK7	Q9JLL0	Q91BG7	Q8AWW5	Q8VIK5	Q8CGA7	Q8VHL7	Q8VHF4	075851	Q8SPM4	8ASX60	Q96KG6	Q8ND91	Q9TVQ2	Q9UDE4	Q9VVK3	Q9VVK0	Q8WYK7	Q9HCS3	09UDL6
,																												
Q8ms81 drosophila	002661 bos taurus	Q8cia2 mus musculu	Q8k0q1 mus musculu	Q9cvg8 mus musculu	Q8vea6 mus musculu	Q92513 mus musculu	075095 homo sapien	Q9tts5 bos taurus	Q8bkk7 mus musculu		xen	Q8aww5 gallus gall	mus	Q8cga7 mus musculu	mus	4 mus	075851 homo sapien		bos t	Q96kg6 homo sapien	Q8nd91 homo sapien	caen			droso	Q8wyk7 homo sapien.	Q9hcs3 homo sapien	Q9ud16 homo sapien

## ALIGNMENTS

PRELIMINARY;

PRT;

251 AA.

Qy .	ДУ	ОУ	ОУ	Que Bes Mat	DT RR
180 QLSALVTPASADAPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQRRLCLPRPCLA 239 	121 CRCDDGGFTCLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGV-TPAIQRSTAQGH 179 	61 GESCDHLHVCDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVL 120 	1 MRGSPLIHLLATSFLCLLSMVCAQLCRTPCTCPWTPPQCPQGVPLVLDGCGCCKVCARRL 60    :	Query Match 90.5%; Score 1302.5; DB 11; Length 251; Best Local Similarity 89.6%; Pred. No. 2.2e-117; Matches 225; Conservative 9; Mismatches 16; Indels 1; Gaps 1;	01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) 01-MAR-2003 (Mouse) 01-MAR-2004 (Mouse) 01-Mary Musculus (Mouse) 02-Mary Musculus (Mouse) 03-Mary Muridae; Murinae; Musculus (Mouse) 03-Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musculus (Mouse) 03-Mary Musculus (Mouse) 03-Mary Muridae; Murinae; Musculus (Musculus (M

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Best Local S
Matches 113
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PROSITE;
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PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99033008; PubMed=9813273;
Cash D.E., Gates P.B., Imokawa Y., Brockes J.P.,
"Identification of newt connective tissue growth
retinoid regulation in limb blastenal cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.
TISSUE-Forelimb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Notophthalmus viridescens (Eas
Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Caudata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Connective tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9PT80;
01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Forelimb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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NCBI_TaxID=8316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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;; PF00093; vwc; 1;
T; SM00041; CT; 1;
T; SM00121; IB; 1;
T; SM00209; TSP1;
T; SM00214; vwc; 1
                                                                                                                                                                                                                                                                                                                                                                                           PS01185; CTCK_1; 1.
TE: PS001225; CTCK_2; 1.
TE: PS001225; CTCK_2; 1.
TE: PS00222; IGF_BINDING; 1
TE: PS0092; TSP1; 1.
TE: PS01208; VWFC; 1.
TE: PS01208; VWFC; 1.
        190
                                             182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222:119-124(1998)
AJ271167; CAB659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00007; Cys_knot; PF00219; IGFBP; 1.
                                                                                                                                                                   71
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                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7271167; CAB65965.1; ...
IPR006208; Cys_knot.
IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1.
IPR001007; VWE_C.
                          SALVTPASADAPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQRRLCLPRPCLA 239
                                                                              LLATSFLCLLSMVCAQLCRTPCTCPWTPPQCPQGVPLVLDGCGCCKVCARRLGESCDHLH
      SSLMR---
                                                                                                                                                               VCDPHRGLFCDFGSRVNKKIGVCTA-KDGAPCVFGGMVYRSGESFQSSCKYQCTCLDGGV
                                                                                                                                                                                                  VCDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRY CDGETEKPNCRVLCRCDDGGF
                                                                                                                                                                                                                                          LLAVALLSWVS---CAQDCSGECRCPNKPPECPAGTSLVM@GCGCCKVCAKQLGELCTEKD
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(TrEMBLrel 13, Last sequence update)
(TrEMBLrel 23, Last annotation update)
tissue growth factor.
                                                                                                                                                                                                                                                                                                                             Conservative
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blastema;
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40.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Eastern newt) (Tritata; Craniata; Vertebata; Salamandroidea;
                                                                                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                               Score 575.5;
Pred. No. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                       3B7E2399F27672C1 CRC64;
                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347
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                                                                                                                                                                                                                                                                                                                          84;
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01-MAR-2003 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Connective tissue growth factor precursor (Connective factor/hypertrophic chondrocyte-specific protein 24).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Cranii
                                                                                                                                                                                                                                                                                  PROSITE;
Signal.
SIGNAL
                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                          SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mukudai Y., Kubota S., Takig Submitted (DEC-2001) to the EMBL; AJ298335; CAC33438.1; EMBL; AF463517; AAL68834.1;
                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gygi
                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ω
                                                                                                                                                                                                                                                                                                                                                             terPro; IPR006208; Cys_knot.

terPro; IPR006207; Cys_knot_C.

terPro; IPR000867; Insl_gro_fac_pr.

terPro; IPR000884; TSP1.

terPro; IPR001007; VWF_C.

am; PF00007; Cys_knot; 1.

am; PF000219; IGFBP; 1.

am; PF000219; IGFBP; 1.

am; PF00039; Vwc; 1.

am; PF00039; Vwc; 1.

an; PF00039; Vwc; 1.

ART; SM00041; CT; 1.

ART; SM000214; VWC; 1.
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236
                    236
                                           176
                                                               183
                                                                                    121
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                                                                                                                                 62
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                                                                                                                                                                                                                               Similarity
                    PCLA
PCEA
                                                                                                 CDDGGFTCLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGVTPAIQRSTAQGHQLS
                                                                                                                                                                                                                                                                                                          PS50092; TSP1;
PS01208; VWFC;
                                                                                                                                                                                                                                                                                                                   PS01185; CTCK_1; 1.
PS01225; CTCK_2; 1.
PS00222; IGF_BINDING;
PS50092; TSP1; 1.
                                                                                                                                                                                             SPLIHLLATSFLCLLSMVCAQLCRTPCTCPWTP-PQCPQGVPLVLDGCGCCKVCARRLGE
                                         AYRLEDTYGPDPTMMRANCLVQTTEWSACSKTCGMGISTRVINDNAFCRLEKQSRLCMVR
                                                                 AL-----
                                                                                     CLDGAVGCVPLCSMDVRLPSPDCPYPRRVKLPGKCCEEWVCDEA--
                                                                                                                               LCTERDPCDHHKGLFCDFGSPANRRIGVCTA-RDGAPCVFSGMVYRSGESFQSSCKYQCT
                                                                                                                                                    SCDHLHVCDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCR
                                                                                                                                                                          SPASLAVALLLALLGPEVRGQECSGQCQCGSGPGPSCPAGVSLVLDGCGCCRVCAKQLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (JAN-2001)
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22
344 AA;
                                                                                                                                                                                                                     Conservative
239
                     239
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                                                     -VTPASADAPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQRRLCLPR
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344
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                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                   Score 551; DB
Pred. No. 5.8e-
25; Mismatches.
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                                                                                                                                                                                                                                                             POTENTIAL.

CONNECTIVE TISSUE GROWTH FACTOR

5 69E639AF69BF1D00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X
                                                                                                                                                                                                                    DB 13;
.8e-45;
es. 94;
                                                                                                                                                                                                                                           DВ
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                                                                                    -KEQTAVGPALA
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RESULT
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ID QBCA67
AC QG
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DT 0
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OC 0
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NGEI_TaxID*8355.

(11 EMBLrel. 05, Last sequence upda ... MAR-2003 (TrEMBLrel. 05, Last sequence upda ... Last annotation up. 05 Connective tissue growth factor XCTGF.

Senopus laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertehramphibia; Batrachia; Anura; Mesobatra.

NCBI_TaxID*8355.
                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 107
                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00007; Cys_knot; Pfam; PF000219; IGFBP; 1. Pfam; PF00090; tsp_1; 1. Pfam; PF00090; tvwc; 1. SMART; SM00021; CT; 1. SMART; SM000214; CT; 1. SMART; SM00214; VWC; 1. SMART; SM00214; VWC; 1. SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                PROSITE;
PROSITE;
PROSITE;
                                Q8CA67 PRELIMINARY; PRT; 354 AA.
Q8CA67;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence up
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation
Nephroblastoma overexpressed.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
InterPro;
InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Ying Z., King M.L.; Submitted (AUG-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         042607
                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                         SEQUENCE
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         NCBI_TaxID=10090;
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; U43523;
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; PS01225; CTCK_2; 1.
; PS50092; TSP1; 1.
; PS01208; VWFC; 1.
                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                         PS01208;
                                                                                                                                                                                                             LLSMVC----AQLCRTPCTCPWTPPQCPQGVPLVLDGCGCCKVCARRLGESCDHLHVCDP
                                                                                                                               LCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGVTPAIQRSTAQGHQLSAL------V
                                                                                                                                                                                                                                    LFALFCWVSDAQECNGECQCPNKVPVCDPGVRMVQDGCGCCKVCSKQLGELCTERDVCDP
                                                                                                                                              TPASADAPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQRRLCLPRPCLA 239
                                                                                                                                                                 HKGLFCDFGSRVNRKIGVCTARE-GAPCVFGGTVYRSGESFQSSCKYQCTCIDGGVGCVP
                                                                                                                                                                                                                                                                                                                                                                                                             IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                             IPR006208; Cys_knot.
IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1.
                                                                                                                                                                                                                                                                       Conservative
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AAB67638.1;
                  Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                       37966 MW;
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45.7%;
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                                                                                                                                                                                                                                                                              Score 550.5;
Pred. No. 6.
                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                       93F221C5DB565A81 CRC64;
                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343
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                                                   update)
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Best Local S
Matches 105
        SMART; SM
SMART; SM
PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                             Pfam;
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                                                                                                      Pfam;
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                                                                                                              InterPro;
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SORRI
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STRAIN-C57BL/6J; TISSUE-Spinal cord;

MEDLINE-22354683; PubMed-12466851;

The FANYOM Consortium,

the RIKEN Genome Exploration Research Group P
"Analysis of the mouse transcriptome based on
60,770 full-length cDMAs.";
Nature 420:563-573(2002).

EMBL; AK039481; BAC30363.1; -
                                                                              Pfam; PF000219; IGFBP; 1.
Pfam; PF000909; tsp_1; 1.
Pfam; PF00093; vwc; 1.
SMART; SW00021; CT; 1.
SMART; SW00121; IB; 1.
SMART; SW00209; TSP1; 1.
SMART; SW00204; VWC; 1.
SMART; SW00214; VWC; 1.
                                                                                                                                                                                                                                   Latinkic B.V., Benett B., Smith J.C.;

"Characterization of Xenopus cyr61.";

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ

EMBL; AF320592; AAK00947.1; -

InterPro; IPR006208; Cys_knot.

InterPro; IPR000307; Cys_knot_C.

InterPro; IPR000384; Tsp1.

InterPro; IPR000384; Tsp1.
                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vel
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 098TX5;
01-JUN-2001 (TrEMBLrel. 17, Cre
01-JUN-2001 (TrEMBLrel. 17, Las
01-MAR-2003 (TrEMBLrel. 23, Las
Secreted cysteine-rich protein
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8355;
                                                                                                                                                                                          PF00007; Cys_knot; PF00219; IGFBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105;
;; PS01185; CTCK_1; 1.
;; PS01225; CTCK_2; 1.
;; PS00222; IGF_BINDING; 1
;; PS50092; TSP1; 1.
;; PS01208; VWFC; 1.
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                                                                                                                                                                                                                            IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 AA;
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Pred. No. 7e-4
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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; Pipidae;
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                  Query Match
Best Local S
Matches 101
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                                                                                                                  Pfam; PF00219; IĞFBP; 1
Pfam; PF00090; tsP_1; 1
Pfam; PF00093; vwc; 1; 1
SMART; SM00041; CT; 1
SMART; SM00121; IB; 1.
SMART; SM00214; VWC; 1.
SMART; SM00204; VWC; 1.
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01-MAY-1999
01-MAR-2003
                                                                            PROSITE;
                                                                                               PROSITE;
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097765;
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InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
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                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
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                                                                                                                                                                                                                                                                                                                                                                          Connective tissue
                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                       Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                       Harding P.A., Brigstock D.R.; "Cloning and sequencing of a porcine connective tissue growth
                                                                                                                                                                                                                                                                                               TISSUE-Uterus;
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    (CTGF)
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                    101;
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                                                                   2; PS01185; CTCK_1; 1.

2; PS01225; CTCK_2; 1.

2; PS00222; IGF_BINDING; 1.

2; PS50092; TSP1; 1.

2; PS01208; VWFC; 1.
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 SFLCLLSM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISTRUTUDNSNCRLVRETRICEVRPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IATRVSNQNRFCQLEIQRRLCLPRPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GMDTNEGELTRKNEFVAVIKGGLKMLPVFGSDPQSHVVENSKCIVQTTSWSQCSKTCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -RSTAGG-----HQLSALV-----TPAS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RCDDGGFTCLPLCSEDVRLPSWDCPRPKRIQVPGKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDCSKTHPCDHTKGLECNFGASSRAIKGICRAKSEGRPCEYNSKIYONGESFQPNCKHQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESCDHLHVCDPSQGLVCQPGAGPGGHGAVCLLDEDDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFLALNPVLAIALLSGFIDLAVSSCPAVCQCPVEVPRCAPGVGLVLDGCGCCKICAKQLN
                                                                                                                                                                                                IPR001007;
                                                                                                                                                                                                       IPR000884; TSP1
                                                                                                                                                                                                                                                                                                                                                                                (TremBLrel. 10, Created)
(TremBLrel. 10, Last sequence update)
(TremBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375
                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                           Ā
                                                                                                                                                                                      Cys_knot;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ξ
                                                                                                                                                                                                                                                                                                                                                                         growth
                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                           35.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.98;
37.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41460 MW;
-VCAQLCRTPCTCPWTPPQ-CPQGVPLVLDGCGCCKVCARRLGESCDHL
                                                          37946 MW;
                                                                                                                                                                                             VWF_C.
                                                                                                                                                                                                                                                                                                                                                                          factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
                   32;
                  Score 505; DB Pred. No. 1.6e 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 517.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78075CA7B380304E CRC64;
                                                         35AB4275AC1D4B3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237
                                                                                                                                                                                                                                                                                                                                                                                                                         349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1e-41;
87;
                                     DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                         A
                            6e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCEVNGRRYLDGETFKPNCRVLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADAPCPNWSTAWGPCSTTCGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EWVCDEAKDPVDEMDDFFNKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EWVCDQGVTPAIQ-----
                                  Length
               indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41;
                  18;
                                                                                                                                                                                                                                                                           factor
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                            Matches
                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q99PPO;
01-JUN-2001
01-JUN-2001
01-MAR-2003
                                                                                                                                                                           PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS01208; VWFC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                            Genomics 69:214-224(2000).
EMBL; AF228049; AAK00729.1; -.
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20487548; PubMed=11031104; Sleeman M.A., Murison J.G., Strachan McGrath A., Bickerstaff P., Grierson
                                                                                                                                                                                                                                                                                                                                                                        Watson J.D.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q99PP0
                                                                                                                                                                                                                                                                                                                                                               "Gene expression in rat dermal papilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185
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                          143 WDCPRPKRIQVPGKCCPEWVCDQGVTPAIQRSTAQGHQLSALVTPASADAPCPNWSTAWG
                                               107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186
                                                                  83
                                                                                      47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                                                                                            94;
                                                                                                                                     Similarity
         LWCRQPRHVRVPGQCCEQWVCDDDARRPRQTALLDTRAFAASGAVEQRYENCIAYTSPWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel.
(TrEMBLrel.)
(TrEMBLrel.)
                                                                                                                                                                   367
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                   Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Rodentia;
                                                                                                                                                                   40613 MW;
                                                                                                                                   35.0%;
43.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17,
17,
23,
                                                                                                                            29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR00687; Insl_gro_fac_pr.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000884; Tspl.
InterPro; IPR001007; VWF_C.
Pfam; PF00007; Cys_knot; 1.
Pfam; PF000219; IGFBP; 1.
Pfam; PF000219; IGFBP; 1.
Pfam; PF00090; tsp_1; 1.
SMARR; SM001041; CT; 1.
SMARR; SM001041; CT; 1.
SMARR; SM001041; CT; 1.
SMARR; SM00104; CT; 1.
                                                                                                                                     24 QLCRTPCTCPWTPPQCPQGVPLVLDGCGCCKVCARRLGESCDHLHVCDPSQGLVCQ-PGA
GPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDDGGFTCLPLCSEDVRLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTFGPDPTMMRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTCLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQGVTPAIQRSTAQGHQLSAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APCDPHKGLFCDFGSPANRKIGVCTA-KDCAPCVFGGTVYRSGESFQSSCKYQCTCLDGA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HVCDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDDGG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFCKWPCECPQAPPRCPLGVSLITDGCECCKICAQQLGDNCTEAAVCDPHRGLYCDYSGD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----VTPASADAPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQRRLCLPRPCLA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                          Score 503.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                               8A4A34C69D3243D2 CRC64;
                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367
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                                                                                                                                                                                                          .3e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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                                                                                                                                                                                                                               DB 11;
                                                                                                                                                                                    ; 68
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                          Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - KDHTVVGPALAAYRLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus.
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164
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164

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                                                                                                                                           Query Match
Best Local 9
                                                                                                                            Matches
                                                                                                                                                                                                                                                                               InterPro; IPR001007; VWF_C.
Pfam; PF00007; Cys_knot; 1.
Pfam; PF000219; IGFBP; 1.
Pfam; PF00090; tsp_1; 1.
Pfam; PF00090; vwc; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00121; TSP1; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        054775;
01-JUN-1998
01-JUN-1998
01-MAR-2003
                                                                                                                                                                                                                PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pennica D., Swanson T.A., Welsh J.W., Roy M.A., Lawrence D.A., Brush J., Taneyhill L.A., Deuel B., Lew M., Watanabe C., Cohen Melham M.F., Finley G.G., Quirke P., Goddard A.D., Hillan K.J., Gurney A.L., Botstein D., Levine A.J.;
"WISP genes are members of the connective tissue growth factor that are up-regulated in wnt-1-transformed cells and aberrantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hashimoto Y., Shindo-okada N., Tani M., Nagamachi Y., Takeuchi K., Shirotshi T., Toma H., Yokota J.; Shirotshi T., Toma H., Yokota J.; "Expression of the Elml gene, a novel gene of the CCN (connective tissue growth factor, Cyr61/Cef10, and neuroblastoma overexpressed gene) family, suppresses In vivo tumor growth and metastasis of K-1735 murine melanoma cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Mammary gland;
MEDLINE-99061933; PubMed-9843955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB004873; BAA24949.1;
EMBL; AF100777; AAC96319.1;
MGD; MGI:1197008; Wisp1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed in human colon tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELM1 OR WISP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              054775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98119879; PubMed=9449709;
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                      47
                     83
                                                                                       24
                                                                                                                                                                                            FS01185; CTCK_1; 1.
FS01225; CTCK_2; 1.
FS50092; TSP1; 1.
FS01208; VWFC; 1.
FS01208; VWFC; 1.
FS01208; VWFC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Med.
                                                                                                                                           Similarity
GPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDDGGFTCLFLCSEDVRLPS
                                                                         QLCRTPCTCPWTPPQCPQGVPLVLDGCGCCKVCARRLGESCDHLHVCDPSQGLVCQ-PGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFCKWPCECPQSPPRCPLGVSLITDGCECCKICAQQLGDNCTEAAICDPHRGLYCDYSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa; Chordata; C
Metazoa; Rodentia; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (TrEMBLrel.
3 (TrEMBLrel.
3 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acad. Sci.
                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187:289-296(1998).
                                                                                                                                             35.0%;
43.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A.
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23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                        Score 503.5;
Pred. No. 2.3e
81; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95:14717-14722(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                              3B7C0569EFAB5E96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367
                                                                                                                                           2.3e-40;
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                                                                                                                                                           DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muridae;
                                                                                                                          ; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         growth factor family
                                                                                                                          Indels
                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murinae;
                                                                                                                                                             367;
                                                                                                                        ω
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                                                                                                                        Gaps
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                                                     106
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR0000884; TSP1.

InterPro; IPR001007; VWF_C.
Pfam; PF00007; Cys_knot; 1.
Pfam; PF000219; IGFBP; 1.
Pfam; PF000909; tsp_1; 1.
Pfam; PF000909; tsp_1; 1.
Pfam; PF000093; VWG; 1.
SMARR; SW000121; IB; 1.
SMARR; SW00120; TSP1; 1.
SMARR; SW00214; VWG; 1.
PR001TE; PS01185; CTCK_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrembLrel. 01-NOV-1999 (TrembLrel. 01-MAR-2003 (TrembLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Izm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYR61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYR61 precursor
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                          Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-1998) to the EMBL; AB015877; BAA78339.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Rat Cyr61 mRNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unoki H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9WTM9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9WTM9
 183
                                    166
                                                                     123
                                                                                                        123
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                                                                                                                                         63
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                                                                                                                                                                                                                                                                                    Similarity
97; Conser
                                                                       CIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDLLGFD
                                                                                         CDDGGFTCLPLCSEDVRLPSWDCPRPKRIQVPGKCCPEWVCDQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                            PS50092;
 ASEVELTRNNELIATGKGSSLKRLPVFGTEPRVLYNPLHAHGQKCIVQTTSWSQCSKSCG
                                                                                                                                         DCSKTQPCDHTKGLECNFGANSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCT
                                                                                                                                                                            SCDHLHVCDPSQGLVCQPGAGPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCR 122
                                                                                                                                                                                                               SSTIKTLAVAVTLLHLTRLALSTCPASCHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNE
                                                                                                                                                                                                                                              SPLIHLLATSFICL-LSMVCAQLCRTPCTCPWTPPQCPQGVPLVLDGCGCCKVCARRLGE
                                                                                                                                                                                                                                                                                                                                                                                                                              PS01208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCSTTCGLGISTRISNVNARCWPEQESRLCNLRPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCSTTCGLGIATRVSNQNRFCQLEIQRRLCLPRPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LWCRQPRHVRVPGQCCEQWVCDDDARRPRQTALLDTRAFAASGAVEQRYENCIAYTSPWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WDCPRPKRIQVPGKCCPEWVCDQGVTPAIQRSTAQGHQLSALVTPASADAPCPNWSTAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPRYAIGVCAQVVGVG-CVLDGVRYTNGESFQPNCRYNCTCIDGTVGCTPLCLSP-RPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yonekura
                                                                                                                                                                                                                                                                                                                                                      25
379 ‡
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Aorta;
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            VWFC;
                                                                                                                                                                                                                                                                                                                                                                                                                                            IGF_BINDING;
TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCK_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Η.,
                                                                                                                                                                                                                                                                                                                                                        41728
                                                                                                                                                                                                                                                                                                   34.9%;
36.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12,
12,
23,
                                  GVTPAIQRSTAQGHQLSALVTPASADA-PCPNWSTAWGPCSTTCG
                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                 Score 503; DB
Pred. No. 2.7e:
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYR61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                        D2ABAFD77B84762B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379
                                                                                                                                                                                                                                                                                                 DB 11;
.7e-40;
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                                                                                                                                                                                                                                                                                                                   Length 379;
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Rattus

34;

Gaps

182

242 209 122

165

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                                                                                                                             Query Match
Best Local S
Matches 96
                                                                                                                                                                                                                                   Pfam; PF00219; IĞFBP; 1.
Pfam; PF00090; tsp_1; 1.
Pfam; PF000093; vwc; 1.
SMART; SM00041; CT; 1.
SMART; SM00209; TSP1; 1.
SMART; SM00209; TSP1; 1.
SMART; SM00214; VwC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    095388;
                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Lung, and Fetal kidney;
MEDLINE-99061933; PubMed-9843955;
MEDLINE-99061933; PubMed-9843955;
MeDLINE-99061933; PubMed-9843955;
Melhan D., Swanson T.A., Welsh J.W., Roy M.A., Bawrence Brush J., Taneyhill L.A., Deuel B., Lew M., Watanabe C., Melham M.F., Finley G.G., Quirke P., Goddard A.Då, Hillan Gurney A.L., Botstein D., Levine A.J.;
"MISP genes are members of the connective tissue growth f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Createg)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TremBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF100779; AAC96321.1; -. EMBL; AF192304; AAF22341.1; -. Genew; HGNC:12769; WISP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 that are up-regulated in wnt-1-transformed cells expressed in human colon tumors.";
Proc. Natl. Acad. Sci. U.S.A. 95:14717-14722(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosenthal
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jonge R.d.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blechschmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                   interPro;
                                                                                                                                                                                                                                                                                                                                                        [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lomo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
            143
                                   107
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                                                        83
                                                                                47
                                                                                                    24
                                                                                                                                                                                                                                                                                                                      PF00007; Cys_knot; 1.
                                                                                                                                                                                     PS01185; CTCK_1; 1.
PS01225; CTCK_2; 1.
PS50092; TSP1; 1.
PS01208; VWFC; 1.
                                                                                                                                       Similarity
WDCPRPKRIQVPGKCCPEWVC-DQGVTPAIQRSTAQGHQLSALVTPASADA---
                                RPRYAIGVCAQVVGVG-CVLDGVRYNNGQSFQPNCKYNCTOLDGAVGCTPLCLR-VRPPR
                                                 GPGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRGDDGGFTCLPLCSEDVRLPS
                                                                              QFCKWPCECPPSPPRCPLGVSLITDGCECCKMCAQQLGDN
                                                                                                    QLCRTPCTCPWTPPQCPQGVPLVLDGCGCCKVCARRLGESGDHLHVCDPSQGLVCQ-PGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGISTRVTNDNPECRLVKETRICEVRPC
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                                                                                                                                                                                                                                                                                                                                           IPR006208; Cys_knot.
IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                             (OCT-1999) to the
                                                                                                                                                                             367
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                                                                                                                             Conservative
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S
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lhabel M., Schattevoy
                                                                                                                                                                         SP1; 1.
WEC; 1.
40331 MW;
                                                                                                                                       34.6%;
                                                                                                                             31;
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                            Score 498.5; DB Pred. No. 7e-40; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                            9F29CA94D69C0502
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goodman I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dette
                                                                                                                                                 DB 4;
                                                                                                                             81;
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WISP-1.
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                                                                                                                                                  Length
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                                                                                                                                                    367;
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Cohen
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baas F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - K.J.,
                                                                                                                             11;
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- PCPNWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee
                                                                                                                            Gaps
                                                                                                      82
                                 164
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                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 83
                                                 095958 PRELIMINARY;
095958;
01-MAY-1999 (TrEMBLrel. 10, Cr
01-MAY-1999 (TrEMBLrel. 10, La
01-MAR-2003 (TrEMBLrel. 23, La
DJ142L7.3 (Connective tissue g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-92096871; P Martinerie C., Perb "Expression of a ge
                              (Fragment)
                                                                                                                                                                                                                                                                                                                                                                  NON_CONS
NON_CONS
NON_TER
SEQUENCE
Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
PROSITE;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken)
Eukaryota; Metazoa; Cho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9PSS6;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                     C. R. Acad. Sci., III, Sci. Vie 313:345-351(1991).
InterPro; IPR0000867; Insl_gro_fac_pr.
InterPro; IPR001007; VWF_C.
SMART; SM00121; IB; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9PSS6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential IGF binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archosauria; Aves;
                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human tissues.
                                                                                                                                                        160
                                                                                                                                                                            204
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                                                                                                                                                                                                                                                                                10
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                                                                                                                                                                                                                                                                                                                           83,
                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  PS00222; IGF_BINDING; PS01208; VWFC; 1.
                                                                                                                                                        CSKSCGMGFSTRVTNRN
                                                                                                                                                                            CSTTCGLGIATRVSNQN
                                                                                                                                                                                                           DCPRPKRIQVPGKCCPEWVCDQGVTPAIQRSTAQGHQLSALVTPASADAPCPNWSTAWGP
                                                                                                                                                                                                                                                    PGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDDGGFTCLPLCSEDVRLPSW
                                                                                                                                                                                                                                                                                CPRPCGGRCPAEPPRCAPGVPAVLDGCGCCLVCARQRGESCSPLLPCDESGGLYCDRGPE
                                                                                                                                                                                                                                                                                            CRTPC--TCPWTPPQCPQGVPLVLDGCGCCKVCARRLGESCDHLHVCDPSQGLVCQPGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPWSPCSTSCGLGVSTRISNVNAQCWPEQESRLCNLRPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGGGAGIC - - - - EGDNCVFDGMIYRNGETFQPSCKYQCTCRDGQIGCLPRCNLGLLLPGP
                                                                                                                                                                                                DCPFPRKIEVPGECCEKWVCDPRDEVLL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LWCPHPRRVSIPGHCCEQWVCEDDAKRP---RKTAP-RDTGAFDAVGEVEAWHRNCIAYT
                               OR LIBC
                                                                                                                                                                                                                                                                                                                                                               154
176
176
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perbal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene encoding a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=1756408
                                                                                                                                                                                                                                                                                                                                                                  155
176
18656 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neognathae;
 Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                   31.6%;
                                                 10, Created)
10, Last sequence update)
23, Last annotation update)
issue growth factor (NOV, GIG) like
                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                            220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                   Score 455; DB 13; Pred. No. 5e-36;
Craniata; Vo
Catarrhini;
                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Fragments).
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Galliformes; Phasian
                                                                                                                                                                                                                                                                                                                                                                   4FA69FFDB79B1C67
                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                     331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     potential IGF binding
 Vertebrata;
i; Hominidae;
                                                                                                     AΑ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phasianidae;
                                                                                                                                                                                                                                                                                                                           59;
                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259
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          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phasianinae;
                                                 protein)
                                                                                                                                                                                                                                                                                                                           32;
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RESULT
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Best Local S
Matches 81
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InterPro; IPR006207; Cys_knot_C.
InterPro; IPR006867; Insl_gro_fac_pr.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000884; TSpl.
Pfam; PF00007; Cys_knot; 1.
Pfam; PF000219; IGFBP; 1.
Pfam; PF00090; tsp_1; 1.
SMARR; SM00041; CT; 1.
SMARR; SM00201; TSP1; 1.
SMARR; SM00121; IB; 1.
SMARR; SM00209; TSP1; 1.
SMARR; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                         095389;
TISSUE-Bone marrow, and Fetal kidney;
MEDLINE-99061933; PubMed-9843955;
Pennica D., Swanson T.A., Welsh J.W., Roy M.
Brush J., Taneyhill L.A., Deuel B., Lew M.,
Melham M.F., Finley G.G., Quirke P., Goddard
                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 01-MAY-1999 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel. Connective tissue growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          van Golen K.L., Davies S., Wu Z.F., Wang Y.F. Chandrasekharappa S., Strawderman M., Ethier "A novel putative IGF-binding, tumor suppress RhoC GTPase, are determinants of the inflamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Mammary gl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases EMBL; z99289; CAB16556.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606
                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                           14
                                                                                                                      P3.

No sapiens (Human).

Netazoa; Chordata; C.

Naryota; Metazoa; Primates; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS01225; CTCK_2; 1.
PS00222; IGF_BINDING;
PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                         WDCPRPKRIQVPGKCCPEWVCDQGVTPAIQRSTAQGHQLSALVTPASADAP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPRYETGVCAC--KSVGCEENQVHYHNGQVFQPNPLFSCLCVSGAIGCTPLFIP--KLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -PGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDDGGFTCLPLCSEDVRLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QFCHWPCKCPQQKPRCPPGVSLVRDGCGCCKICAKQPGEICNEADLCDPHKGLYCDYSVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             -GGKKSDQSNC--SLEPLLQQLST---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36909 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.8%;
36.7%;
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                                                                                                                                                                                                 10, Created)
10, Last sequence update)
23, Last annotation update)
h factor related protein WISP-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 372;
Pred. No. 9
                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D109C2FDCA1DF549 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang Y.F., Bucana C.D.,
, Ethier S.P., Merajver
suppressor protein, LIB
inflammatory breast can
   Goddard A.D.,
                                                                                                                                                                                                                                                                                           354
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nes 91;
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 M.A., Lawrence D
, Watanabe C., C
rd A.D., Hillan
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jver S.D.;
, LIBC, and
   Cohen
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                 Lee J
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Query Match
Best Local
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Pfam; PF00219; IGFBP; 1.
Pfam; PF00090; tsp_1; 1.
Pfam; PF00090; tsp_1; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM001209; TSP1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01222; IGF_BINDING
PROSITE; PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gurney A.L., Botstein D., Levine A.J.;
"WISP genes are members of the connective tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               that are up-regulated in wnt-1-transformed expressed in human colon tumors.";
                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:12771; WISP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S./
EMBL; AF100781; AAC96323.1;
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                                 197
                                                                   163
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                                                                                                                                                                                                                                                                        82;
                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                         QLCRTPCTCPWTPPQCPQGVPLVLDGCGCCKVCARRLGESCDHLHVCDPSQGLVCQPGAG
QATKWTPCSRTCGMGISNRVTNENSNCEMRKEKRLCYIQPC
               WDCPRPKRIQVPGKCCPEWVCDQGVTPAIQRSTAQGHQLSALVTPASADAP-----CPN
                                                                                                                                                                                                     QFCHWPCKCPQQKPRCPPGVSLVRDGCGCCKICAKQPGEICNEADLCDPHKGLYCDYSVD
                                                                                                                                                                  - PGGHGAVCLLDEDDGSCEVNGRRYLDGETFKPNCRVLCRCDDGGFTCLPLCSEDVRLPS
                                                                   SHCSGAK----GGKKSDQSNC--SLEPLLQQLST----SYKTMPAYRNLPLIWKKKCLV
                                                                                                                                  RPRYETGVCAYLVAVG-CEFNQVHYHNGQVFQPNPLFSCLCVSGAIGCTPLFIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR006208; Cys_knot.
IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                          354 AA;
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                           IGF_BINDING;
TSP1; 1.
                                                                                                                                                                                                                                                                                                                                          39292 MW;
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37.1%;
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323.1; -.
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                          67F48D0D5C2F5EE3 CRC64;
                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                        91;
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 252
                                 237
                                                                                                                                                                                                                                                                                                          354;
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                                                                                                                                    -KLAG
                                                                                                    196
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                                                                                                                                    162
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Anding B., Long Y.;

"Cloning of a new gene down-regulated in the smale "Cloning of a new gene down-regulated in the smale state of the smale stat Q9UID7; PRELIMINARY; Q9UID7; 01-MAY-2000 (TrEMBLrel. 1 01-MAY-2000 (TrEMBLrel. 1 01-MAR-2003 (TrEMBLrel. 2 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI\_TaxID=9606; TISSUE=Kidney; SEQUENCE OF 1-107 FROM z 13, 13, 23, Last sequence update)
Last annotation updat Created) Craniata; Vertebrata; Catarrhini; Hominidae, 334 ₿ Hominidae; update) small-cell databases Euteleostomi;

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Search completed: July 25, 2003, 12:37:14 Job time: 98 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00041; CT; 1.

SMART; SM00219; TSP1; 1.

SMART; SM00214; VEP1; 1.

PROSITE; PS01225; CTCK_2; 1.

PROSITE; PS50092; TSP1; 1.

PROSITE; PS01208; VWFC; 1.

SEQUENCE 334 AA; 37246 MW; 9188987A7352E948 CRC64;
                                                                                                                                                                                 174 STAQGHQLSALVTPASADAPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQRRLCL 233
                                                                                                                                                                                                                                     115 VCDEDSIKDPMEDQDGLLGKELGFDASEVELTRNNELIAVGKGSSLKRIPVFGMEPRIRY 174
                                                                               111
222 VRPC 225
                                                                                                                                                        175 NPLOGOK------CIVQTTSWSQCSKTCGTGTSTRVTNDNPECRLVKETRICE 221
                                                                                                                                                                                                                                                                                                                   234 PRPC 237
                                                                                                                                                                                                                                                                                 162 VCDQ------
                                                                                                                                                                                                                                                                                                                                                                                                                             49 GCGCCKVCARRLGESCDHL-HVCDP-----SQGLVCQGGAGPGGHGAVCLLDEDDGSCE 101
                                                                                                                                                                                                                                                                                                                                                                                                  2 GCGTHP-----NLCIHLGHTASPTSYKHHTKGLECNEGASSTALKGICRAQSEGRPCE 54
                                                                                                                                                                                                                                                              *-----GVTPAIQR 173
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Total number of hits satisfying chosen parameters:
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Maximum Match 10
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Maximum DB seq length: 2000000000
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Perfect score:
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753
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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gb_sts:*
gb_sy:*
gb_un:*
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gb_ph:*
gb_p1:*
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gb_htg:*
gb_in:*
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                                                                                em_htg_mus:*
em_htg_pln:*
em_htg_rod:*
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em_pl:*
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em_or:*
em_ov:*
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em_hum:*
em_in:*
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em_un:*
em_htgo_other: *
              em_htgo_hum: *
em_htgo_mus: *
                                                     em_htg_vrt:*
                                                                    em_htg_mam:*
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em_htg_inv: *
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Pred. No.

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the number of results predicted by chance to have

REFERENCE AUTHORS

Rattus. 1 (bases 1 to 1741) 2hang,R., Averboukh,L., Zhu,W., Zhang,H., Jo,H., Dempsey,P.J.,

Rattus norvegicus. Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; RESULT 1
AF259981
LOCUS
DEFINITION

AF259981 1741 bp mRNA linear ROD 09-MAY-2000 Rattus norvegicus CCN family protein COP-1 (COp-1) mRNA, complete

ALIGNMENTS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

> AF259981 AF259981.1

GI:7739780

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Direct Submission
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Identification of rCop-1, a new member of the Coas a negative regulator for cell transformation Mol. Cell. Biol. 18 (10), 6131-6141 (1998) 98414629 9742130
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Botstein, D.A., Cohen, R.L., Goddard, A.D., Gurney, A
Lawrence, D.A., Levine, A.J., Pennica, D., Roy, M. Ann
WISP polypeptides and nucleic acids encoding same
Patent: US 6387657-A 17 14-MAY-2002;
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Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L.,
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and
WISP polypeptides and nucleic acids encoding same
WISP polypeptides and nucleic acids encoding same
Patent: US 6387657-A 18 14-MAY-2002;
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                                                                                                                                                                                                                                                                                                    Submitted (23-OCT-1998) Molecular Oncology, Way, South San Francisco, CA 94080, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus connective (Wisp2) mRNA, complete c AF100778
                                                                                                                                                                                                                                                                                                                                     Direct Submission
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/protein_id="AAC96320.1"
/db_xref="GI:4028579"
/db_xref="GI:4028579"
/taanslation="MNGMPLHHLLAISFLCILSMVYSQLCPAPCACPWTPPQCPPGVP
LVLDGCGCCRVCARRLGESCDHLHVCDPSQGLVCQPGAGPSGRGAVCLFEEDDGSCEV
                                                                WISP-2"
                                                                                                                          /gene="Wisp2"
257. .1012
                                                                                                                                                                                          /db_xref="taxon:10090"
/cell_line="C57MG"
/cell_type="epithelial"
/tissue_type="mammary"
                                                                             /codon_start=1
/product="connective tissue
                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                             /gene="Wisp2"
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NQNRFCQLEIQRRLCLSRPCLASRSHGSWNSAF"

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No. 1.6e-150;
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                 GGGCAGGCCCTGGCGCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGGTAGCTGT
                                                      GGGGAGTCCTGCGACCTGCATGTCTGCGACCCCAGCCAGGGCCTGGTTTGTCAGCCT
                                                                                 CCGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTCGAGTGTGTGCCCGGAGGCTG
                                                                                          CAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGTAAAGTGTGTGCACGGAGGCTG
        GGGGCAGGCCCCAGTGGCCGTGGTGCTGTGCCTCTTCGAAGAGGATGACGGGAGCTGT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Murida I (bases 1 to 1739) Rumar, S., Hand, A.T., Connor, J.R., Dodds, R.A., Ryan Trill, J.J., Fisher, S.M., Nuttall, M.E., Lipshutz, D. Hwang, S. M., Votta, B.J., James, I.E., Rieman, D.J., G. Lee, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (04-FEB-1999)
SmithKline Beecham, 709
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Kumar, S. and Zou, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor-like cDNA from hof osteoblast functions
J. Biol. Chem. 274 (24),
99287915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identification and cloning
                                                                       /gene="Ctgfl"
/gene="Ctgfl"
/note="similar to the Mus musculus WISP-2 protein encoded in the sequence presented in GenBank Accession Number AF100778; putative growth factor; CTGF-1; contains IGF binding (IGFBD), Von Willebrand Factor type C (VWC) repet and thrombospondin type I (TSP1) domains; member of the CCN (CTGF/Cyr61/Nov) family; lacks the fourth carbox-terminal (CT) domain present in other members of the CCN family"
                                                                                                                                                                                                                                          /translation="MRONPLIHLLAISFLCILSMVYSQLCPAPCACPWTPPQCPPGVPLVLDGCGCCRVCARRLGESCDHLHVCDPSQGLVCQPGAGPSGRGAVCLFEEDDGSCEVMGRRYLDGETEKPNCRVTLCRCDDGGFTCLPLCSEDVRLPSWDCPRPRRLQVPGRCCPEWCCPLAYLORDAVMQPAIQPSSAQGHQLSALVTPASADGPCPNWSTAWGPCSTTCGLGIATRVSNQNRFCQLEIQRRLCLSRFCLASRSHGSWNSAF"
1 480 c 489 g 395 t
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242. .997
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1. .1739
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/db_xref="GI:4337060"
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/db_xref="taxon:10090"
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Sutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                    Score 654.2;
Pred. No. 2.3
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Swedeland Rd., King of Prussia, PA
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tz, D.B., Zo
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Gowen, M.
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                                                                                                                                                                                                                                                                    Polypeptidic compositions and methods Patent: WO 0105836-A 31 25-JAN-2001; Genentech, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31 from AX076919
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                        CAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGTAAAGTGTGTGCACGGAGGCTG
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             CTGGGAGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGCCGGGTATGTGCACGGCGGCTG
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/db_xref="taxon:9606"
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79.9%;
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Pred. No. 3.3e-114;
0; Mismatches 151;
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Sequence
AX464186
                                                                                                                                                                      Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E. Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Wattanabe,C.K., Wood,W.L. and Zhang,Z.
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Mammalia; Eutheria;
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                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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Primates;
                      Score 510.4; DB 6;
Pred. No. 3.3e-114;
0; Mismatches 151;
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Kumar,
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1283)

Kumar, S., Hand, A.T., Connor, J.C., Dodds, R.A., Ryan, P.J., Trill, J.G., Fisher, S.M., Slemmon, J.R., Lipshutz, D.B., Bartholomew, V., James, I.E., Rieman, D.J., Goven, M. and Lee, J.C Identification and cloning of CTGF-L from human osteoblasts, novel cysteine rich protein containing an IGF binding domain Bone 23 (5), S240 (1998)
                                                                                         Homo
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Submitted (11-AUG-1998)
SmithKline Beecham, 709
USA
QNRFCRLETQRRLCLSRPCPPSRGRSPQNSAF"
a 418 c 389 g 241 t
                                          /protein_id="AAC70350.1"
/db_xref="GI:3462836"
/db_xref="GI:3462836"
/translation="MRGTPKTHLLAFSLLCLLSKVRTQLCPTPCTCPWPPPRCPLGVP
/translation="MRGTPKTHLLAFSLLCLLSKVRTQLCPTPCTCPWPPRCPLGVP
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NGRLYREGETFQPHCSIRCRCEDGGFTCVPLCSEDVRLPSWDCPHPRRVEVLGKCCPE
WVCGQGGGGLGTQPLPAQGPQFSGLVSSLPPGVPCPEWSTAWGPCSTTCGLGMATRVSN
                                                                                                                                                                                                                                                           /note="CTGF-L; encodes IGF binding (IGFB), v factor type C (VWC) and thrombospondin type domains; member of the CCN (CTGF/cyr61/nov) the fourth carboxy-terminal domain present i members of the CCN family"
                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="20"
/map="20q12-q13"
/cell_type="prim
                                                                                                                                                                                                                 /product="connective tissue
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                           osteoblast"
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Ouery Match
67.8%; Score 510.4; DB 9; Length 1283;
Best Local Similarity 79.9%; Pred. No. 3.3e-114;
Matches 601; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

241 GGGGCAGGCCCTGGCGGCCATGGGGCTGTGTGTGTCTCTTGGATGAGGATGACGGTAGCTGT

420

248 300 308 360 368

428

369 TGCCGCTGCGAGGACGGCGGCTTCACCTGCGTGCGCTGTGCAGCGAGGATGTGCGGCTG
421 CCCAGCTGGGACTGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGCCCCGAG

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RESULT 9
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Botstein,D.A., Cohen,R.L., Goddard,A.D.,
Lawrence,D.A., Levine,A.J., Pennica,D., F
WISP polypeptides and nucleic acids encod
Patent: US 6387657-A 13 14-MAY-2002;
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                                           CCCAGCTGGGACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGCCCCGAG
                                                                                    TGCCGCTGTGATGACGGTGGCCTTCACCTGCCTGCCGCTGTGCAGTGAGGATGTGCGGCTG
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                                CCCAGCTGGGACTGCCCCCACCCCAGGAGGGTCGAGGTCCTGGGCCAAGTGCTGCCCTGAG
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Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., FLAWrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and WISP polypeptides and nucleic acids encoding same Patent: US 6387657-A 14 14-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown
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                                                                                                                 GGGGCAGGCCCTGGCGCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGGTAGCTGT
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                               TGCCGCTGTGATGACGGTGGCTTCACCTGCCTGCCGCTGTGCAGTGAGGATGTGCGGCTG 420
                                                                        GAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAACCCAATTGCAGGGTCCTG
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                                                                                                       GGGGCAGGACCCGGTGGCCGGGGGGCCCTGTGCCTCTTGGCAGAGGACGACAGCAGCTGT
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Pred. No. 3.3e-114;
0; Mismatches 151;
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+ US r
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PAT

20-JUN-2002

741 720 681 621 600 561

; DB 9; 1.3e-114; 1es 151;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 1309).
Rowles, J. and Gendler, S.
Direct Submission
Submitted (25-UUN-1998) Blochemistry and
Clinic Scottsdale, 13400 E. Shea Blvd.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1309)

ROWLES, J. and Gendler, S.

CT58, a new member of the connective interacts with the breast cancer asso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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-protein_id="AAC26794.1"
-protein_i
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bait"
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/gene="CT58"
/note="contains three of four modules found in growth factor as regulators related to connective cissue growth factor as described in FEBS Letters, 327:125-130,1993; identified in yeast two-hybrid screen using the epithelial mucin MUC1 and the statement of the statemen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="CT58"
7. .759
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/product="connective
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1. .1309
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/db_xref="taxon:9606"
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Eutheria; Primates; Catarrhini; Hominidae;
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Scottsdale, Az 85259, USI
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Lee, J., Brush, J., Tanevh., Gohen, R.L., Melh.
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red. No. 3.3e
Mismatches
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n,M.F., Finley,G
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.W., Roy,M.A., Lawrence,D.A., Deuel,B., Lew,M., Watanabe,C.G., Quirke,P., Goddard,A.D.,
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Proc. Natl. Acad. Sci. U.S.A. 95 (25), 14717-14722 (1998)
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Submitted (23-OCT-1998) Molecular Oncology,
Way, South San Francisco, CA 94080, USA
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/tissue_type="lung"
/dev_stage="fetus"
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                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 36 Row: m Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA 91: 4507922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (03-DEC-2001) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Geno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@nail.nih.gov
Tissue Procurement: CLONTECH
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Institute, 31 Center Drive, Room 11A03,
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                                                                                                                                         /clone="MGC:22271 IMAGE:4691574"
/tlssue_type="Lung"
/clone_lib="NHH_MGC_77"
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                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="LocusID:8839"
/db_xref="taxon:9606"
                                                                                                                     /note="Vector:
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(Dickson, Mark) mcd@paxil.stanford.edu
M., Schmutz, J., Grimwood, J., Rodrique
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Botstein,D.A., Cohen,R.L., Goddard,A.D.,
Lawrence,D.A., Levine,A.J., Pennica,D.,
WISP polypeptides and nucleic acids enco
Patent: US 6387657-A 38 14-MAY-2002;
Location/Qualifiers
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CCACAAAACAGTGCCTTC
              TCATGGAACAGTGCTTTC
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Pred. No. 6.2e-112;
0; Mismatches 148;
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Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.
WISP polypeptides and nucleic acids encoding same
Patent: US 6387657-A 39 14-MAY-2002;
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## ALIGNMENTS

RESULT 1 AAZ07517 Heparin-induced CCN-like protein; HICP; cell-associated activity; ss; cardiovascular disorder; aberrant cell proliferation; fibrotic disorder. AAZ07517; AAZ07517 standard; cDNA; 753 BP Castellot JJ; 19-MAR-1998; 18-MAR-1999; 23-SEP-1999 WO9947556-A2 Rattus sp Rat HICP polypeptide coding sequence 26-NOV-1999 (first entry) (TUFT ) TUFTS COLLEGE. 98US-0044273. 99WO-US05999.

sequ

WPI; 1999-562060/47. P-PSDB; AAY27434.

Nucleic acid sequences encoding rat heparin-induced CCN-like protein, used in methods to identify modulators or in diagnostic applications

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides a rat heparin-induced cCN-like protein (HICP) protein. Agents that stimulate or inhibit HICP protein activity or expression, antisense HICP nucleic acid molecules and HICP antibodies, can be used to modulate cell-associated activity. HICP modulators can be used to treat disorders characterized by abergant HICP protein activity or expression. Probes capable of hybridizing to HICP mRNA or antibodies specific for HICP can be used to detect HICP activity in a biological sample. HICP can be used to treat disorders, such as a cardiovascular or fibrotic disorder, characterized by aberrant cell proliferation. The present sequence represents the coding sequence of rat HICP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This cDNA encodes a rat heparin-induced CCN-like protein (HICP) protein. Agents that stimulate or inhibit HICP protein activity or expression, antisense HICP nucleic acid molecules and HICP antibodies, can be used to modulate cell-associated activity. HICP modulators can be used to treat disorders characterized by aberrant HICP protein activity or expression. Probes capable of hybridizing to HICP mRNA or antibodies specific for HICP can be used to detect HICP activity in a biological sample. HICP can be used to treat disorders, such as a cardiovascular or fibrotic can be used to treat disorders, such as a cardiovascular or fibrotic
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cardiovascular disorder; aberrant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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specific for HICP can
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WISP-2

protein

nucleotide

sequence

SEQ

IJ

entry)

AAX76488

standard;

DNA;

1734

ВP

WNT-1 induced secreted protein; connective tissue growth factor; leukaemia; lymphoid malignancy;

factor;

WISP-1; WISP-2; haematopoiesis-related

WISP-3; NO:17

arteriosclerosis; disorder; CTGF;

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                                          GACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCAAGGACACCAACTTTCTGCC
                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                            The present invention describes Wnt-1 induced sected polypeptides, CC WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 CC and WISP-3 have homology to connective tissue growth factor (CTGP). CC Products from the present invention can be used to treat WISP-related CC disorders such as breast, ovarian, and colon cancer or melanoma. The CC used to treat other diseases e.g. benign and malignant tumours, CC leukaemia and lymphoid malignancies, neuronal, glial, astrocytal, and blastocoelic disorders, haematopolesis-related disorders, it issue-growth CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney CC disorders, bone-related disorders such as osteoporosis, trauma such as CC burns, incisions, and other wounds, connective tissue disorders, catabolic states, testicular-related disorders, and inflammatory, CC angiogenic and immunologic disorders including argeriosclerosis. The CC consecutive can also be used for detection and diagnosis especially of CC individuals with neoplastic cell growth or proliferation. The products can be used in the production of transgenic or knock-out animals.

CC Calle
                                                                                                                                                                                                                         Query Match
Best Local S
Matches 702
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29-OCT-1997;
03-FEB-1998;
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                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 178-179; 284pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawrence
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702; Conser
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                        GGGGAGTCCTGCGACCTGCATGTCTGCGACCCCAGCCAGGGCCTGGTTTGTCAGCCT
                                                                                     CAGGGGGTACCCCTGGTGCTGGATGGCTGTGGGCTGCTGTAAAGTGTGTGCACGGAGGCTG
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                                                                                                                          GTGTATTCCCAGCTGTGCCCAGCACCCTGTGCCTTTGGACACCACCCCAGTGCCCA
 GGGGCAGGCCCTGGCGGCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGGTAGCTGT
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nilarity 93.0%;
Conservative
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98US-0073612.
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                                                                                                                                                                                                                        Score 659; DB Pred. No. 7.4e 0; Mismatches
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Roy MA,
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∕o⊚d WI;
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                                                                                      14-APR-1998;
29-OCT-1997;
03-FEB-1998;
                              Botstein
Lawrence
                                                                                                                                                                                                                                   tissue-growth disorder; skin aisuruer, commercial kidney disorder; bone-related disorder; osteoporosis; traukidney disorder; affarder; catabolic state; inflammation;
                                                                                                                                                                                                    Mus
                                                                                                                                                                                                                                                                                 connective
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                                                                                                                                    29-OCT-1998;
                                                                                                                                                          06-MAY-1999
                                                                                                                                                                               W09921998-A1
                                                                                                                                                                                                                           testicular-related disorder; angiogenesis;
                                                                                                                                                                                                                                                                                                                    Mouse
                                                                                                                                                                                                                                                                                                                                          06-AUG-1999
                                                                (GETH )
                                                                                                                                                                                                                                                        NNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour connective tissue growth factor; cancer; melanoma; arteriosclerosis; leukaemia; lymphoid malignancy; haematopoiesis-related disorder; leukaemia; lymphoid malignancy; haematopoiesis-related disorder; lesion; lissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion;
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                            Goddard A, o
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Roy MA,
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The present invention describes Wnt-1 induced secreted polypeptides, CC WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-3 have homology to connective tissue growth factor (CTGF). CC Products from the present invention can be used to treat WISP-related CC disorders such as breast, ovarian, and colon cancer or melanoma. The CC products can be used to treat arteriosclerosis. The products can also be used to treat other diseases e.g. benign and malignant tumours, CC leukaemia and lymphoid malignancies, neuronal, glial, astrocytal, by the products can also be used to treat other diseases e.g. benign and malignant tumours, CC hypothalamic and other glandular, macrophagal, epithelial, stromal, and CD blastocoelic disorders, haematopoiesis-related disorders, kidney CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney CC disorders, bone-related disorders such as osteoporosis, trauma such as burns, incisions, and other wounds, connective tissue disorders, CC catabolic states, testicular-related disorders, and inflammatory, CC angiogenic and immunologic disorders including arteriosclerosis. The CC products can also be used for detection and diagnosis especially of CC individuals with neoplastic cell growth or proliferation. The products can be used in the production of transgenic or knock-out animals.

CC antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                    CCCAGCTGGGACTGCCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGCCCCGAG
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                           GCCTGGGGCCCCTGCTCAACCACCTGTGGGCCTGGGCATAGCCACCCGAGTGTCCAACCAG
                                                                       CAACTTTCTGCCCTTGTCACTCCTGCATCTGCCGATGGCCCCTGTCCAAACTGGAGCACA
                                                                                                CAACTTTCTGCCCTTGTCACTCCTGCCTCTGCTGATGCTCCTTGTCCAAATTGGAGCACA
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93.0%;
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Pred. No. 2e-167;
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Query Match
Best Local Similarity
Matches 601; Conserv
                                                                                                                   This sequence encodes the EGF-like homologue PRO261.
The invention relates to antibodies (Ab) that bind to any of the polypeptides (I) designated PRO187; PRO533; PRO214; PRO246; PRO246 or EBAF-2. The Ab, or other agents that inhibit expression and/or activity of (I) are used: (i) to inhibit growth of tumours; and (ii) as diagnostic/prognostic reagents for detection or quantification of (I) in cells or tissues, by standard immunoassays, wi overexpression being indicative of cancer. For therapeutic use, the Ab may be conjugated to a toxin, chemotherapeutic agent or radioisotope. Genes expressing (I), many of which are growth factor homologues, are overexpressed in some cases of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-NOV-1997;
17-SEP-1997;
17-SEP-1997;
18-SEP-1997;
15-OCT-1997;
17-OCT-1997;
17-OCT-1997;
24-OCT-1997;
29-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-229532/19.
P-PSDB; AAY05285.
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97US-0059114.

97US-0059157.

97US-0059263.

97US-0062125.

97US-0062815.

97US-0062816.

97US-0063704.
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79.9%;
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growth; cancer;
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Pred. No. 8.2e-
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RRESULT 7
AAA30048
AID AAA304
AC AAA3
XX AAA2
DT 09-P
DT 09-P
AX ANLL
KW ANLL
KW PRO3
KW Cell
KW Cell
XX ANLL
XX HOMC
XX WO21
                                                                                                                                                                                 Antibody; PRO187;
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    23-MAR-2000
                                                                                Homo sapiens.
                                                                                                                        antibody
                                                                                                                                           17; tumour
growth; pr
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                                                                                                                                         0187; PRO533; PRO214; PRO240; PRO211; PI
ur growth inhibitor; cancer; diagnosis;
proliferation; growth factor; ADEPT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a human PRO261 nucleotide sequence. PRO261 is a CC growth factor. The invention relates to isolated antibodies which bind to CC a polypeptide. The "PRO" polypeptides are encoded by genes which are over CC expressed in the genome of tumour cells. Vectors and host cells comprising the nucleic acid encoding the antibodies are used in the production of the antibodies. The antibodies are used for diagnosing a tumour in a mammal. The antibodies are used for inhibiting the growth of tumour cells and identifying compounds CC that inhibit a biological or immunological activity of and/or expression CC that inhibit a biological or immunological activity of and/or expression CC of a PRO187, PRO531, PRO534, PRO240, PRO211, PRO230, PRO261, PRO266 or PRO317 polypeptide. The antibody can be used in antibody dependent enzyme endiated prodrug therapy (ADEFT) by conjugating the antibody to a compound component of the antibodies can be fluorescently labelled and monitored by light concorsopy, flow cytometry or fluorimetry for diagnosis and prognosis of cumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 601
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10-SEP-1998;
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ge; ear; proliferation; glucose; free fatty acid; ;
te; A-peptide; factor VIIA; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC AAS21244-AAS21518 encode for novel human secretory and transmembrane CC PRO polypeptides. The PRO polypeptides are useful to detect other CPRO polypeptides, to link bloactive molecules to cells expressing CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, CC breast, prostate, rectal, cervical or liver tumours by comparing PRO CC polypeptide expression in a cell sample to that in a control sample. CC some of the 275 sequences are also useful to stimulate the release of CC tumour necrosis factor-alpha (TMF-alpha) from human blood, the CC proliferation or differentiation of chondrocytes, the proliferation or CC gene expression in pericyte cells, the release of proteoglycans from CC artilage, the proliferation of inner ear utricular supporting cells or CC of T-lymphocytes, the release of a cycokine from peripheral blood CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by Skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide CC factor VIIA. The PRO polypeptides can be used in assays to identify CC molecules involved in binding interactions. The polynucleotides encoding CC propolypeptides can be used to generate probes, antisense RNA/DNA, CC transgenic or knock out animals and can be used in gene therapy.
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Best Local Similarity
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                                  CCCAGCTGGGACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGCCCCGAG
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  CCCAGCTGGGACTGCCCCCACCCCAGGAGGGTCGAGGTCCTGGGCAAGTGCTGCCCTGAG
                                                                                           TGCCGCTGCGAGGACGGCGGCTTCACCTGCGTGCCGCTGTGCAGCGAGGATGTGCGGCTG
                                                                                                                       TGCCGCTGTGATGACGGTGGCTTCACCTGCCTGCCGCTGTGCAGTGAGGATGTGCGGCTG
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ME, Goddard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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79.9%;
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A, Godowski PJ, Gurney l
Tumas D, Watanabe CK, Wo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T; 0
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Wood WI, Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other;
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ገ Z;
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RESULT 9
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XX W
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26-JUL-1999;
08-SEP-1999;
13-SEP-1999;
15-SEP-1999;
05-CCT-1999;
29-NOV-1999;
02-DEC-1999;
           The present invention relates to PRO proteins and coding sequences. The present sequence is the coding sequence for one such PRO protein. It was found that the PRO genes are amplified in the genome of tumour cells. The gene amplification is expected to be associated with the overexpression of the gene product and contributes to tumourlyenesis. Therefore, antagonists of PRO proteins are useful for the treatment of benign or malignant tumours, leukaemias, lymphoid malignancies and other disorders such as neuronal, glial, astroytal, hypothalamic, glandular, altroytal, hypothalamic, glandular,
                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic;
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DB; AAB68598.
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99US-0145598.
99WO-US20594.
99WO-US20944.
99WO-US21090.
99WO-US21090.
99WO-US28214.
99WO-US28564.
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immunologic
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RESULT 10
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XC AAC97
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KW cardi
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Best Local Sim:
Matches 601;
Human; angiogenesis-associated protein; PRO; endothelial cell growth; cardiac hypertrophy; cardiovascular disorder; endothelial disorder; angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1266
                                         Human angiogenesis-associated
                                                               28-FEB-2001
                                                                                    AAC97451;
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                                                                                                         standard;
                                                                                                                                                                                                                 CCCAGCTGGGACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGCCCCAGGCTGGGCTGGGGAAGTGCTGCCCCTGAGCCCCGAGGTGGGTCCTGGGCAAGTGCTGCCCTGAG
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Pred.
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No. 8.3
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CC The invention relates to novel human angiogenesis-associated proteins CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding CPRO proteins. The invention also relates to vectors and host cells. CC comprising a PRO nucleic acid, the recombinant production of a PRO CC protein, PRO antibodies specific for a PRO protein, fusion protein, and compounds which inhibit the expression of a PRO protein and CC compounds which inhibit the expression of a PRO protein and CC compounds which inhibit the expression of a PRO gene. The invention CC additionally encompasses methods of identifying modulators of PRO CC expression or activity; diagnosing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting CC mutations in a PRO gene, or the expression level of a PRO gene within a CC particular tissue; treating a cardiovascular, endothelial or angiogenic CC disorder via the administration of a PRO protein, PRO nucleic acid, or CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial or antagonist; a retroviral gene therapy vector comprising a CC disorder via the administration of a PRO-induced angiogenesis via the CC administration of a PRO proteins, or an agonist or antagonist thereof. CC agonists and PRO proteins, or an agonist or antagonist thereof. CC administration of a PRO proteins, antibodies against PRO proteins, PRO CC atheroselerosis, oscoporosis, mycardial infarction, hypertension, CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, Huntington's CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's CC disease, or stroke. PRO proteins, as hybridisation probes to component production of PRO proteins, as hybridisation probes to component production of PRO proteins, to analyze cidentity to PRO proteins, to analyze creatic disorders, and in
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Human connective tissue growth

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This nucleotide sequence codes for human connective tissue growth CC factor-3 (CTGF-3) protein (see AAWA7946), a novel member of the CG growth factor superfamily. It was discovered in a cDNA library CC derived from human osteoblasts. The gene has also been identified CC in cDNA libraries from ovary, testis, heart, lung, skeletal muscle, CC adrenal medulla, adrenal cortex, thymus, prostate, small intestine CC are vectors, host cells and recombinant methods for provided CC cross, host cells and recombinant methods for producing CC cross-3 polypeptides. CTGF-3 nucleic acid sequences or their CC tragments, e.g. primers or probes, can be used to diseases where CG-3 expression is enhanced, e.g. cancer, arthritis, CC decreased such as in osteoporosis. Disorders characterised by CC administering CTGF-3 polypeptides and anti-CTGF-3 can be treated by administering CTGF-3 polypeptides and anti-CTGF-3 antibodies,
                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 601; Conserv
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Pred. No. 8.3e-128;
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                                                                                                                                                                                                                                                                                                                                                                                                tissue-growth disorder; skin disorder; desmoplasia; ribrotic kidney disorder; bone-related disorder; osteoporosis; trauma; connective tissue disorder; catabolic state; inflammation;
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CC Products from the present invention can be used to treat WISP-related CC disorders such as breast, ovarian, and colon cancer or melanoma. The CC products can be used to treat arteriosclerosis. The products can also be cused to treat other diseases e.g. benign and malignant tumours. CC leukaemia and lymphoid malignancies, neuronal, glial, astrocytal, cc hypothalamic and other glandular, macrophagal, epithelial, stromal, and CC blastocoelic disorders, haematopoissis-related disorders, tissue-growth CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney CC disorders, bone-related disorders such as osteoporosis, trauma such as:

CC catabolic states, testicular-related disorders, and inflammatory, CC anglogenic and immunologic disorders including arteriosclerosis. The products can also be used for detection and diagnosis especially of CC individuals with neoplastic cell growth or proliferation. The products can be used in the production of transgenic or knock-out animals.
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Best Local S
Matches 601
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The specification describes a pharmaceutical composition, comprising a growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent inhibits the action of at least one specific adverse protein, i.e. a protease, that is upregulated in a damaged tissue such as a wound environment. Growth factors which are included in the composition of the invention are platelet-derived growth factor (PGF), fibroblast growth factor (FGF), connective tissue derived growth factor (TGF), keratinocyte-derived growth factor (KGF), transforming growth factor (BGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF), epidermal growth factor (EGF), vascular endothelial growth factor (VEGF), and chrysalin. Inhibitors which are included in the
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                                                                                                                                                                                     Disclosure;
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RESULT 14
AAX16595
ID AAX16
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AC AAX16
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DT 29-AF
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 29-APR-1999
                                            AAX16595
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                                                                                                                                                                                                                                         TTTTCTGGCCTTGTCTCTTCCCTGCCCCCTGGTGTCCCCTGCCCAGAATGGAGCACGCCC
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Claim 4;

Fig

1; 63pp;

English.

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connective tissue growth factor; platelet-derived growth factor; keloid; connective tissue disorder; cancer; ankylosing spondylitis; scleroderma; atherosclerosis; Dupuytren's contracture; eosinophilic fasciitis; relty syndrome; Goodpasture's disease; Hunter syndrome; Hurler syndrome; Marfan syndrome; nodular fasciitis; osteogenesis imperfecta; restenosis; rheumatoid arthritis; systemic lupus erythematosus; ss.
                                                                                                                                                    New polynucleotide preventing and trea
                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                        Corley
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DB; AAW94616.
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                                                                                                                                                     cancer
                                                                                                                                                              useful
                                                                                                                                                                                                                                                                                                                                                                                                                  PDGF family;
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tissue disorders including ankylosing spondylitis, atherosclerosis, Dupuytren's contracture, eosinophilic fasciitis, Felty syndrome, Goodpasture's disease, Hunter syndrome, Hurler syndrome, keloids, Marfan syndrome, nodular fasciitis, osteogenesis imperfecta, polyarthritis nodosa, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, and restenosis following angioplasty. HGFLP antibodies and polynucleotides can also be used in diagnostic assays for conditions or diseases characterised by GRFLP expression. superfamily of growth factors. Antisense oligonucleotides and HGFLI antagonists can be used to treat or prevent cancer, and connective The present sequence encodes human growth factor-like protein ch has homology to connective tissue growth factor (CTGF) ( ch are members of the platelet derived growth factor (PDGF growth factor (PDGF) and HGFLP and fisp-12,

Sequence 1522 BP; 279 A; 496 Ç; 459 G; 288 T; 0 other;

Query Match Best Local S Matches 601

h 67.8%; Similarity 79.9%; O1; Conservative

0;

Score 510.4; DB 20 Pred. No. 8.8e-128; 0; Mismatches 151;

20;

1522

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Gaps

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                                                               CAGGGGGTACCCCTGGTGCTGGATGGCTGTGGGCTGCTGAAAGTGTGTGCACGGAGGCTG
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GGGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGGCCAGGGCCTGGTCTGCCAGCCC
                                                   CTGGGAGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGCCGGGTATGTGCACGGCGGCTG
                                                                                                       GTGCGTACCCAGCTGTGCCCGACACCATGTACCTGCCCCTGGCCACCTCCCCGATGCCCG
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                                                                                                Rosen
                                                                                                                              (HUMA-)
                                                                                                                                                                          31-JAN-2000;
04-FEB-2000;
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Ruben
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                                                                                                                              HUMAN GENOME SCI INC
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; 2000US-0180628.
; 2000US-0231968.
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tibacterial; virucide;
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fungicide; human;
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17 isolated nucleic acid molecules encoding human secreted proteins, r used to preventing, treating or ameliorating a medical condition .

Claim 1; Page 427-428; 482pp; English.

CC The invention provides novel human secreted proteins and polynucleotides concoding them. The secreted proteins can be expressed by standard concombinant methodology. The secreted proteins and polynucleotides are cused to prevent, treat or ameliorate a medical condition in e.g. humans, concombinant methodology. The secreted proteins and polynucleotides are cused to prevent, treat or ameliorate a medical condition. The antibodies to mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can concombinate the condition of the condition of the condition of the proteins associated with the condition of the condition of

Sequence 1337 BP; 257 A; 427 C; 396 G; 252 T; 5 other;

Query Match Best Local S Matches 600 241 227 181 167 121 107 al Similarity 600; Conserv 61 47 GTGTGTGCCCAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAGTGCCCA GGGGCAGGCCCTGGCGGCCATGGGGGCTGTGTGTGTCTCTTGGATGAGGATGACGGTAGCTGT CAGGGGGTACCCCTGGTGCTGGATGGCTGTGGGCTGTAAAGTGTGTGCACGGAGGCTG GGGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGGGCCCTGGTCTGCCAGCCC CTGGGAGTACCCCTGGTGCTGGATGGCTGTGGCTGCCGGGTATGTGCACGGCGGCTG Conservative 67.7%; 1; Score 510; DB 22; Pred. No. 1.1e-127; 1; Mismatches 151; Length 1337; Indels 0 Gaps 120 166 106 300 180 286 240 226

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US-09-08-715-1
US-09-08-715-1
US-09-08-716-714-1
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US-09-182-145-1
US-09-182-145-1
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Sequence 2, Appli	Sequence 27, Appl	Sequence 25, Appl	Sequence 28, Appl	Sequence 117, App	Sequence 1, Appli	Sequence 26, Appl	-	Sequence 29, Appl	Sequence 31, Appl	•	Sequence 35, Appl	Sequence 34, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 23, Appl	Sequence 3, Appli	Sequence 1, Appli

## ALIGNMENTS

CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 17 GENERAL INFORMATION:

APPLICANT: Botstein, David A.

APPLICANT: Cohen, Robert

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Levine, Arnold J.

APPLICANT: Levine, Arnold J.

APPLICANT: Pennica, Diane

APPLICANT: Pennica, Diane ; TYPE: DNA; ORGANISM: Mus musculus US-09-182-145-17 Sequence 17, Application Patent No. 6387657 Matches Query Match
Best Local Similarity LENGTH: 1734 121 317 181 702; ب CAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGTAAAGTGTGTGCACGGAGGCTG GGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGGCCAGGGCCTGGTTTGTCAGCCT GTGTATTCCCAGCTGTGCCCAGCACCCTGTGCCTGTCCTTGGACACCACCCCAGTGCCCA CCGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTCGAGTGTGTGCACGGAGGCTG Conservative 87.5%; 93.0%; US/09182145B 0; Score 659; DB 4; Pred. No. 8.5e-161; D; Mismatches 50; Length 1734; ACIDS ENCODING Indels w --SAME Gaps 316 180 240 436 376 60

Gaps

180 . 1359 120

1419 60

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Sequence 18, Application US/09182145B
Patent No. 6387657
GENERAL INFORMATION:
APPLICANT: Botstein, David A.
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Levine, Arnold J.
APPLICANT: Hood, William I.
APPLICANT: Wood, WILLIAM I.
APPLIC
                                               ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-182-145-18
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Patent No. 6387657
GENERAL INFORMATION:
                                          APPLICANT:
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           APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P1176R2
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NUMBER: US/09/182,145B
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US-09-182-145-13
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EARLIER APPLICATION NUMBER: US 60/063,704

EARLIER FILING DATE: 1997-10-29

EARLIER APPLICATION NUMBER: US 60/073,612

EARLIER FILING DATE: 1998-02-04

EARLIER APPLICATION NUMBER: US 60/081,695

EARLIER FILING DATE: 1998-04-14

NUMBER OF SEQ ID NOS: 156

SEQ ID NO 13

LENGTH: 1293
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Pred. No. 1.4e-122;
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APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Pennica, Diane
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACI
FILE REFERENCE: P11762
CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT APPLICATION NUMBER: US 60/063,704
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-10-29
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/081,695
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LENGTH: 1293
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Pred. No. 1.4e-122;
0; Mismatches 151;
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INFORMATION:

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APPLICANT: BOTSTEEIN, David A.
APPLICANT: Goddard, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Pennica, Diane
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIPTILE REFERENCE: P117682
CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
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Patent No. 6387657
 CGCAGGTACCTGGATGGAGAGCCTTTAAACCCAATTGCAGGGTCCTGTGCCGCTGTGAT
                                                         CCACTGATCCATCTTCTGGCCACTTCCTTCCTCTGCCTT&TCTCATGGTGTGTGTGCCCAG
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Pred. No. 2.9e-120;
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                                                                                                   GRGANISM: Artificial
FEATURE:
NAME/KEY: misc_featu
LOCATION: 1-841
COTHER INFORMATION: S
PATENT NO. 6387657
US-09-182-145-39
                                                                                                                                                                                                                                                            APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Pennica, Diane
APPLICANT: Wood, William I.
TITLE OF INVENTION. WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAMI
FILE REFERENCE: P1176R2
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER FILING DATE: 1997-10-29
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-04-14
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                                           Query Match
Best Local Sim
Matches 599;
                                                                                                                                                                                                                     NUMBER OF SEQ ID
SEQ ID NO 39
LENGTH: 841
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APPLICANT:
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                                                                                                                                                                                                          TYPE: DNA
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o. 6387657
                                                           Similarity
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Hillan, Kenneth J.
Lawrence, David A.
ATGAGGGCCACTGATCCATCTTCTGGCCACTTCCTTCCTCTGCCTTCTCTAATG
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1-841
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                                           Score 496.4; I
Pred. No. 5.2e-
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밁 Ş ; TYPE: DNA ; ORGANISM: Homo US-09-182-145-38

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UMBER OF SEQ ID Q ID NO 38 LENGTH: 738

Query Match
Best Local Similarity
Matches 590; Conserv

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                                                                                                                                                                                                                                                                         Sequence 1, Application Patent No. 5408040
                                                                                                                                                                                                                                                           GENERAL INFORMATION:
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                            APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH
                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                             670
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   APPLICATION DATA:
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               PatentIn Release #1.0,
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                 Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
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NAME: Wetherell, Jr. Ph.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 619-455-5100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                             CTCCACCCGGGTTACCAATGACAACGCCTCCTGCAGGCTAGAGAAGCAGAGCCGCCTGTG
                                                                        AGCCACCCGAGTGTCCAACCAGAACCGATTCTGCCAACTGGAGATCCAACGCCGCCTGTG
                                                                                                       CAACTGCCTGGTCCAGACCACAGAGTGGAGCGCCTGTTCCAAGACCTGTGGGATGGGCAT
                                                                                                                         TCCTTGTCCAAATTGGAGCACAGCCTGGGGCCCCTGCTCAACCACCTGTGGGGCTGGGCAT
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31,678
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Pred. No. 4.5e-33;
0; Mismatches 265
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,680
FILING DATE: 10-FEB-1995
CLASSIFICATION: 435
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APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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CLONE: DB60R32
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LOCATION:
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SOFTWARE: PatentI
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                               TGAGGATGACGGTAGCTGTGAGGTGAATGGCCGCAGGTACC
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CAAAGATGGTGCTCCCTGCATCTTCGGTGGTACGGTGTACC
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                                                                   GGGCCTCTTCTGTGACTTCGGCTCCCCGGCCAACCGCAAGATCGGCGTGTG----CACCGC
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                  Score 163; DB 1;
Pred. No. 4.5e-33;
D; Mismatches 265
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Patent No. 5770209
GENERAL INFORMATION:
                                                                                               TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                   NAME: Wetherell, Jr. Ph.D., REGISTRATION NUMBER: 31,678 REFERENCE/DOCKET NUMBER: PD TELECOMMUNICATION INFORMATION: TELEPHONE: 619-455-5100
                                                                                                                                                                                                                                             FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                            TYPE: nucleio
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08 FILING DATE: 02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                               TOPOLOGY:
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; LOCATION:
US-08-459-717-1
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Best Local Simi
Matches 351;
                                                                                                                                                       Sequence 1, Application US/08712302 Patent No. 5783187
                                                                                               GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE:
FEATURE:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                      CORRESPONDENCE ADDRESS
                    CITY: LA JOLLA
STATE: CA
COUNTRY: US
ZIP: 92037
                                                        STREET:
                                                               ADDRESSEE: Spensley Horn Jubas STREET: 4225 Executive Square,
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Pred. No. 4.5e-33;
0; Mismatches 265; Indels
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Suite 14
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CAAAGATGGTGCTCCCTGCATCTTCGGTGGTACGGTGTACCGCAGCGGAGAGTCCTTCCA

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AGTGTGTGCACGGAGGCTGGGGGGAGTCCTGCGACCTGCATGTCTGCGACCCCAGCCA

CGTCTGCGCCAAGCAGCTGGGCGAGCTGTGCACCGAGCGCGACCCCTGCGACCCGCACAA

362 221 GACACCACCCAGTGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTAA 161

Conservative

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Mismatches

265;

Indels

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Gaps

GCCGGCGCGCGCGCGGCGGGCGTGAGCCTCGTGCTGGACGGCTGCTGCTGCCG

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TCCTTGTCCAAATTGGAGCACAGCCTGGGGCCCCTGCTCAACCACCTGTGGGCTTGGGCAT

TGCCCTCGCGGCTTACCGACTGGAAGACACGTTTGGCCCCAGACCCAACTATGATTAGAGC

CGGGAAATGCTGCGAGGAGTGGGTGTGTGACGAGCCCAAGGACCAAACCGTGGTTGGGCC

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CAGTGAGGATGTGCGGCTGCCCAGCTGGGACTGCCCACGCCCCAAGAGAATACAGGTGCC

461

AGGAAAGTGCTGCCCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGCGCTC

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; NAME/KEY:
; LOCATION:
US-08-712-302-1
   Query Match
Best Local
                                                                                                                                                                                                                             TELEFAX: 619-455-5110 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 619-455-5100
                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.:
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                           FEATURE:
                                                                                                                       MOLECULE TYPE: c
IMMEDIATE SOURCE:
                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/386,680 FILING DATE: 10-FEB-1995
                                                                                                            CLONE:
                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 11-SEP-1996
                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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 Similarity
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130..1177
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SYSTEM: PC-DOS/MS-DOS
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21.6%; 56.2%;
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Score 163; DB 1;
Pred. No. 4.5e-33;
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                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.I
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH
NUMBER OF SEQUENCES: 2
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MOLECULE TYPE:
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                                                                                                                                                                                                                           NAME/KEY:
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4225 Executive Square,
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Pred. No. 4.5e-33;
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US-09-097-179-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Groten
APPLICANT: Bradha
                                                                                                                                                                                                                            SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                CITY:
STATE:
                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 92037
                              NAME: Wetherell, Jr. REGISTRATION NUMBER:
                                                                                                                      FILING DATE: 10-FEI APPLICATION NUMBER:
                                                                                                                                    APPLICATION NUMBER: US 0 FILING DATE: 10-FEB-1995
                                                                                                                                                                                   CLASSIFICATION:
                                                                                         FILING DATE:
APPLICATION NUMBER:
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                    REFERENCE/DOCKET
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VENTION: CONNECTIVE TISSUE GROWTH FACTOR
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                                                                                                                                                                                                                                                                                                                                                                Jolla
                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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25 Executive Square,
                    NUMBER:
                                                                                                                                                                                                                                            Release #1.0,
                                                                                            US/07/752,427
                                                                                                                                                     US 08/386,680
                                                                                                                        US/08/167,628
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; LOCATION:
US-09-097-179-1
         Sequence 1, Application US/09080715
Patent No. 6190804
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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IMMEDIATE SOURCE:
CLONE: DB60R32
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TYPE: nucleic acid
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    INVENTION:
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Jr., Douglas M.,
CONNECTIVE TISSUE GROWTH FACTOR
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2075 base pairs TYPE: nucleic acid STRANDEDNESS: single
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56.2%;
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ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/752,427 FILING DATE: ADDRESSEE: Spensley Horn Jubas & Lubitz STREET: 4225 Executive Square, Suite 1400 CAGTGAGGATGTGCGGCTGCCCAGCTGGGACTGCCCAAGAGAAATACAGGTGCC CGTCTGCGCCAAGCAGCTGGGGGGAGCTGTGCACCGAGCGCGGAGCCCACAA AGGAAAGTGCTGCCCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGCGCTC CAAAGATGGTGCTCCCTGCATCTTCGGTGGTACGGTGTACCGCAGCGGAGAGTCCTTCCA GGGCCTGGTTTGTCAGCCTGGGGCAĞGCCCTGGCGATGGGGCTGTGTGTCTCTTGGA AGTGTGTGCACGGAGGCTGGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGCCA GAGCAGCTGCAAGTACCAGTGCACGTGCCTGGACGGGGCGGTGGGCTGCATGCCCCTGTG GGGCCTCTTCTGTGACTTCGGCTCCCCGGCCAACCGCAAGATCGGCGTGTG----CACCGC CAGCATGGACGTTCGTCTGCCCAGCCCTGACTGCCCCTTCCCGAGGAGGGTCAAGCTGCC US/09/080,715 US/08/167,628 Score 163; DB 4; Pred. No. 4.5e-33; D; Mismatches 265 Σ Length 2075; 9 Gaps 479 419 461 401 341 281 362 221 302 521 599 539

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US-09-142-569-7
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                                                                                                      Matches 351;
                                                                                                                                      Query Match
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APPLICANT: Lau, Lest
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                      NAME/KEY: misc_feature
OTHER INFORMATION: "CTGF |
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/142,569
FILING DATE: 02-Apr-1999
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
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                                                                                                                      Similarity
                                                     GACACCACCCAGTGCCCACAGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGTAA 161
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AGTGTGTGCACGGAGGCTGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGCCA 221
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                                   GCCGGCGCGCGCGCGGGCGGGCGTGAGCCTCGTGCTGGACGGCTGCGGCTGCTGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Illinois
                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 312/474-63
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Clough, David W
REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
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                                                                                                   Score 163; DB 4;
Pred. No. 4.5e-33;
0; Mismatches 265
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                                                                                                                                    Length 2075;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application:
              TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    SOFTWARE: PatentIn Relicurrent APPLICATION DATA:
APPLICATION NUMBER: PC
                                                               REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 074
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                   TELEPHONE: 619 -678-5099
                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 92037
                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                         FILING DATE:
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Search completed: July 28, 2003, Job time: 43.1673 secs
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; LOCATION:
PCT-US96-08140-1
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Best Local Similarity 56.2%;
Matches 351; Conservative
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MOLECULE TYPE: cD
IMMEDIATE SOURCE:
CLONE: CTGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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Pred. No. 4.5e-33;
0; Mismatches 265; Indels 9;
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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re greater than or equal to the score of the result being printed,
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: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq3:*
: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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Copyright (c) 1993 - 2003 Compu
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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   US-10-010-408-3

US-10-010-408-1

US-10-0112-267-17

US-10-112-267-18

US-10-117-267-18

US-10-137-866-319

US-10-146-726-319

US-10-146-788-319

US-10-146-788-319

US-10-152-380-319

US-10-152-380-319

US-10-123-049-319

US-10-123-049-319

US-10-123-049-319

US-10-123-049-319

US-10-123-043-319

US-10-123-043-319
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8368.853 Million cell updates/sec
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12, Appl
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17, Appl
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RESULT 1  US-10-010-408-3  Sequence 3, A; Publication N GENERAL INF GENERAL INF CORRES; COMPUT COMPU		111 112 113 114 115 116 117 117 117 117 117 117 117 117 117
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-408-3  tion No. US200200  AL INFORMATION: APPLICATIC: STATE: Mass: COUNTRY: US ZIF: 02109 COMPUTER READABL MEDIUM TYPE COMPUTER: I O2109 COMPUTER: MASS: SOFTWARE: FOPERATING: SOFTWARE: FILING DATE CLASSIFICATION APPLICATION CLASSIFICATION APPLICATION TILING DATE REGISTRATIC APPLICATION APPLICATION APPLICATION TILING DATE APPLICATION TELEPAX: MAME: AMY E REGISTRATIC TELECOMMUNICATIO TELEPAX: (6 MAGION FOR SEQ I SEQUENCE CHARACT		444444444444444444444444444444444444444
-3  Applicat: Applicat: No. US200  WEORMATION  SO OF INVER  ER OF EQUI  CITY: BOS  STREET: COUNTRY: CO		6677
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D8  Therefor  Th	ALIGNMENTS	US-10-176-918-319 US-10-176-921-319 US-10-137-865-319 US-10-142-474-319 US-10-142-431-319 US-10-142-419-319 US-10-142-419-319 US-10-142-423-319 US-10-123-262-319 US-10-121-550-319 US-10-121-550-319 US-10-123-261-319 US-10-123-261-319 US-10-123-261-319 US-10-123-261-319 US-10-123-281-319 US-10-123-296-319 US-10-124-928-319 US-10-124-819-319 US-10-124-819-319 US-10-124-819-319 US-10-140-925-319 US-10-140-925-319 US-10-140-925-319 US-10-140-925-319 US-10-140-925-319 US-10-140-925-319 US-10-140-925-319 US-10-140-925-319 US-10-140-925-319 US-10-124-812-319 US-10-124-823-319 US-10-124-823-319 US-10-124-823-319 US-10-124-823-319 US-10-124-823-319 US-10-124-823-319 US-10-124-823-319 US-10-127-825A-319 US-10-127-825A-319 US-10-127-825A-319
Heparin-Induced CCN-Like		Sequence 319
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SEQUENCE CHARACTERISTICS:

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NAME/KEY: CDS
LOCATION: 1..750
SEQUENCE DESCRIPTION: SEQ ID
US-10-010-408-3
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RESULT 2
US-10-010-408-1
; Sequence 1, Application US/10010408
; Publication No. US20020165185A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 753; Conservative 0
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
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Pred. No. 7.4e-206;
); Mismatches 0;
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Matches 753
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NAME/KEY: CDS
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LOCATION: 249..1001
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SEQUENCE DESCRIPTION: SEQ
US-10-010-408-1
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ETLING DATE: 07-Dec-2001
CLASSIFICATION: CUNKnown>
PRIOR APPLICATION: CUNKnown>
PRIOR APPLICATION UNMER: 09/044,273
APPLICATION NOMBER: 09/044,273
FILING DATE: MARCH 19,198
APPLICATION NUMBER: 4UNKnown>
FILING DATE: MARCH 19,198
APPLICATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
TELEPHONE: (617)227-7400
TELEPHONE: (617)424-4214
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; al Similarity 100.0%; 753; Conservative 0
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GGGCAGGCCCTGGCGCCATGGGGCTGTCTGTCTCTTGGATGAGGATGACGGTAGCTGT
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STRANDEDNESS: single
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COUNTRY: USA
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NVENTION: No. US20020165185Alel Heparin-Induced
and Uses Therefor
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US-10-010-408-12
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Publication No. US20020165185A1

GENERAL INFORMATION:

APPLICANT: John J. Castellot, Jr.

APPLICANT: John J. Castellot, Jr.

TITLE OF INVENTION: No. US20020165185A1e1 Heparin-Induced CCN-Like

and Uses Therefor
                                                                                 APPLICATION NUMBER: 09/044,273
FILING DATE: MATCH 19, 1998
APPLICATION NUMBER: CUNKNOWN>
FILING DATE: CUNKNOWN>
FILING DATE: CUNKNOWN>
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. MANDRENS 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   CURRENT
    MOLECULE
                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
RRENT APPLICATION DATA:
APPLICATION UMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: LAHIVE & COCKE
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGAGCCACAGCTCATGGAACAGTGCTTTCTAA 1001
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US-10-112-267-17
; Sequence 17, Application US/10112267
; Publication No. US20030068678A1
; GENERAL INFORMATION:
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; LOCATION: 1..681
; SEQUENCE DESCRIPTION: SEQ
US-10-010-408-12
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APPLICANT: Botstein, I
APPLICANT: Cohen, Rob
APPLICANT: Goddard, A
APPLICANT: Gurney, Au
APPLICANT: Hillan, Ke
APPLICANT: Lawrence,
APPLICANT: Levine, Av
APPLICANT: Pennica, I
APPLICANT: Roy, Marga
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Best Local Similarity
Matches 681; Conserv
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                                       Goddard, Audrey
Gurney, Austin L.
Hillan, Kenneth J.
Lawrence, David A.
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Levine, Arnold J.
Pennica, Diane
Roy, Margaret Ann
                                                                                                 Cohen, Robert
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                                                                                                              David A
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Pred. No. 3e-185;
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FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/10/112,267
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION
PRIOR FILING DATE: EARLIER FILING DATE: 199
PRIOR FILING DATE: EARLIER FILING DATE: 199
PRIOR FILING DATE: EARLIER FILING DATE: 199
PRIOR APPLICATION NUMBER: EARLIER APPLICATION
PRIOR APPLICATION NUMBER: EARLIER APPLICATION
PRIOR APPLICATION NUMBER: EARLIER APPLICATION
PRIOR FILING DATE: EARLIER FILING DATE: 199
PRIOR APPLICATION NUMBER: EARLIER APPLICATION
PRIOR FILING DATE: EARLIER FILING DATE: 199
NUMBER OF SEQ ID NOS: 156
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TITLE OF INVENTION: WISP POLYPEPTIDES AND
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ORGANISM: Mus musculus
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hes 702;
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STH: 1734
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GCCAGGAGCCACAGCTCATGGAACAGTGCTTTCTA
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                                              Conservative
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93.0%;
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Pred. No. 6.6e-179;
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G DATE: 1998-10-29

R APPLICATION NUMBER: U

IG DATE: 1997-10-29

R APPLICATION NUMBER: U

IG DATE: 1998-02-04

IG DATE: 1998-04-14
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; TYPE: DNA
; ORGANISM: Mus I
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CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION
PRIOR FILING DATE: EARLIER FILING DATE: 1996
PRIOR APPLICATION NUMBER: EARLIER APPLICATION
PRIOR FILING DATE: EARLIER FILING DATE: 11906
PRIOR APPLICATION NUMBER: EARLIER APPLICATION
PRIOR FILING DATE: EARLIER FILING DATE: 11906
PRIOR FILING DATE: EARLIER FILING DATE: 11906
PRIOR FILING DATE: EARLIER FILING DATE: 11907
PRIOR FILING DATE: DATE: 11907
PRIOR FILING DATE: EARLIER FILING DATE: 11907
PRIOR FILING DATE: DATE: DATE: 11907
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PRIOR FILING DATE: DA
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US-10-112-267-18/c
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APPLICANT: Botstein, David
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 18
LENGTH: 1734
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Best Local
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Local Similarity 93.0%;
les 702; Conservative
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Gurney, Austin L.
Hillan, Kenneth J.
Lawrence, David A.
                                           CCCAGCTGGGACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGCCCCGAG
                                                                                                                                     TGCCGCTGTGATGACGGTGGCTTCACCTGCCTGCCGCTGTGCAGTGAGGATGTGCGGCTG
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Wood, William I.
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Pred. No. 6.6e-179;
0; Mismatches 50;
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G DATE: 1998-10-29
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PRIOR FILING DATE: 1998-03-20 PRIOR APPLICATION NUMBER: 60/079294 PRIOR APPLICATION NUMBER: 60/079663 PRIOR APPLICATION NUMBER: 60/079663 PRIOR FILING DATE: 1998-02-27 PRIOR APPLICATION NUMBER: 60/079728	APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER:	APPLICATION NUMBER: FILING DATE: 1997-11 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0	FILING DATE: 1997-1 APPLICATION NUMBER: FILING DATE: 1997-1 APPLICATION NUMBER: FILING DATE: 1997-1 APPLICATION NUMBER: FILING DATE: 1997-1	י ש ש ש ש ש י	חמת ממ	י ש א ש א ש א ש א	PRIOR APPLICATION NUMBER: 60/06350 PRIOR FILING DATE: 1997-10-28 PRIOR FILING DATE: 1997-10-28 PRIOR FILING DATE: 1997-10-29 PRIOR FILING DATE: 1997-10-29 PRIOR FILING DATE: 1997-10-29 PRIOR APPLICATION NUMBER: 60/063733 PRIOR FILING DATE: 1997-10-29 PRIOR FILING DATE: 1997-10-29	ת שש שש ש נדים דים דיי	י הימ הימי הימי הימ	; PRIOR APPLICATION NUMBER: 60/062285; PRIOR FILING DATE: 1997-10-17; PRIOR APPLICATION NUMBER: 60/062287; PRIOR FILING DATE: 1997-10-17; PRIOR FILING DATE: 1997-10-17.

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OR APPLICATION NUMBER: 60/081818
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OR APPLICATION NUMBER: 60/083322
OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/083645
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RESULT 7
US-10-146-726-319
; Sequence 319, Application US/10; Publication No. US20030129690A1; GENERAL INFORMATION:
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Desnoyers, Luc
Filvaroff, Ellen
                               Baker, Kevin P.
Beresini, Maureen
                                                                                                                     AGGAGCCACAGCTCATGGAACAGTGCTTTCTA
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79.9%;
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Pred. No. 2.1e
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NUMBER: 60/090863

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CURRENT APPLICATION NUMBER: US/10/146,726

CURRENT FILING DATE: 2002-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prior Application removed - See File Wrapper NUMBER OF SEQ ID NOS: 550
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                                                       CTTTCTGCCCTTGTCACTCCTGCCTCTGATGCTCCTTGTCCAAATTGGAGCACAGCC
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TGGGGACCCTGCTCGACCACCTGTGGGCTGGGCCATGGCCACCCGGGTGTCCAACCAGAAC
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Watanabe, Colin K
Wood, William
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Gurney, Austin L.
Sherwood, Steven
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Stewart, Timothy A.
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; SEQ ID NO 319
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; ORGANISM: HOMO S
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US-10-146-727-319
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Best Local S
Matches 601
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C312
CURRENT APPLICATION NUMBER: US/10/146,727
CURRENT FILING DATE: 2002-05-15
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Wood, William
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Stewart, Timothy A
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Filvaroff, Ellen
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Pred. No. 2.1e-136;
D; Mismatches 151;
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; ORGANISM: HOMO
US-10-146-788-319
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US-10-146-788-319
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                                                                                                                                                Query Match
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 319
LENGTH: 1266
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C322
                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/146,788
CURRENT FILING DATE: 2002-05-15
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sharwood, Steven
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Wood, William
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APPLICANT: Zhang, Zemin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C397
CURRENT APPLICATION NUMBER: US/10/152,380
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Smith, Victoria
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Filvaroff, Ellen
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; Sequence 319, Application; Publication No. US2003012; GENERAL INFORMATION:
APPLICANT: Baker, Kevin FAPPLICANT: Beresini, Mau
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Prior Application removed -
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 319
LENGTH: 1266
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Beresini, Maureen
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o. US20030129695A1
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CURRENT FILING DATE: 2002-05-22
Prior Application removed - See file Wrap;
NUMBER OF SEQ ID NOS: 550
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LENGTH: 1266
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C412
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TGGGGCCCCTGCTCAACCACCTGTGGGCTGGGCATAGCCACCCGAGTGTCCAACCAGAAC
                       TTTTCTGGCCTTGTCTCTTCCCTGCCCCCTGGTGTCCCCTGCCCAGAATGGAGCACGGCC
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                                                                                                                                                                                                                                                                           GGGGCAGGCCCTGGCGGCCATGGGGCTGTGTGTGTCTCTTGGATGAGGATGAGGGTAGCTGT
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                                                                                                                                                                                                                                                                                                                                                             CTGGGAGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGCCGGGTATGTGCACGGCGGCTG
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumas,Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stewart, Timothy A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DeForge, Laura
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Pred. No. 2.1e-136;
0; Mismatches 151;
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GENERAL INFORMATION:

APPLICANT: Baker Kevin P
APPLICANT: Beresini, Mau
APPLICANT: Deforge, Laur
APPLICANT: Desnoyers, Lu
APPLICANT: Filvaroff, Eli
APPLICANT: Gao, Wei-Qian
APPLICANT: Gao, Wei-Qian
APPLICANT: Goddard, Audre
APPLICANT: Goddard, Audre
APPLICANT: Goddwski, Pau,
APPLICANT: Graney, Austi
APPLICANT: Sherwood, Ster
APPLICANT: Smith, Victor
                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/028,072

CURRENT EILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/05914

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059122

PRIOR APPLICATION NUMBER: 60/059122

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059263

PRIOR APPLICATION NUMBER: 60/05935

PRIOR APPLICATION NUMBER: 60/05935

PRIOR APPLICATION NUMBER: 60/059368

PRIOR FILING DATE: 1997-09-19

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059368

PRIOR FILING DATE: 1997-09-19

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059368

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059368
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R FILING DATE:
R APPLICATION N
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desnoyers, Luc
Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerritsen, Mary E
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b. US20030004311A1
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E: 1997-09-24
N NUMBER: 60/062250
E: 1997-10-17
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                                                                                                                                                                                        NUMBER: 60/062285: 1997-10-17
                                                             NUMBER: 60/062816: 1997-10-24
                                                                                                       NUMBER: 60/
: 1997-10-24
                                                                                                                                              NUMBER: 60/062287: 1997-10-17
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                        1997-10-24
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                                           60/063045
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OR FILING DATE: 1998-02-04
OR APPLICATION NUMBER: 60/074086
OR FILING DATE: 1998-02-09
OR APPLICATION NUMBER: 60/074092
OR FILING DATE: 1998-02-09
OR APPLICATION NUMBER: 60/077791
OR FILING DATE: 1998-03-12
OR APPLICATION NUMBER: 60/078910
OR APPLICATION NUMBER: 60/079294
                                                                                                                                                           DR APPLICATION NUMBER: 60/079663
DR FILLING DATE: 1998-02-27
DR APPLICATION NUMBER: 60/079728
DR FILLING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/080165
DR FILLING DATE: 1998-03-31
DR FILLING DATE: 1998-03-31
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DR FILING DATE: 1997-11-12
DR APPLICATION NUMBER: 60/065846
DR FILING DATE: 1997-11-17
DR APPLICATION NUMBER: 60/066364
DR FILING DATE: 1997-11-21
DR APPLICATION NUMBER: 60/066453
DR APPLICATION NUMBER: 60/066511
DR FILLING DATE: 1997-11-24
               R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-04-09
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-04-14
R APPLICATION NUMBER: 60/08
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R FILING DATE: 1997-12-11

R FILING DATE: 1997-12-11

R APPLICATION NUMBER: 60/069694

R FILING DATE: 1997-12-16

R APPLICATION NUMBER: 60/072320

R FILING DATE: 1998-01-23
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DR FILING DATE: 1997-10-29

R FILING DATE: 1997-10-29

DR APPLICATION NUMBER: 60/063755

DR FILING DATE: 1997-10-17
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APPLICATION NUMBER: 60/069278
APPLICATION 1997-12-11
APPLICATION 0ATE: 1997-12-11
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APPLICATION NUMBER: 60/0
TTYNG DATE: 1997-10-24
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                                                                                                                          APPLICATION NUMBER: 60/
FILING DATE: 1998-04-09
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FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/
FILING DATE: 1997-12-11
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FILING DATE: 1997-10-28
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                                                                                                                                                60/081203
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Query Match 67.1
Best Local Similarity 79.1
Matches 601; Conservative
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                                                                                     OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090445
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090538
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090863
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-01
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091519
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091982
OR FILING DATE: 1998-07-07
                                                                                                                                                                                                                                                                                                            OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084637
OR APPLICATION NUMBER: 60/085149
OR FILING DATE: 1998-05-12
OR APPLICATION NUMBER: 60/08532
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/08533
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/08539
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085697
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/08579
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/086414
OR FILING DATE: 1998-05-22
OR APPLICATION NUMBER: 60/086430
OR FILING DATE: 1998-05-22
OR APPLICATION NUMBER: 60/086430
OR FILING DATE: 1998-05-22
OR APPLICATION NUMBER: 60/088026
OR FILING DATE: 1998-05-20
OR APPLICATION NUMBER: 60/088026
OR FILING DATE: 1998-05-20
OR APPLICATION NUMBER: 60/088730
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088741
OR APPLICATION NUMBER: 60/088610
OR APPLICATION NUMBER: 60/088610
OR APPLICATION NUMBER: 60/088610
OR APPLICATION NUMBER: 60/088959
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/089532
OR APPLICATION NUMBER: 60/089532
OR APPLICATION NUMBER: 60/089532
OR APPLICATION NUMBER: 60/08996
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/08993
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/084600
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FILING DATE: 1998-04-28
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FILING DATE:
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1998-05-07
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             Score 510.4;
Pred. No. 2.1e
0; Mismatches
                 0
                                   .1e-13
                                                    В
                                                    15;
                 Indels
                                                  Length 1266;
               0;
                 Gaps
                 0
                                            Sequence 319, Application US/10121049
Publication No. US20030022239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desoryers, Luc
APPLICANT: Desoryers, Luc
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Godwski, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
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US-10-121-049-319
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: APPLICANT: Zbang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE PO!
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3330RLC17
: CURRENT APPLICATION NUMBER: US/10/121,049
: CURRENT FILLING DATE: 2002-04-12
: P10r Application removed - See File Wrapper: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 319
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Best Local Similarity 79.9%;
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 319
LENGTH: 1266
TYPE: DNA
ORGANISM: Homo Sapien
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Publication No. US20030022328A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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Best Local Similarity
Matches 601; Conserv
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CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
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NUMBER OF SEQ ID NOS: 550
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Best Local Similarity
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                                                                                                                                                                   Matches
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C160
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Watanabe, Colin K
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Stewart, Timothy A.
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Pred. No. 2.1e-136;
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Search completed: July 28, 2003, 21:31:59
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## ALIGNMENTS

11058	FEATURES Source
High quality sequence stop: 697.	
http://image.llnl.gov	
found through the T.M.A.G.E. Consortium/LLNL at:	
Clone distribution: MGC clone distribution information can be	
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
cDNA Library Preparation: Life Technologies, Inc.	
Tissue Procurement: Invitrogen	
Email: cgapbs-r@mail.nih.gov	
Contact: Robert Strausberg, Ph.D.	COMMENT
Unpublished (1999)	JOURNAL
National Institutes of Health, Mammalian Gene Collection (MGC)	TITLE
NIH-MGC http://mgc.nci.nih.gov/.	AUTHORS
1 (bases 1 to 1058)	REFERENCE
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Homo sapiens	ORGANISM
human.	SOURCE
EST.	KEYWORDS
BM805088.1 GI:19121911	VERSION
BM805088	ACCESSION
5', mRNA sequence.	
AGENCOURT_6490429 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5725937	DEFINITION
BM805088 1058 bp mRNA linear EST 05-MAR-2002	LOCUS
	BM805088

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BASE COUNT
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/clone_lib="NIH_MGC_125"
/lab_host="DH10B"
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Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1:3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."

a 423 c 294 g 200 t 2 others
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79.8%;
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Pred. No. 1.2e-114;
0; .Mismatches 152;
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587; Conser
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2045 row: k column: 04
High quality sequence stop: 752.
Location/Qualifiers
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5', mRNA sequence.
B0279131
B0279131.1 GI:20489339
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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National Institutes of Health, M
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1 (bases 1 to 979)
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/db_xref="taxon:9606"
/clone="IMAGE:5805819"
/clone=lib="MIH_MGC_107"
/tissue_type="adenocarcinoma, cell line"
/tissue_type="adenocarci
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Eutheria; Primates; Catarrhini; Hominidae;
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80.2%;
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603039845F1 NIH_MGC_115
                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11450 row: 1 column: 11
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                                                                                                                                                                                                                                                               quality sequence stop: 865
/note="Organ: pooled brain, lung, testis; vector: pcMV-SpORT6; Site_1: NotI; Site_2: EcoRV (destroyed); I source anonymous pool of 6 male brains, age range 23-2; male lung, age 27; and 1 male testis, age 69. Library oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by
                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5180650"
/clone_lib="NHH_MGC_115"
                                                                                                                                         /lab_host="DH10B"
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     Metazoa; Chordata; Craniata;
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National Institutes of Health, M
Unpublished (1999)
Contact: Robert Strausberg, Ph.D
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High quality sequence stop: 714.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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GTGGGTATGTGACCAGGGAGTGACACCGGCGATCC-AGCGCTCCACGGCGCAAGGACACC
                                                                                                                                                                              CTGCCGCTGCGAGGACGGCGGCTTCACCTGCGTGCCGCTGTGCAGCGAGGATGTGCGGCT
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/clone=lib="NIH_MGC_40"
/clone_lib="NIH_MGC_40"
/tissue_type="carcinoma, cell line"
/note="OTB7; Site_1: xhoI;
/note="OTGAN : porB7; Site_1: xhoI;
/note="Corgan: cona made by oligo-dT priming.

Directionally cloned into EcorI/%hoI sites using the
following 5' adaptor: GGCAGGAG(G), Library constructed by
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/db_xref="taxon:9606"
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Location/Qualifiers
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1 (Dases 1 to 651)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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603185392F1 NIH_MGC_42
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CCTTGGACACCACCCCAGTGCCCACAGGGGGGTACCCCTGGTGCTGGATGGCTGTGGCTGC 156
                                                                         TCCCTCCTCTGCCTCTCAAAGGTGCGTACCCAGCTGTGCCCGACACCATGTACCTGC
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                                                                                                                                                Conservative
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//clone_lib="NHH_MGC_42"
//tissue_type="epithelioid carcinoma cell line"
//lab_bost="PH10B (phage=resistant)"
//note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
//note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
//site_2: ECONI; CONA made by oligo-dT priming.
Directionally cloned into ECONI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size=selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NHH_MGC Library. | "
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/db_xref="taxon:9606"
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Eutheria; Primates;
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80.1%;
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                                                                                cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLI DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCML870 row: a column: 23 High quality sequence stop: 778.
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603185689F1 NIH_MGC_42
                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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Mammalia; Eutheria;
1 (bases 1 to 916)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5258398"
/clone_lib="NIH_MGC_42"
/tissue_type="epithelioid carcinoma/lab_host="DH10B (phage-resistant)"
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Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library. ["
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79.0%;
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Pred. No. 1.4e-94;
0; Mismatches 146;
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SSULT 7
1921531
1921531
1006 bp mRNA linear EST 12-MAR-2002
ETINITION AGENCOURT_6708025 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5753009
5', mRNA sequence.
CESSION BM921531.1 GI:19371910
EXEMPLE ST. 1006 bp mRNA linear EST 12-MAR-2002
EST. 1007 bp mRNA linear EST 12-MAR-2002
EST. 1
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ORGANISM
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Best Local Similarity
Matches 585; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; V
Mammalla; Eutherla; Primates; Catarrhini;
1 (bases 1 to 1006)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 593.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: LLAM12788 row: b column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://image.llnl.gov
GGGACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTCCCCCGAGTGGGTAT
                                                       GCGAGGACGGCGCTTCACCTGCGTGCCGCTGTGCAGCGATGTGTGCGCGCTGCCCAGCT
                                                                                                                                                                                                                         GCCCTGGCGGCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGGTAGCTGTGAGGTGA 307
                                                                                                                                                                                                                                                                        CCTGCGACCAACTCCACGTCTGCGACGCCAGCCAGGGCCTGGTCTGCCAGCCCGGGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAGCCCACTGATCCATCTTCTGGCCACTTCCTTCTCTCTGGCCTTCTCTCAATGGTGTG
                                                                                          GTGATGACGGTGGCTTCACCTGCCTGCCGCTGTGCAGTGAGGATGTGCGGCTGCCCAGCT
                                                                                                                               ACGGCCGCCTGTATCGGGAAGGGGAACCTTCCAGCCCCÄCTGCAGCATCCGCTGCCGCT
                                                                                                                                                                ATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAACCCCAATTGCAGGGTCCTGTGCCGCT 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5753009"
/clone_lib="NIH_MGC_115"
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77.5%;
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Site_2: EcoRV (destroyed); RNA
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BQ073722
LOCUS
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Query Match
Best Local Sim
Matches 532;
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AGENCOURT_7046577 NIH_MGC_101
5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: L/LRL047 row: k column: 19 High quality sequence stop: 517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 1073)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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BQ073722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A - - GGAGCCACAGCTCATGGAACAGTGCTTTCTAA
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                                                                                                              166
                                                                                                     /tissue_type="epidermoid carcinoma, cell line"
/tab_host="bH10B (phage resistant)"
/nab_host="bH10B (phage resistant)"
/note="Drgan: lung; Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

56 a 384 c 347 g 176 t
                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5806602"
/clone_lib="NIH_MGC_101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metazoa; Chordata;
Eutheria; Primates;
                        55.5%;
79.5%;
                        Score 417.8; DB 1 Pred. No. 2.8e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp mRNA linear EST 02-APR-2002
1 Homo sapiens cDNA clone IMAGE:5806602
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                                          DB 14;
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution informat

found through the I.M.A.G.E. Consortium/LLNL at:
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Location/Qualifiers
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/tissue_type="medulla"
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/clone="IMAGE:5169065"
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Tissue Procurement: ATCC
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National Institutes of Health, M
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/clone_Lib="NMGE.42"
/clone_Lib="NMH_MGC.42"
/tissue_type="epithelioid carcinoma cell line"
/tiste_1: XhoI;
/the_Torgan: pancreas; Vector: pOTB7; Site_1: XhoI;
/the_Torgan: pancreas; Vector: potgan: pancreas; 
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
plate: LLAM11408 row: n column: 07
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BI825652.1 GI:15937202
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Location/Qualifiers
                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5164614"
/clone=1b="NHHMGC_119"
/tissue_type="medulia"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Sit
Site_2: EcoRV (destroyed); RNA source normal
anonymous male age 27. Library is oligo-dT
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BM046275
603626088F1 NIH_MGC_40 Hd
mRNA sequence.
BM046275
BM046275.1 GI:16775542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 790)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
CCTCTGCTGATGCTCCTTGTCCAAATTGGAGCACAGCCTGGGGGCCCCTGCTCAACCACCT
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                                                                               CACCGGCGATCCAGCGCTCCACGGCGCAAGGACACCAACTTTCTGCCCTTGTCACTCCTG
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//tab_host="DBHOB (phage-resistant)"
/note="organ: prostate; Vector: pOTB7; Site_1: XhoI;
/note="organ: prostate; Vector: pOTB7; Site_1: XhoI;
/note="organ: prostate; Vector: pOTB7; Site_2: EcoRI; CDNA made by oligo-dT priming.

Site_2: EcoRI; CDNA made by oligo-dT priming the Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NHLMGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:5452480"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections of the collections of the
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5', mRNA sequence.
BQ952960
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Tissue Procurement: DCTD/DTP
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Plate: LLCM2669 row: m column:
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Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                               Similarity
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CDNA Library Arrayed by: The I.M.A.G.E: Consortium (LLA
DNA Sequencing by: Agencourt Blosclence Corporation
Clone distribution: MGC clone distribution information
                                                                                                                                      GCTGCTGTAAAGTGTGTGCACGGAGGCTGGGGGAGTCGTGCGACCACCTGCATGTCTGCG
                                           ACCCCAGCCAGGGCCTGGTTTGTCAGCCTGGGGCAGGGCCTGGCGGCCATGGGGCTGTGT
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                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                    /tissue_type="carcinoma, cell line"
/lab_host="DHIOB (phage resistant)"
/note="Organ: prostate; Vector; pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI, XhoI sites using the following 5 adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
a 305 c 457 g 131 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6484123"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NIH_MGC_40"
                                                                                                                                                                                                                             49.8%;
78.1%;
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709 Swedeland Road, F
Tel: 610-270-7245
Fax: 610-270-5598
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Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. &
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HNC57-1-D9.R HNC
                                                                                                                                                                                                                                                   Email: sanjay_kumar-1@gsk.com
Seq primer: T7.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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BG928868
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                     97
                                           /note="Vector: psport I; Site_1:
Directional"
                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_sref="taxon:9606"
/clome_lib="HNC (Human Normal
/tissue_type="cartilage"
/lab_host="E.coli_DH10_B"
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Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 1251)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                found through the I.M.A.G.E. Consortium/LLNL http://lmage.llnl.gov Plate: LLCM2670 row: n column: 21
                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                  BQ961357.1
                                                                                                         cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
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                                                      quality sequence stop: 465
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                            Location/Qualifiers
1. .1251
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Homo sapiens cDNA clone
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CCCAGCTGGGACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGCCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:6484532"
/clone_lib="NIH_MGC_40"
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/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
/site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: EcoRI; cDNA finto EcoRI/XhoI sites using the following 5' adaptor: GGCACCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
78 a 393 c 546 g 131 t 3 others
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Search completed: Job time: 1337.44 July 29, 2003, 02:51:36 δÃ Вþ Š 밁 Qγ д δÃ В δÃ 밁 Qy В δÃ g γ

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Minimum DB
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Result No. Score Match 145540 145540 176107 176107 185612 185612 193395 142143 149483 180464 200050 66908 150484 154881 157691 167691 167691 179236 226303 137964 1734 1734 107260 51 51 1734 61072 216757 1739 Length В AR210325 AF100778 AL731698 AX464186 AF083500 ARZ10323 ARZ10323 ARZ10323 ARZ100780 BC017782 ARZ10371 AX076923 ARZ10375 AR AC112856 AC122102 AC103349 AL646068 AC119914 AC107112 AR210338 AX076919 AC126895 AR210324 AC110904 AC116351 AC010446 AC091173 IJ AC114696 AC067881 AC126895 Rattus no AC095418 Rattus no AC126895 Rattus no AR210324 Sequence AR210325 Sequence AF210778 Mus muscu AL731698 Mouse DNA AL669906 Mus muscu AR210337 Sequence AR210338 Sequence AX076919 Sequence AX076919 Sequence AX464186 Sequence AF083500 Homo sap1 AF210323 Sequence AR210323 Sequence AR210323 Sequence AR2103782 Homo sap1 AF100780 Homo sap1 AF100780 Homo sap1 AR139352 Human DNA AR210371 Sequence AX076923 Sequence AX076923 Sequence AX076923 Sequence AX076923 Rattus no AP002393 Homo sap1 AC108655 Rattus no AP002393 Homo sap1 AC0105227 Homo sap1 AC0105227 Homo sap1 AC0105251 Homo sap1 AC010526 Rattus no AC112856 Rattus no AC112102 Rattus no AC107112 Rattus no AC107112 Rattus no AC107112 Rattus no AC107112 Rattus no AC1071112 Rattus muscu AC1131741 Mus muscu AC01331741 Mus muscu Description AL672068 Mouse DNA AF259981 Rattus nc

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Zhang,R., Averboukh,L., Zhu,W., Zhang,H., Jo,H., Dempsey,P.J.,	1 (bases 1 to 1741)	Rattus.	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Rattus norvegicus	Rattus norvegicus.		AF259981.1 GI:7739780	AF259981	cds.	Rattus norvegicus CCN family protein COP-1 (Cop-1) mRNA, complete	AF259981 1741 bp mRNA linear ROD 09-MAY-2000		

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                                         AGCGATCCCTGCTCTGTCTGAGGTAGGCGGAGCAGGTĞACCAGCTCCAGTTCTCTGGTTC
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/note="secreted protein"
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                                Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Blouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Chen, R., Chen, Z., Chowdhry, L., Christopoulos, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hulk, S., Hume, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Jouahh, S., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Lozado, R.J., Lu, X., Lucier, R., Martindale, A., Martinez, E., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Morgan, M., Morris, S., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Massey, E., McLeod, R., Payton, B., Weerey, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pull, B., Lewis, L., Perez, L., Peters, L., Pickens, R., Parimus, E., Pull, B., Lewis, L., Perez, L., Peters, L., Soott, G., Shen, H., Shooshtari, N., Sisson, I., Sodegrer, S., Soott, G., Shen, H., Shooshtari, N., Stanley, H., Stone, H., Sutch, A., Tandrisa, A., Tamerisa, A., Tamerisa, K., Tang, H.,
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Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Taylor, T., Telfrod, B., Thomas, N., Thomas, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williamson,A., Wileczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-JUL-2002) Human Genome Sec
of Molecular and Human Genetics, Baylor
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 137964)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center project name: CZHG
Center clone name: CH230-301E4
Consensus quality: By341 bases at least Q30
Consensus quality: 93422 bases at least Q30
Consensus quality: 93422 bases at least Q30
Consensus quality: 93506 bases at least Q30
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NOTE: This is a 'working draft' sequence. It currently consists of 49 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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be preserved
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Alsbrooks, S.L., Adio-Oduola, B., Ali osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Blarbooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Blarbooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Blarbooks, S.L., Bankenburg, K., Bonnin, D., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowke, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chaeko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., 
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Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Maylinez, E., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Pickens, R., Primus, E., Pu, L. L., Quilles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward Moore, S., Warren, R., Washington, C., Watlingson, S., Wulliams, G., williamson, A., Wilcz, R., Wooden, S., Worley, K., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Virson, D., Virson, D., Virson, R., G., Wulliams, G., and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 10, 2002 this sequence version scales.
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Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 226303)
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of re
Assembly program: Phrap; version 0.990329
Consensus quality: 185950 bases at least 030
Consensus quality: 193076 bases at least 020
                                                                                                                                                                                                                                                                                                       Center project name: GCDF
Center clone name: CH230-7C10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Baylor College of Medicine
Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                 Project Information
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AUTHORS

\* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).

\* NOTE: This is a 'working draft' sequence. It currently

\* Consists of 51 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence soon as it is available and preserved. 1052 1152 2287 2387 2387 3434 3534 4615 4715 1051: contig of 1051 b 1151: gap of unknown 1 2286: contig of 1105 b 2386: gap of unknown 1 3433: contig of 1047 b 3533: gap of unknown 1 4614: contig of 1081 b 4714: gap of unknown 1 6581: contig of 1867 b 6681: gap of unknown 1 of 1051 bp in unknown length the accession number will bp in length bp in ģ length bp in length length in length length length length length

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Rattus norvegicus.
Rattus norvegicus
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Mammalia; Eutheria; i
Rattus.
1 (bases 1 to 137964)
Muzny,D.M., Adams,C.,
                                                                                                                                    AC126895 137964 bp DNA linear Rattus norvegicus clone CH230-301E4, *** SEQUENCING ***, 49 unordered pieces AC126895 AC126895 1 GI:21724040
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Rodentia;
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   Adio-Oduola, B.,
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                                                 Craniata; Vertebrata; I
Sciurognathi; Muridae;
   Ali-osman, F.R.,
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5117 others Length 226303;

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Gaps

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Euteleostomi;
; Murinae;

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rans of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence

accession number will

not known and their order in this sequence record is

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Falls, T. Ferraguto, D. Plagg, N. Ford, J. Estolid, C., Estolid, T. Ferraguto, D. Plagg, N. Ford, J. Frantz, P. Fantz, P. Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hennandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hennandez, O., Hodgson, A., Holloway, C., Hollins, B., Hennandez, O., Hober, J., Huber, J., Johason, R., Jollvet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Liu, W., Joulseged, H., Lozado, R., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R., Lucier, A., Lucier, R., Luna, R., Ma, J., Lozado, R., J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Lozado, R., Mapua, P., Martin, R., Martindale, A., Martinez, E., Mansey, E., Mawhiney, E., McLeod, M.P., Meagor, M., Mei, G., Metzker, M., Miner, G., Miner, S., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Paec, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shan, H., Shooshtard, M., Sisson, I., Shore, H., Shooshtard, M., Shoon, R., Wang, O., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Wulliamson, A., Warren, R., Washington, C., Watlington, S., Wulliamson, A., Waczyk, R., Wooden, S., Watlington, S., Wulliamson, A., Waczyk, R., Wooden, S., Nelson, D., Wulliamson, A., Waczyk, R., Wooden, S., Nelson, D., Wang, S., Shoo, H., Shooshtard, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-JUL-2002) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 137964)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 137964) Worley, K.C. Direct Submission
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                                                                                                                                                                                                                            Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 10
Assembly program: Phrap; version 0.5
Consensus quality: 89474 bases at 16a
Consensus quality: 93422 bases at 16a
Consensus quality: 96506 bases at 16a
NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 49 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: GZHG
Center clone name: CH230-301E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Baylor Co
Center code: BCM
Web site: http://
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---- Genome Center
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Sequence 17
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1 (bases 1 to 1734)
Botstein, D.A., Cohen, R.L., Goddard, A.D., Gurney, A
Lawrence, D.A., Levine, A.J., Pennica, D., Roy, M. Ann
WISP polypeptides and nucleic acids encoding same
                                                   Unknown
                                                              Unknown.
                                          Unclassified.
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
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83138: contig
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97339: contig
97439: gap of
103534: gap of
103634: gap of
107180: contig
107180: contig
115201: contig
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137964: contig
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Roy, M.Ann. and
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Mus musculus connective t
(Wisp2) mRNA, complete cd
AF100778.1 GI:4028578
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AR210325
AR210325.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 1734)
Pennica,D., Swanson,T.A., Welsh,J.W., Roy,M.A., Lawre
Lee,J., Brush,J., Taneyhill,L.A., Deuel,B., Lew,M., W
Cohen,R.L., Melhem,M.F., Finley,G.G., Quirke,P., Godd
Hillan,K.J., Gurney,A.L., Botstein,D. and Levine,A.J.
MISP genes are members of the connective tissue growt
family that are up-regulated in wnt-1-transformed cel
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90; Conserv
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Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurr
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,A
WISP polypeptides and nucleic acids encoding
Patent: US 6387657-A 18 14-MAY-2002;
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                 growth factor
                                        Goddard, A.D.,
     cells and
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                                                       Watanabe, C.,
                                                                                          Euteleostomi; 
; Murinae; Mus
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1 Wood, W.I.
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               Submitted (24-MAY-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: Clongerequest@sanger.ac.uk On May 25, 2002 this sequence version replaced gi:21213601. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a small overlap as described above.
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Way, South San Francisco, CA 94080, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/db_xref="G1:4028579"
/translation="MRGNPLIHLLAISFLCIDENVYSOLCPAPCACPWTPPOCPPGVP
/translation="MRGNPLIHLLAISFLCIDENVYSOLCPAPCACPWTPPOCPPGVP
LVLDGCGCCRVCARRLGESCDHLHVCDPSQGDVCLPGAGPSGRGAVCLFFEEDDGSCEV
MGRRYLDGETFKNCRVLCRCDDGGFTCLFLGSEDVRLPSWDCPRPRRIQVPGGCCPE
WYCDQAIWQPAIOPSSAGGHOLSALVTPASAGGPCPNWSTAWGPCSTTCGLGIATRVS
NONRFCQLEIQRRLCLSRPCLASRSHGSWNSAF"
a 491 c 495 g 393 t
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257. .1012
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/db_xref="taxon:10090"
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/note="transformed by Wnt-1"
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as follows unless otherwise noted: all
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Assembly program: XGAP4; version 4.5 Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 211865 bases at least Q40 Consensus quality: 213403 bases at least Q30 Consensus quality: 214139 bases at least Q20 Insert size: 214757; sum-of-contigs Insert size: 234243; 1.8% error; agarose-fp Quality coverage: 6.29x in Q20 bases; sum-of-con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBLO 15A, UK. E-mail enguiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 25, 2002 this sequence version replaced gi:18181793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL669906 216757 bp DNA linea Mus musculus chromosome 2 clone RP23-217C2, *** PROGRESS ***, 21 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
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                                                                                                                                                                                                                                                                                                                                                                                          Center project name: bM217C2
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE1; HTGS_CANCELLED
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134553 134652: gap of 100 bp in length 134653 141202: contig of 6550 bp in length 141203 141302: gap of 100 bp 101 length 141303 145808: contig of 4506 bp in length 145809 145908: gap of 100 bp 151572: gap of 100 bp 101 length 151673 151672: gap of 100 bp 101 length 151673 151678: gap of 100 bp 101 length 151673 150786: contig of 18014 bp in length 160887 160786: days of 100 bp 101 length 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160887 160
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119874 134552: contig of 14679 bp in length
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65990 66089; gap of 100 pp
66090 84635: contig of 18546 bp in length
84636 84735: gap of 100 bp
84736 87399: contig of 2664 bp in length
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4001 4100: gap of 100 bp
4101 15267: contig of 11167 bp in length
15268 15367: gap of 100 hm
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                                                       /note="assembly_fragment:03544
fragment_chain:1"
39772. .46360
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fragment_chain:1"
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fragment_chain:1"
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34970: contig of 19603 bp in length
35070: gap of 100 bp
35071: contig of 4601 bp in length
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460: gap of 100 bp
49809: contia ~f^^
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98601: contig of 11102 bp in length
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fragment_chain:3"
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49910...54509
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fragment_chain:6"
213978. .216757
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fragment_chain:5"
169787. .2000as
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51573 c 51904 g
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46461. .49809
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fragment_chain:4"
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fragment_chain:2"
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fragment_chain:6"
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fragment_chain:5" .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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Pred. No. 5.9e-38;
0; Mismatches 0;
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                                                                                               p mRNA linear ROD 12-OCT-1999
growth factor-like protein precursor
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AR210337
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AR210337
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J. Biol. Chem. 274 (24), 17123-17131 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1739)
Kumar,S., Hand,A.T., Connor,J.R., Dodds;R.A., Ryan,P.J., Trill,J.J., Fisher,S.M., Nuttall,M.E., @ipshutz,D.B., Zou,C., Hwang,S.M., Votta,B.J., James,I.E., Rieman,D.J., Gowen,M. and
                              AR210337.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (04-FEB-1999)
SmithKline Beecham, 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor-like cDNA from human osteoblasts encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification and cloning of a connective tissue growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee, J.C
                                                                                                                                                                                                        TGTCAGCCTGGGGCAGGCCC 499
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                                                          38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to the Mus musculus WISP-2 protein encoded by the sequence presented in GénBank Accession Number AF100778; putative growth factor; CTGF-L; contains IGF binding (IGFBD), Von Willebrand Factor type C (VWC) repeat and thrombospondin type I (TSP1) domains; member of the CCN (CTGF/Cyr61/Nov) family; lacks the fourth carboxy terminal (CT) domain present in other members of
                                                                                                                                                                                                                                                                                                                                          NGRRYLDGETFKPNORVLCRCDDGGFTCLPÅCSEDVRLPSWDCPRPRRIOVPGRCCPE
WVCDQAVMQPAIQPSSAQGHQUSALVTPASÅDGPCPNNSTAWGPCSTTCGLGIATRVS
NQNRECQLEIQRRLCLSRPCLASSRHGSWNSAE,"
480 c 489 g 395 t
                                                                                                                                                                                                                                                                                                                                                                                                   /protein_1d="AAD18058.1"
/db_xref="GI:4337060"
/translation="MRGNPLIHLAISFLCTISMVYSQLCPAPCACPWTPPQCPPGVP
LYLDGCGCCRVCARRLGESCDHLHVCDPSQGLVCQPGAGPSGRGAVCLFEEDDGSCEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 precursor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="connective tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Ctgfl"
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l. .1739
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/db_xref="taxon:10090"
                                                       from
                                                                                                                                                                                                                                                             4.7%; 5cc
100.0%; Pr
                                                         patent
                                                                                                                                                                                                                                                                  Score 80; DB; Pred. No. 3.7. 0; Mismatches
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Swedeland Rd., King of Prussia, PA
                                                         38 bp
6387657.
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3.7e-32;
hes 0;
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1 Similarity . 100.0%;
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Sequence
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1 (bases 1 to 841)

Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurn Lawrence,D.A., Levine,A.J., Pennica,D., Roy,MISP polypeptides and nucleic acids encoding Patent: US 6387657-A 39 14 MAY 2002;
                                                                                                                                                                                                                                                                                                                                                                               Similarity
32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wisp polypeptides and nucleic acids encoding same Patent; US 6387657-A 38 14-MAY-2002; Location/Qualifiers
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1 (bases 1 to 738)

Botstein,D.A., Cohen,R.L., Goddard,A.D.,
Lawrence,D.A., Levine,A.J., Pennica,D., 1
                                                                   Polypeptidic compositions and method Patent: WO 0105836-A 31 25-JAN-2001;
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1266)
                                                     Genentech, Inc. (US)
                                                                                                           Botstein, D., Goddard, A.,
                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                             AX076919.1
                                                                                                                                                                                                                                                      AX076919
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                                                                                                Wood, W.I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="unknown"
297 c 280 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
272 c 238 g
/organism="Homo sapiens"
/db_xref="taxon:9606"
                              1. .1266
                                        Location/Qualifiers
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                       1266 bp
WO0105836.
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US 6387657.
                                                                                                           Gurney, A.L.,
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1.3e-05;
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                                                                                 treatment of
                                                                                                             Roy, M.A.
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d Wood, W.I.
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AX464186
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1283)

Kumar,S., Hand,A.T., Connor,J.C., Dodds,R.A., Ryan,P.J.,

Trill,J.G., Fisher,S.M., Slemmon,J.R., Lipshutz,D.B.,

Bartholomew,V., James,I.E., Rieman,D.J., Gowen,M. and Lee,J.C.

Identification and cloning of CTGF-L from human osteoblasts, a novel cysteine rich protein containing an IGF binding domain Bone 23 (5), S240 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E., Gao,W.G., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K., Wood,W.L. and Zhang,Z.

Secreted and transmembrane polypeptides and nucleic acids encoding
Direct Submission
Direct Submission
Submitted (11-AUG-1998) Bone & Cartilage Biology, UW 2109,
Submitted (19-AUG-1998) Bone & Cartilage Biology, UW 2109,
SwithKline Beecham, 709 Swedeland Road, King of Prussia, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                              Kumar,S
                                                                                                                                                                                                                                                                                                                                          AF083500 1283 bp mRNA linear Homo sapiens connective tissue growth factor-like
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/db_xref="taxon:9606"
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Search completed: July 28, 2003, 21:14:39 Job time: 4755.55 secs
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/db_xref="GI:3465836"
/translation="MRGTPKTHLLAFSLLCLLSKVRTQLCPTPCTCPWPPPRCPLGVP
LVLDGCGCCRVCARRLGEPCDQLHVCDASQGLVCQPGAGPGGRGALCLLAEDDSSCEV
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/db_xref="taxon:9606"
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100.0%; Pr
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

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## ALIGNMENTS

RESULT 1 AAZ07516 AA207516 standard; cDNA; 1708

BP

AAZ07516;

26-NOV-1999 (first entry)

Rat HICP polypeptide encoding cDNA

Heparin-induced CCN-like protein; HICP; cell-associated activity; ss; cardiovascular disorder; aberrant cell proliferation; fibrotic disorder.

Rattus sp.

WO9947556-A2

23-SEP-1999

18-MAR-1999; 99WO-US05999

19-MAR-1998; 98US-0044273

(TUFT ) TUFTS COLLEGE.

Castellot JJ;

WPI; 1999-562060/47. P-PSDB; AAY27434.

Nucleic acid sequences encoding rat heparin-induced CCN-like protein, used in methods to identify modulators or in diagnostic applications

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Matches 1708; Conserv
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                                                      TGCGGCTGCCCAGCTGGGACTGCCCAACGACGACAAGAAGAAGAAGACAGTGCCAAGAAAAGACTGCT
                                                                                                                    CTGTCAGCTTGTCCTAAAGTCTTAGCACTTGTGGTGGCTTGGGCTTCACACACTGTCAGA
                       GCCCCGAGTGGGTATGTGACCAGGGAGTGACACCGGCGA∯CCAGCGCTCCACGGCGCAAG
                                                                                     GGAGGCTGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCAGCCCAGGGCCTGGTTT
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Best Local Similarity

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                                                                                                                                     gene
19-SEP-2001;
                          28-MAR-2002
                                                                                                          osteopenia;
                                                                                                                         bone
                                                                                                                                                                                                            17-JUL-2002
                                                                                                                                                                                                                                                                  ABL59575 standard;
                                                    WO200224943-A2
                                                                                                                    OST; osteoregenerative; parathyroid hormone; tibiae; osteopathic; therapy; parathyroid hormone receptor ligand; bone disorder; formation disorder; bone resorption disorder; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 CCCCTGGTGCTGGATGGCTGTGGGCTGCTGTAAAGTGTGTGCACGGAGGCTGGGGGGAGTCC
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                                                                                                                                                                                                                                                                                                                                                                                          GACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAG#GCTGCCCCGAGTGGGTATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCCGCAGGTACCTGGATGGAGAGACCTTTAAACCCAAT#GCAGGGTCCTGTGCCGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCGACCACCTGCATGTCTGCGACCCCAGCCAGGCCTGGTTTGTCAGCCTGGGGCAGGC
                                                                                                                                                                                                                                                                                                                                     AGCTCATGGAACAGTGCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCAAGGACACCAACTTTCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACCAGGGAGTGACACCGGCGATCCAGGGCTCCACGGCGCGAAGGACACCAACTTTCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGACGGTGGCTTCACCTGCCGGCTGTGCAGTGAGGATGTGCGGCTGCCCAGCTGG
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                                                                                                                                                                               gene fragment SEQ ID
                                                                                                          osteopetrosis; gene;
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2001WO-US29548
                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                         entry)
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                                                                                                                                                                                                                                                                                                                                                    DЬ
                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC test cell population (CP) comprising cells expressing nucleic acid sequences (S) of OSTI-47 and 48, with a test agent, measuring nucleic acid companies of the ligand and agent by the difference in expression levels. Also described is a method (M2) for treating a bone disorder in a subject by administering to the subject an agent that modulates the expression or companies to the subject an agent that modulates the expression or companies that modulates the expression or companies that modulates the expression or companies to its modulate the expression of OST 1-48, and can also be used to modulate the expression of OST 1-48, and can also be used in gene companies (M) is useful for identifying parathyroid hormone receptor ligands (I) or osteoregenerative agents. OST gene sequence can be used for assessing the osteoregenerative activity of a test agent in a companies of companies of a treatment of a bone disorder in a companies to raise anti-OST antibodies (II). Parathyroid hormone receptor ligands: (I) identified by (MI) are useful for treating bone companies. The present sequence represents an OST23 gene fragment contained from rat tibiae, from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 404; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method (M1) for identifying parathyroid hormone receptor ligands (I) and osteoregenerative agents by contacting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 45; Page 22; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying parathyroid hormone receptor ligands and osteoregenerative
agents involves detecting the expression of nucleic acids which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Horesovsky GJ,
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(GLAX ) GLAXO GROUP I
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                                                                                                                                                                                181
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           361
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                                                                                                                                                                                                                                    TCTGGCAGGCCAGGGCCTTTCTCTTCAGCATGAGAAAGACAAGGG
                                                                                CTTTGTATTTTCAGGAATGCACATCTCTTAAGCACTCGCAAAACAGGAAGGCTCCACACC 1609
                                                                                                                                     GAACATGAAGAGATGAATCACACTGTCCTTAAGAAATTCCTGAAAGTCCAGGAACTTGAG
                                                                                                                                                                                                                                                                                                                                                   GAACATGAAGAGATGAATCACACTGTCCTTAAGAAATTCCTCAAAGTCCAGGAACTTGAG
                                                                                                                                                                                CTTCCCTGACCTGAGAACACCCTGCCTGCTCGGGAAGTATTCAGGGGCAGAATTCTCTGT
                                                                                                                                                                                              CTTCCCTGACCTGAGAACACCCTGCCTGCTCGGGAAGTATTCAGGGGCAGAATTCTCTGT
                                                                                                                                                                                                                                                                                             ACCGTGCTGGGGATAAGGTCAATGTTAGGACCAGACAGCAGATTGCCTGAAACTTCCAAT
                                                                                                                                                                                                                                                                                                                        ACCGTGCTGGGGATAAGGTCAATGTTAGGACCAGACAGCAGATTGCCTGAAACTTCCAAT
           TCTGGCAGGCCAGGGCCTTTCTCTTCAGCATGAGAAAAGACAAGGG
                                                                   CTTTGTATTTCAGGAATGCACATCTCTTAAGCACTCGCAAAACAGGAAGGCTCCACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Noel LS,
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                                                                                                                                                                                                                                                                                                                                                                                                                      20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; 108 C; 99 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 354;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                       ; DB 24; Length 439;
4e-162;
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                       1654
                                                                                                                                                                                                                                                                                                                                                                                                            0;
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1549

240

300

360

1489

1429

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180

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RESULT 5
AAZ07519
В
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Best Local
                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                The invention provides a rat heparin-induced CCN-like protein (HICP) protein. Agents that stimulate or inhibit HICP protein activity or expression, antisense HICP nucleic acid molecules and HICP antibodies, can be used to modulate cell-associated activity. HICP modulators can be used to treat disorders characterized by abberrant HICP protein activity or expression. Probes capable of hybridizing to HICP make or antibodies specific for HICP can be used to detect HICP activity in a biological sample. HICP can be used to treat disorders, such as a cardiovascular or fibrotic disorder, characterized by aberrant cell proliferation. The present sequence represents a nucleotide sequence encoding the insulinlike growth factor binding protein (IGFBP) domain of HICP polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heparin-induced CCN-like protein; HICP; cell-associated activity; cardiovascular disorder; aberrant cell proliferation; fibrotic diinsulin-like growth factor binding protein; IGFBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used
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                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 104; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TUFT
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DB; AAY27438.
                         498
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 181
                                                   121
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                                                                                                                                                                                                           210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid sequences encoding rat heparin-induced CCN-like protein, methods to identify modulators or in diagnostic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TUFTS
                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                               210
                                                                                                                                                     TGCGACCACCTGCATGTCTGCGACCCCAGCCAGGCCTGGTTTGTCAGCCTGGGGCAGGC
                                                                                                    CCCCTGGTGCTGGATGGCTGTGGGCTGTAAAGTGTGTGCACGGAGGCTGGGGGAGTCC
                                                                                                                CCCCTGGTGCTGGATGGCTGTGGCTGTAAAGTGTGTGCACGGAGGCTGGGGGGAGTCC
                                                                                                                                                                                CAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAGTGCCCACAGGGGGGTA
CCTGGCGGCCATGGGGCTGTGTCTCTTG
                        CCTGGCGGCCATGGGGCTGTGTGTCTCTTG 527
                                                  TGCGACCACCTGCATGTCTGCGACCCCAGCCAGGCCTGGTTTGTCAGCCTGGGGCAGGC
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                             BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0044273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US05999
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                                                                                                                                                                                                                   Score 210;
Pred. No.
                                                                                                                                                                                                                                                            74 G;
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                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                            44 T; 0 other;
                                                                                                                                                                                                        6.2e-92;
210
                                                                                                                                                                                                                                    DB 20;
                                                                                                                                                                                                                                 Length 210;
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disorder;
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                                                  180
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RESULT

26-NOV-1999 AAZ07520;

(first entry)

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AAZ07518
ID AAZ0
                                                                 RESULT 7
AAZ07520
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Best Local
                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                    The invention provides a rat heparin-induced CCN-like protein (HICP) protein. Agents that stimulate or inhibit HICP protein activity or expression, antisense HICP nucleic acid molecules and HICP antibodies, can be used to modulate cell-associated activity. HICP modulators can be used to treat disorders characterized by abservant HICP modulators can be used to reapression. Probes capable of hybridizing to HICP mRNA or antibodies specific for HICP can be used to detect HICP activity in a biological sample. HICP can be used to treat disorders, such as a cardiovascular or fibrotic disorder, characterized by aberrant cell proliferation. The present sequence represents a CDNA encoding the Von Willebrand C (VWC) a domain of the HICP polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heparin-induced CCN-like protein; HICP; cell-associated activity; ss; cardiovascular disorder; aberrant cell proliferation; fibrotic disorder; Von Willebrand C domain; VWC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid sequences encoding rat heparin-induced CCN-like protein, used in methods to identify modulators or in diagnostic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-562060/47.
P-PSDB; AAY27436.
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                                                  AAZ07520 standard;
                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Castellot JJ;
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177; Conserv
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                                                                                                                                                                                           CTGTGCCGCTGTGATGACGGTGGCTTCACCTGCCTGCCGCTGTGCAGTGAGGATGTGCGG
                                                                                                                                                                                                                                                                                                                                               177
                                                                                                                                   CTGCCCAGCTGGGACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGC 722
                                                                                                                       CTGCCCAGCTGGGACTGCCCACGCCCCAAGAGAATACAGGTGCCAGGAAAGTGCTGC
                                                                                                                                                                             CTGTGCCGCTGTGATGACGGTGGCTTCACCTGCCTGCCGCTGTGCAGTGAGGATGTGCGG
                                                                                                                                                                                                                                    TGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAACCCCAATTGCAGGGTC
                                                                                                                                                                                                                                                            TGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAACCCAATTGCAGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 103;
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                               BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0044273
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                                                                                                                                                                                                                                                                                                                                             35 A; 47 C; 60 G;
                                                   cDNA; 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                   10.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177
                                                                                                                                                                                                                                                                                        Score 177; DB; Pred. No. 7.5
                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
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                                                                                                                                                                                                                                                                                                                                               35 T;
                                                                                                                                                                                                                                                                                        DB 20;
7.5e-76;
hes 0;
                                                                                                                                                                                                                                                                                                                                               0 other;
                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                        0;
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RESULT 8
AAX76489,
ID AAX7
XX
AC AAX7
XX
AC AAX7
XX
DT 06-A
XX
DE Mous
XX
KW WNT-
KW Conn
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                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 174
                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides a rat heparin-induced CCN-like protein (HICP) protein. Agents that stimulate or inhibit HICP protein activity or expression, antisense HICP nucleic acid molecules and HICP antibodies, can be used to modulate cell-associated activity HICP modulators can be used to treat disorders characterized by aberrand HICP protein activity or expression. Probes capable of hybridizing to HICP mRNA or antibodies specific for HICP can be used to detect HICP activity in a biological sample. HICP can be used to treat disorders, such as a cardiovascular or fibrotic disorder, characterized by aberrant cell proliferation. The present sequence represents a nucleotide sequence encoding the thrombospondin 1 (TSP1) domain of the HICP polypeptide.
                                                                            06-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 105; 108pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-562060/47.
P-PSDB; AAY27439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Castellot JJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombospondin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heparin-induced CCN-like cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat HICP TSP1
              connective
                          WNT-1 induced secreted protein; WISP-1; WISP-2;
                                                   Mouse
                                                                                                                           AAX76489 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TUFT ) TUFTS
                                                                                                                                                                                                               945
                                                                                                                                                                                                                                                                                                             825
                                                                                                                                                                                         121
                                                                                                                                                                                                                                                               885
                                                                                                                                                                                                                                                                                                                                     174;
                                                 WISP-2 protein complementary nucleotide sequence
                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                      _
                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid sequences encoding rat heparin-induced CCN-like protein, methods to identify modulators or in diagnostic applications
                                                                                                                                                                                     GCCACCCGAGTGTCCAACCAGAACCGATTCTGCCAACTGGAGATCCAACGCCGCCTGTGT
                                                                                                                                                                                                                                                                                    CCTTGTCCAAATTGGAGCACAGCCTGGGGCCCCTGCTCAACCACCTGTGGGCTGGGCATA
lymphoid malignancy: F
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                      BP;
                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain
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                                                                                                                                                                                                                                                                                                                                                                                     36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain;
                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                     A; 62 C;
                                                                                                                                                                                                                                                                                                                                                10.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; HICP; cell-ass@ciated activity; ss;
aberrant cell prolifera@lon; fibrotic disorc
                                                                                                                                                                                                                                                                                                                                   Score 174; DB; Pred. No. 2.2.0; Mismatches
                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                     45 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA
  haematopoiesis-related
               cancer; melanoma;
                                                                                                                                                                                                                                                                                                                                                                                     31 T;
                                                                                                                                                                                                                                                                                                                                             2.2e-74;
                                                                                                                                                                                                                                                                                                                                                                                     0 other;
                                                                                                                                                                                                                                                                                                                                                            DB 20;
                                                                                                                                                                                                                                                                                                                                     0
                          WISP-3; CTGF; tumour;
                                                                                                                                                                                                                                                                                                                                                           Length 174;
                                                                                                                                                                                                                                                                                                                                     Indels
               arteriosclerosis;
  disorder
                                                   SEQ ID
                                                                                                                                                                                                                                                                                                                                     0;
                                                   NO:18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorder;
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                                                                                                                                                                                        174
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RESULT 9
AAX76488
ID AAX7
XX
AC AAX7
XC AAX7
XX
DT 06-A
XX
MOUS

AAX76488 standard;

DNA;

1734

06-AUG-1999

(first entry)

Mouse WISP-2 protein nucleotide sequence

SEQ

ij

NO:17

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                                                                                                                                                                                                                                                                CC The present invention describes Wnt-1 induced secreted polypeptides, CC WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 CC and WISP-3 have homology to connective tissue growth factor (CTGF). CC Products from the present invention can be used to treat WISP-related CC products can be used to treat arteriosclerosis. The products can also be used to treat other diseases e.g. benign and malignant tumours, CC leukaemia and lymphoid malignancies, neuronal, glial, astrocytal, CC hypothalamic and other glandular, macrophagal, epithelial, stromal, and CD hlastocoelic disorders, haematopoiesis-related disorders, tissue-growth CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney CC disorders, bone-related disorders such as osteoporosis, trauma such as CC burns, incisions, and other wounds, connective tissue disorders. The products can also be used for detertion and diamnosis esnociality of products can also be used for detertion and diamnosis esnociality of
                                                                                                               Matches
                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-APR-1998;
29-OCT-1997;
03-FEB-1998;
                                                                                                                                                                                                              products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The products can be used in the production of transgenic or knock-out animals. Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion; kidney disorder; bone-related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation; testicular-related disorder; angiogenesis; immunological disorder; ss
                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 179-180; 284pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Botstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-OCT-1998;
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                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolated Wnt-1 induced secreted polypeptides, WISP-1,
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532
                         470
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                                                                                                                              Similarity
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                                                    GGGCCTGGTTTGTCAGCCTGGGGCAGGCCC 499
                                                                                                            5.3%;
ilarity 100.0%;
Conservative
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Levine AJ,
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97US-0063704.
98US-0073612.
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                                                                                                                                                                      Α,
                                                                                                                                                                       229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goddard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pennica
                                                                                                                                                                      c;
                                                                                                               0;
                                                                                                                              Score 90;
Pred. No.
                                                                                                                                                                       238
                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 A,
                                                                                                                                                                      G; 127
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Roy MA,
                                                                                                                                            DB
                                                                                                                              1.9e-33;
                                                                                                                                                                       T; 0
                                                                                                                                            20;
                                                                                                                                                                         other;
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                                                                                                                                         Length 753;
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Wood WI;
                                                                                                                 Indels
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ABN30189
ID ABN3
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Best Local S
Matches 90
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Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour; connective tissue growth factor; cancer; melanoma; arteriosclerosis; leukaemia; lymphoid malignancy; haematopoiesis-related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion; kidney disorder; bone-related disorder; osteoporosis; trauma; burn; kidney disorder; bone-related disorder; osteoporosis; trauma; burn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-1999
                ABN30189
                                                                                                                                                                                                                                                                                         Sequence 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Wnt-1 induced secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
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29-OCT-1997;
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testicular-related disorder; angiogenesis; in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1999-337420/28
                                                                                               478
                                                                                                                             470
                                                                                                                                                             418
                                                                                                                                                                                             410
                                                                                                                                                                                                                            90;
                                                                                                                                                                                                                                          Similarity
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                standard; DNA;
                                                                                                                                                                          AGTGTGTGCACGGAGGCTGGGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGCCA 469
                                                                                                                             GGGCCTGGTTTGTCAGCCTGGGGCAGGCCC 499
                                                                                                                                                         AGTGTGCACGGAGGCTGGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 178-179;
                                                                                                                                                                                                                         5.3%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                         BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cohen RL,
Levine AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0081695.
97US-0063704.
98US-0073612.
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                                                                                                                                                                                                                                                                                         355 A; 491 C; 495 G;
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Pennica D,
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                          Score 90; pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roy MA,
                                                                                                                                                                                                                                                                                         393 T; 0
                                                                                                                                                                                                                                                         DB 20;
                                                                                             507
                                                                                                                                                                                                                                            1.9e-33;
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                                                                                                                                                                                                                                                      Length 1734;
                                                                                                                                                                                                                                                                                         other;
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                                                                                                                                                                                                                         Gaps
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RESULT 11 ABA72245 ID ABA72 XX

ABA72245

standard; DNA; 199

ВP

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0;

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QΥ
                                                                                                                                                               messenger NNAs that populate a (sub-)transcriptome, where the CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises comprises several oligonucleotides, each capable of hybridising selectively to a comprise of the genome, which encodes one or more messenger RNAs plice variants. The oligonucleotide libraries are useful for detecting mnNas from a companient of the penome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mnNas from a companient of the corresponding transcriptome, and in companient transcripts and splice variants of human or animal companient transcripts and splice variants of human or animal companient to detect transcripts of a sub-transcriptome under a companient to detect transcripts of a sub-transcriptome under a companient to detect developmental specific genes such as those genes conjugated in specific tissue under a specific pathological conjugated in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABNS9589 represent colliponucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.

CC N.B. The sequence data for this patent did not form part of the printed control of the printed control of the printed of the printed control of the printed of the printed of the printed of the printed control of the printed of the printed control of the printed control of the printed of the print
                                                                                Matches
                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developmental-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-2000;
02-MAY-2001;
                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes oligonucleotide libraries for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID 2937; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COMP-) COMPUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-2002
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                                                                                                   Local
                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                        1559
                                                                                54;
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                                                                                                   Similarity
TTCAGGAATGCACATCTCTTAAGCACTCGCAAAACAGGAAGGCTCCACACCTCT 1612
                                                                                                                                                               65
                                                                                                                                                               BP;
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                                                                              Conservative
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2001US-287724P
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                                                                                                                                                               21 A;
                                                                                                                                                               20 C;
                                                                                                                      3.2%;
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                                                                              0;
                                                                                                                                                               13 G; 11 T; 0 other;
                                                                                                 Score 54;
Pred. No.
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                                                                                Mismatches
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                                                                                                                      DB 24;
                                                                                                 6.7e-16;
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                                                                                                                      Length 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA transcript;
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                                                                                Indels
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                         congenital
                                                                                                           Human; gene expression; heart; microan cardiovascular disease; hypertension;
                                                                                                                                                                                  Probe
                                                                                                                                                                                                                                                                                                                   ABA38112 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human
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                                            Homo sapiens
                                                                                                                                                                                                                            23-JAN-2002
                                                                                                                                                                                                                                                                        ABA38112;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome-derived single exon nucleic acid probes useful ing gene expression in human fetal liver.
                                                                                                                                                                               #16578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            foetal liver single exon nucleic acid probe #20550.
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                                                                                         heart
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2000US-0207456.
2000US-0608408.
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2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 32 A; 65 C; 73 G;
                                                                                                                                                                             for gene expression
                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO 20550; 639pp + sequence listing; English.
                                                                                         disease;
                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.9%;
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                                                                                                           heart; microarray; vascular system;
hypertension; cardiac arkhythmia;
                                                                                                                                                                                                                                                                                                                     199
                                                                                         88
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3.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                 160
                                                                                                         arrhythmia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 199;
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                                                                                                                                   probe;
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WO200157274-A2

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                                                                                                                                                                                                                                                                                                                                                                                             present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from human heart from the human heart via microarrays. By measuring gene expression, probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular spe.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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hearts
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                                                                                                                              Human; brain expressed e microarray; Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn
                                       30-JAN-2001;
                                                           09-AUG-2001
                                                                               WO200157275-A2
                                                                                                  Homo sapiens
                                                                                                                     epilepsy;
                                                                                                                                                              Human
                                                                                                                                                                                 05-NOV-2001
                                                                                                                                                                                                     AAK20667;
                                                                                                                                                                                                                        AAK20667 standard;
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4;
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27-SEP-2000;
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                                                                                                                                                            brain expressed single
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32; Conserv
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                                                                                                                      cancer;
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; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                       32 A;
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                                                                                                                                          exon;
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                                                                                                                               disease;
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Pred. No.
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                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                       73 G;
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                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                               e expression analysis; probe;
multiple sclerosis; schizophrenia;
                                                                                                                                                            probe
                                                                                                                                                                                                                                                                                                                                                      29 T;
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Matches 32
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26-MAY-2000;
30-JUN-2000;
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
               Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human bone marrow - \,
                                                                                                              Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single
brains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human bone marrow expressed
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27-SEP-2000;
                                                                                                                                                                                                                                            03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK46811 standard;
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                                                                                                                                                                                                                         -SEP-2000;
                                                                       2001-488900/53
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L Similarity 100.0%;
32; Conservative
                                                                                                                                               MOLECULAR DYNAMICS INC
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cancer; leukaemia; lymj
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2000US-0024263.
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26-MAY-2000;
30-JUN-2000;
                                                                 microarray, which can be used for measuring human gene expression in sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the print specification, but was obtained in electronic format directly from WI
                                                                                                                                                                                                                The present invention relates to human single exon nucleic acid probe (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cance such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                           at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                analyzing
                                                                                                                                                                                                                                                                                                                                                                                               Human
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21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe #15682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                     SEQ
                                                                                                                                                                                                                                                                                                                                                                gene expression
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                ID No 15682; 487pp;
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Pred. No.
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1: /cgn2_6/ptodata/1,
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3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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US-09-213-768-1
US-09-182-145-110
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RESULT 2
US-09-182-145-18/c
; Sequence 18, Application US/09182145B
; Patent No. 6387657
; GENERAL INFORMATION:
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TTGTCA	ACGGAG         ACGGAG	5.39 100.0 vative	JUCANT: COhen, Robert LICANT: Goddard, Austry LICANT: Gurney, Austrin L. LICANT: Hillan, Kenneth J. LICANT: Levine, Arnold J. LICANT: Levine, Arnold J. LICANT: Pennica, Diane LICANT: Pennica, Diane LICANT: Wood, William I. LICANT: Wood, William I. LIE OF INVENTION: WISP POLXF LE REFERENCE: P1176R2 REENT APPLICATION NUMBER: US REENT APPLICATION NUMBER: US LIER APPLICATION NUMBER: US LIER FILING DATE: 1998-10-2 LIER FILING DATE: 1998-02-0 LIER APPLICATION NUMBER: US LIER APPLICATION NUMBER: US LIER FILING DATE: 1998-04-1 HER OF SEQ ID NOS: 156 ID NO 17 ID N	lon US		2517 2517 2517 3280 3865 6803 6803 7874	933 1308 1491 1743 1743 1743 1797 1821 1974 2329 2329 2329
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GGGCCTGGTTTGTCAGCCTGGGGCAGGCCC 499	AGTGTGTGCACGGAGGCTGGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGCCAG	Score 90; DB 4; Length; Pred. No. 1.9e-34; 0; Mismatches 0; Inde	ANT: Cohen, Robert ANT: Goddard, Audrey ANT: Goddard, Austin L. ANT: Hillan, Kenneth J. ANT: Lawrence, David A. ANT: Levine, Arnold J. ANT: Levine, Arnold J. ANT: Wood, William I. OF INVERTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS EFERENCE: P1176R2 EFERENCE: P1176R2 T APPLICATION NUMBER: US/09/182,145B T FILING DATE: 1998-10-29 R APPLICATION NUMBER: US 60/063,704 R FILING DATE: 1997-10-29 R APPLICATION NUMBER: US 60/063,704 R FILING DATE: 1998-02-04 R APPLICATION NUMBER: US 60/073,612 R FILING DATE: 1998-02-04 R APPLICATION NUMBER: US 60/081,695 R FILING DATE: 1998-04-14 NO 17 H: 1734 DNA ISM: Mus musculus -145-17	/09182145B A.	ALIGNMENTS	US-08-987-743-16 US-08-916-935-4 US-09-484-970B-43 US-09-149-476-296 US-08-665-259-19 US-08-762-500-19 US-08-762-500-19	US-08-987-743-1 US-08-987-743-5 US-09-62-249A-3 US-08-665-259-20 US-08-762-500-20 US-09-149-476-90 US-08-762-500-78 US-08-455-559-9 US-09-145-060-9 PCT-US94-00657-9
		1734; lels 0; Gaps	ENCODING SAME			16, 43, 19, 19, 19,	Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 20, Appl Sequence 20, Appl Sequence 90, Appl Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli
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\PPLICANT: Botstein, \PPLICANT: Cohen, Ro

Robert

David A

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                                            ; ORGANISM: Homo sapiens
US-09-182-145-38
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Hilan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
                                                                                                     SEQ ID NO 38
LENGTH: 738
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LENGTH: 1734
  Query Match
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CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER APPLICATION NUMBER: US 60/081,695
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CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
                                                                                                                                                                 EARLIER APPLICATION NUMBER: US 60/081,695 EARLIER FILING DATE: 1998-04-14
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APPLICANT: WOOd, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
                                                                                                                                                                                                                                                                                                                                RPPLICANT: ROY, MATGATEL ANN
APPLICANT: WOOD, WIlliam I.
ITTLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
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RESULT 5
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SEQ ID NO 39
LENGTH: 841
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NAME/KEY: misc_feature
LOCATION: 1-841
OTHER LINFORMATION: Sequence is synthesized
Patent No. 6387657
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                                                                               APPLICANT:
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APPLICANT: Wood, William I.
TITLE:OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
FILE REFERENCE: P1176R2
                           APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC
                                                                                                            APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
                                                                                                                                                               APPLICANT: Cohen, Robert APPLICANT: Goddard, Audr
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 CURRENT
             FILE REFERENCE: P1176R2
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NO. 6387657
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APPLICATION NUMBER: US/09/182,145B
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32; Conserv
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Pennica, Diane
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100.0%;
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; ORGANISM: Homo sapiens
US-09-182-145-13
                                                                                                                                        US-09-182-145-117
                                                                                                                                                              RESULT 7
                                                                                       Sequence 117, Application US/09182145B Patent No. 6387657 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 14
LENGTH: 1293
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SEQ ID NO 13
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APPLICANT: Botstein, David A. APPLICANT: Cohen, Robert APPLICANT: Goddard, Audrey APPLICANT: Gurney, Austin L. APPLICANT: Hillan, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-04-14
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CURRENT FILING DATE: 1998-10-29
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APPLICANT: WOOD, William I.
ITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cohen, Robert
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RESULT 8
US-09-385-982-220/c
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LENGTH: 51
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Best Local
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/385,9 CURRENT FILING DATE: 1999-08-30 EARLIER APPLICATION NUMBER: 09/328,111 EARLIER FILING DATE: 1999-06-08 EARLIER APPLICATION NUMBER: 60/117,393 EARLIER FILING DATE: 1999-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/182,145B CURRENT FILING DATE: 1998-10-29 EARLIER APPLICATION NUMBER: US 60/063,704 EARLIER FILING DATE: 1997-10-29 EARLIER APPLICATION NUMBER: US 60/073,612 EARLIER FILING DATE: 1998-02-04 EARLIER FILING DATE: 1998-02-04 EARLIER APPLICATION NUMBER: US 60/081,695 EARLIER FILING DATE: 1998-04-14
                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: 60/098,639 EARLIER FILING DATE: 1998-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(616)
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                                                                                                                                                                                                                                      LENGTH: 61
TYPE: DNA
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617 TGATGACGGTGGCTTCACC 635
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Levine, Arnold J.
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RESULT 9 US-09-149-476-225/c Sequence 225, Appl

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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/02
RR FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/03
R FILING DATE: 1997-08-22
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R FILING DATE: 1997-08-22
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FILING DATE:
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APPLICATION NUMBER:
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/043,311
FILING DATE: 1997-04-11
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GENERAL INFORMATION:
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APPLICANT: Brenda F. Baker
APPLICANT: Lex M. Cowsert
APPLICANT: Lex M. Cowsert
FILE OF INVENTION: ANTISENSE MODULATION OF SENTRIN EXP
FILE REFERENCE: RTS-0026
CURRENT APPLICATION NUMBER: US/09/213,768
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 47
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APPLICATION NUMBER: 60/1
FILING DATE: 1997-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/043,576 FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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19; Conserv
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ilarity 100.0%;
Conservative (
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: 1997-08-22
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: 1997-10-02
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1997-04-11
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Pred. No.
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; LOCATION: (130)..(1539)
US-09-668-680-13
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; LOCATION: (136)..(441)
US:09-213-768-1
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Best Local S
Matches 19
                                                                                                                  Sequence 2, Application US/09213768 Patent No. 5985664 GENERAL INFORMATION:
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SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 13
            APPLICANT: Brenda F. Baker
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTIGENSE MODULATION OF SENTRIN EXPRESSION
FILE REFERENCE: RTS-0026
FULE REFERENCE: RTS-0026
CURRENT APPLICATION NUMBER: US/09/213,768
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Xu, Chongjun
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6436703el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 790CIP2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/668,680 CURRENT FILING DATE: 2000-09-22 PRIOR APPLICATION NUMBER: 09/649,167 PRIOR FILING DATE: 2000-08-23
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                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1539
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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19; Conserv
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6436703
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Wang, Jian-Rui
Xue, Aidong J.
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Xu, Chongjun
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; DATABASE ACCESSION NUMBER: L07860 ; DATABASE ENTRY DATE: 1993-11-02 . US-09-313-930-1
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OTHER INFORMATION: PCR Primer US-09-213-768-2
                               RESULT 15
US-08-259-451-10
                                                                                              В
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US-09-313-930-1/c
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Best Local Similarity
Matches 18; Conserv
Sequence 10, Application US/08259451 Patent No. 6406841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dean, Nicholas M.
TITLE OF INVENTION: Antisense Oligonucleotide Modulation
TITLE OF INVENTION: Kinase C-delta Expression
FILE REFERENCE: ISPH 0357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (59)..(2089)
PUBLICATION INFORMATION:
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NAME/KEY: CDS
LOCATION: (59)
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                                                                                                                                                                                                                                                                    ISSUE: 2
PAGES: 171-181
DATE: 1993-08-19
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                                                                                                                                                                                                                                                                                                                                                    TITLE: Molecular and biochemical characterization of a TITLE: recombinant human PKC-delta family member
                                                                                                                                                                                                                                                                                                                      /OLUME: 1174
                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS: Burns, D.
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                                                                                                                                                                                                                                                                                                                                     JOURNAL: Biochim. Biophys. Acta
                                                                                              1185 GCAGAGTACTCTCCTCTG 1168
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Loomis, C. R.
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Basta, P. V.
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Rankl, N. B.
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Ballas, L. M.
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100.0%; Pred. No.
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Patent No. 6406841 GENERAL INFORMATION:

APPLICANT:

Lee, Helen Swanson, Pı

Priscilla A.

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
MEDIUM TYPE: storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOSTWARE: WOODPERCT: STORAGE
OPERATING SYSTEM: MS-DOS
SOSTWARE: WOODPERCT: US/08/259,451
FILING DATE: 20-JUN-1994
CLASSIFICATION NUMBER: US/08/259,451
FILING DATE: 20-JUN-1994
CLASSIFICATION NUMBER: US/08/086,415
FILING DATE: 01-JUL-1993
ATTORNEY/ACENT IMFORMATION:
NAME: Daniel W. Collins
REGISTRATION NUMBER: 31,912
REFERENCE/DOCKET NUMBER: 5381.US.P1
TELEPHONE: (708) 937-6365
TELEFAX: (708) 938-2623
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2949 base pairs
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
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Search completed: July 28, 2003, 15:58:52 Job time: 94.3356 secs
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                                                                                                                                                   Query Match 1.1%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 32 Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064
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APPLICANT:
APPLICANT:
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APPLICANT: Tate, Cynthia
TITLE OF INVENTION: HTLV-IINRA Compositions
TITLE OF INVENTION: and Assays for Detecting HTLV Infection
NUMBER OF SEQUENCES: 19
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                                                                           Peterson, Bryan
Edwards, Michelle
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Johnson, Joan E.
Motley, Cheryl T.
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Chan, Emerson W.
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Rosenblatt, Joseph D.
Chen, Irvin S. Y.
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('ggn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

('ggn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

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//cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq3:*
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US-10-010-408-10
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## ALIGNMENTS

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Sequence 1, Application US/10010408

Publication No. US20020165185A1

GENERAL INFORMATION:
APPLICANT: John J. Castellot, Jr.
APPLICANT: John J. Castellot, Jr.
APPLICANT: John J. Castellot, Jr.
TITLE OF INVENTION: No. US20020165185A1el Heparin-Induced CCN-Like Molecules
and Uses Therefor

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: MASSachusetts
COUNTRY: USA

COMPUTER: ISSACHUSETTS
COMPUTER: ISSACHUSETTS
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: ISSACHUSETS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATION NUMBER: US/10/010,408
FILING DATE: O7-Dec-2001
CLASSIFICATION NUMBER: US/10/010,408
FILING DATE: WASTON NUMBER: US/10/010,408
APPLICATION US/10
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LOCATION: 249..1001
SEQUENCE DESCRIPTION: SEQ
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Local Similarity
ches 1708; Conserv
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
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          RESULT 2
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; Publication No. US20020165185A1
; GENERAL INFORMATION:
APPLICANT: John J. Castellot, Cast
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STREET: 28 State St. CITY: Boston
STATE: Massach
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     Boston
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                                                                   Castellot, Jr.
4: No. US20020165185A1el
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LOCATION: 1..750
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/010,408 FILING DATE: 07-Dec-2001 CLASSIFICATION: <Unknown>
 TGGGTATGTGACCAGGGAGTGACACCGGCGATCCAGCGCTCCACGGCGCAAGGACACCAA 788
                                                                                                         TGCCGCTGTGATGACGGTGGCTTCACCTGCCTGCCCTGTGCAGTGAGGATGTGCGGCTG
                                                                                                                                                     GAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAACCCCAATTGCAGGGTCCTG
                                                                                                                                                                                                                  GGGGCAGGCCCTGGCGGCCATGGGGCTGTGTGTCTCTTGGATGAGGATGACGGTAGCTGT
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/044,273
FILING DATE: March 19, 1998
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                          TGCCGCTGTGATGACGGTGGCTTCACCTGCCTGCCGCTGTGCAGTGAGGATGTGCGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: MBI-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOR SEQ ID NO: 3:
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                                            LOCATION: 1.681; SEQUENCE DESCRIPTION: $1.000.12
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US-10-010-408-12
; Sequence 12, Application US/10010408
; Publication No. US20020165185A1
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Query Match
Best Local Similarity
Matches 681; Conserv
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GENERAL INFORMATION:
APPLICANT: John J. Castellot, Jr.
APPLICANT: John J. Castellot, Jr.
APPLICANT: OF INVENTION: No. US20020165185Alel Heparin-Induced CCN-Like Molecules
                                                                                                                                                                                                              TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/044,273

FILING DATE: March 19, 1998

APPLICATION NUMBER: <Unknown>
FILING DATE: CUnknown>
FILING DATE: CUnknown>
ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras

REGISTRATION NUMBER: 36,207

REGISTRATION NUMBER: MBI-004

TELEPRENEN: 6617,227-7400

TELEPROME: 6617,227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02109

COMDUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,408

FILING DATE: 07-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                     FEATURE:
                                                                                                                                     MOLECULE TYPE:
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TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Massachusetts
COUNTRY: USA
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 Conservative
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              39.9%;
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; Score 681; DB
b; Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                     Sequence 23, Application US/09956622A Publication No. US20030091973A1 GENERAL INFORMATION:
SEQ ID NO 23
LENCTH: 439
TYPE: DNA
ORGANISM: Rattus norvegicus
5-09-956-622A-23
                                                                                                                 APPLICANT: Horesovsky, Gregory J
APPLICANT: No. US20030091973A11 II, L. Staton
APPLICANT: Raha, Debasish
TITLE OF INVENTION: Method of Identifying Osteorégenerative
TITLE OF INVENTION: Differential Gene Expression
FILE REFERENCE: 21402-445
CURRENT APPLICATION NUMBER: US/09/956,622A
                                                          PRIOR APPLICATION NUMBER: 60/233,579
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin ver. 2.1
                                                                                                         CURRENT FILING DATE:
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Best Local
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: John J. Castellot, Jr.
TITLE OF INVENTION: No. US20020165185Alel Heparin-Induced
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                        REFERENCE//DOCKET NUMBER: MBI-004
TELECOMMUNICATION INFORMATION:
TELLEHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                             APPLICATION NUMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFFICATION: -CUNKNOWN>
PRIOR APPLICATION DATA:
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CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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FILING DATE: <Unknown>
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Street
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Pred. No. 3e-178;
D; Mismatches
                                                                                                                                                                                                                                                    Version
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US-10-010-408-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                INFORMATION FOR SEQ ID NO: 5:
                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/044,273

FILING DATE: March 19, 1998

APPLICATION NUMBER: <Unknown>
FILING DATE: CInknown>
ATTORNEY/AGENT INFORMATION:

NAME: Any E. Mandragouras

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MBI-004

TELEPHONE: (617)227-7400

TELEPHONE: (617)242-4214

TELEPHONE: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: John J. Castellot, Jr.
TITLE OF INVENTION: No. US20020165185Alel Heparin-Induced CCN-Like Molecules
and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..210
SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linea
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 CAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCCCACCCCAGTGCCCACAGGGGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378 CCCCTGGTGCTGGATGGCTGTGGCTGCTGTAAAGTGTGTGCACGGAGGCTGGGGGAGTCC 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCTGTGCCGGACACCCTGTACCTGTCCTTGGACACCACCCCAGTGCCCACAGGGGGGTA
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTGGCGGCCATGGGGCTGTGTGTCTCTTG 527
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                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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100.0%; Pr
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Pred. No. 2.2e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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; LOCATION: 1..177;
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-010-408-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          APPLICATION NUMBER: 09/044,273
FILING DATE: March 19,1998
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
FILING DATE: <Unknown>
ATTORREY/ACENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
NAME/KEY: CDS
LOCATION: 1.174
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: John J. Castellot, Jr.
TITLE OF INVENTION: No. US20020165185Alel Heparin-Induced CCN-Like Molecules
and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                            FEATURE:
                                                                            MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  606 CTGTGCCGCTGTGATGACGGTGGCTTCACCTGCCTGCCGCTGTGCAGTGAGGATGTGCGG 665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         666 CTGCCCAGCTGGGACTGCCCACGCCCCAAGAGATACAGGTGCCAGGAAAGTGCTGC 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTGAGGTGAATGGCCGCAGGTACCTGGATGGAGAGACCTTTAAACCCCAATTGCAGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
                                                                                               TOPOLOGY:
                                                                                                                   STRANDEDNESS: single
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    NO:
    10:
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RESULT 9
US-10-112-267-18/c
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                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-112-267-17
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                                     Sequence 18, Application US/101 Publication No. US20030068678A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/101 Publication No. US20030068678A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Botstein, I
APPLICANT: Cohen, Rol
APPLICANT: Goddard, A
APPLICANT: Gurney, A
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/112,267

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145E

PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704

PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29

PRIOR PILICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14*

NUMBER OF SEQ ID NOS: 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT: Botstein, APPLICANT: Cohen, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: P1176R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WOOD, WIIIIAM I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          945 CTGCCCAGACCCTGCCTGGCAGCCAGGAGCCACAGCTCATGGAACAGTGCTTTC 998
                                                                                                                                                                        478
                                                                                                                                                                                         470 GGGCCTGGTTTGTCAGCCTGGGGCAGGCCC 499
                                                                                                                                                                                                                                              418 AGTGTGTGCACGGAGGCTGGGGGAGTCCTGCGACCACCTĞCATGTCTGCGACCCCAGCCA 477
                                                                                                                                                                                                                                                                   410 AGTGTGTGCACGGAGGCTGGGGGAGTCCTGCGACCCTGCATGTCTGCGACCCCAGCCA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       885 GCCACCCGAGTGTCCAACCAGAACCGATTCTGCCAACTGGAGATCCAACGCCGCCTGTGT
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                                                                                                                                                                                                                                                                                                                        90;
                                                                                                                                                                                                                                                                                                                                      5.3%;
Similarity 100.0%;
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Gurney, Austin L.
Hillan, Kenneth J.
Lawrence, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCACCCGAGTGTCCAACCAGAACCAGATTCTGCCAACTGGAGATCCAACGCCGCCTGTGT
                                                                      Application US/10112267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cohen, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roy, Margaret Ann
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Levine, Arnold J.
Pennica, Diane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10112267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.2%;
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Pred. No.
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Pred. No. 3
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2.1e-37;
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                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
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Best Local
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SEQ ID NO 18
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CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145E

PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704

PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612

PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
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                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                                                                                   FILING DATE: 2001-01-30
                                                APPLICATION NUMBER: PCT/US01/0066/
FILING DATE: 2001-01-30
                                                                                                                         APPLICATION NUMBER: PCT/US01/00667
                     APPLICATION NUMBER: PCT/US01/00669
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Wood, William I.
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Hillan, Kenneth J.
Lawrence, David A.
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2001-01-30
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100.0%; Pred. No.
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APPLICATION NUMBER: PCT/US01/00668

2001-01-30 NUMBER: PCT 2001-01-30

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RESULT 11
US-09-864-761-6698
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26
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CURRENT APPLICATION NUMBER: US/09/864,761
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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ORGANISM: Homo sapiens
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LENGTH: 199
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                                                                                                     FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                APPLICATION NUMBER: US 09/632,366 FILING DATE: 2000-08-03
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FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
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                                                                   APPLICATION NUMBER: PCT/US01/00666
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32; Conserv
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Chen, Wensheng
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EXPRESSED IN BRAIN, SIGNAL - 1.7
NT HIT: AF083500.1, EVALUE 1.00e-108
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EXPRESSED IN HEART, SIGNAL = 1.9
EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
EXPRESSED IN BONE MARROW, SIGNAL = 1.8
EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
EXPRESSED IN HELA, SIGNAL = 2.7
                                         2001-01-30
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PCT/US01/00667
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40. 2.1e-06; 0;
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Best Local
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Publication No.
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
                                                                 TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/10/112,267
CURRENT FILING DATE: 2002-03-27
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                                                                                                                                                                                                  Hillan, Kenneth J.
Lawrence, David A.
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No. US20030068678A1
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D IN FETAL LIVER, SIGNAL = 1
D IN BONE MARROW, SIGNAL = 1
D IN ADULT LIVER, SIGNAL = 1
D IN HELA, SIGNAL = 2.7
D IN HELA, SIGNAL = 2.7
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Pred. No.
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RESULT 1
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SEQ ID NO 38

LENGTH: 738
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TYPE: DNA
ORGANISM: Homo sapiens
US-10-112-267-38
              Sequence 319, Application US/10137866 Publication No. US20030129689A1 GENERAL INFORMATION:
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APPLICANT: Cohen, Rob
APPLICANT: Goddard, A
APPLICANT: Gurney, AL
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SEQ ID NO 39
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Publication No.
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Best Local :
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/112,267
CURRENT FILING DATE: 2002-03-27
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
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NAME/KEY: misc_feature
LOCATION: 1-841
OTHER INFORMATION: Sequence is synthesized.
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TYPE: DNA
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Hillan, Kenneth J.
Lawrence, David A.
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G DATE: 1997-10-29
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APPLICATION NUMBER: 60/062285
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FILING DATE: 1997-09-17
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APPLICATION NUMBER: 60/063733
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FILING DATE: 1997-10-24
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          Gao, Wei-Qiang
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Filvaroff, Ellen
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DeForge, Laura
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60/078910 60/077791 60/074092 60/074086 60/073612 60/072320 60/069694 60/069334 60/069278 60/069212 60/066770 60/066511 60/066453 60/066364 60/065846 60/065186

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APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
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NE RS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
NE RS	
NE AL	AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
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Program for University 451 Eckstei 451 Eckstei Tel: 319 33 Fax: 319 33 Email: msoa The sequenc oligonucleo	COMMENT Contact: Soares, MB
University 451 Eckstei Tel: 319 33 Fax: 319 33 Email: msoa The sequenc oligonucleo	Program for Rat Gene Discovery and Mapping
451 Eckstei Tel: 319 33 Fax: 319 33 Email: msoa The sequenc ollgonucleo	University of Iowa
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rax: 3.19 33 Email: msoa The sequenc oligonucleo strand cDNA	Tel: 319 335 8250
Email: msoa The sequenc oligonucleo strand cDNA	Fax: 319 335 9565
The sequenc oligonucleo strand cDNA	Email: msoares@blue.weeg.uiowa.edu
oligonucleo strand cDNA	The sequence contained an oligo-dT track that was present in the
strand cDNA	oligonucleotide that was used to prime the synthesis of first
	strand cDNA and therefore this may represent a bonafide poly A

FEATURES

source

including CYO, CZO, DAO, DBO, DDO, DDO, and DEO
COTTESPONDING to plates R-CYO-BXY
R-CZO-BYA through R-CZO-BYI, R-CZO-BZB-C, R-DAO-BYJ
through R-DAO-BYP, R-DAO-BZD through R-DAO-BYQ
through R-DBO-BZA, R-DCO-BZI through R-DAO-BZH, R-CO-CAY
through R-DBO-BAA, R-DCO-BZI through R-DCO-BZQ, R-CO-CAY
through R-DBO-CBA, R-DDO-BZR through R-DEO-CAA.

R-DDO-CBB-C, and R-DEO-CAB through R-DEO-CAA.

The corresponding plates are R-CNO-BKF through R-CNO-BLD,
R-CNO-BLG, R-CNO-BMB and R-CNO-BKF through R-CNO-BLD,
R-CNO-BLG, R-CNO-BMB, and R-CNO-BKF through R-CNO-BLD,
R-CNO-BLG R-CNO-BMB, and R-CNO-BKF through R-CNO-BLD,
R-CNO-BLG R-CNO-BMB, and R-CNO-BKF R-CNO-BML.

This pool represented 5% of the final driver population.

h) a pool of the 28 most abundant clones in the CNO pool corresponding to the following addresses: bkx-a-01-0-UI, bkx-d-01-0-UI, bkx-d-01-0-UI,

TAG\_SEQ-GACCA"

BASE COUNT 177 a 176 c 198 g 211 t

ORIGIN

Query Match Best Local Similarity

29.3**%**; 99.5**%**;

Score 501; DB 14; Pred. No. 1.6e-238;

Length 762;

δÃ B δÃ B Q Вb 50 밁 Ş Qy 밁 ρ 밁 Вp 밁 Matches 651; 1393 1333 1273 1213 403 1093 GCTCTTGGCTGCAGTTAACTGTCCTGCTTGGATTCACTGTGTAGAGCCACTGAGCGATCC 1152 1033 CATCCTCAGCAAATGACCCTAGGACCAGGCCCTGGACTGCTGGTAGATGCTCTTCTCCAT 1092 463 523 583 643 703 TGTCCTTAAGAAATTCCTGAAAGTCCAGGAACTTGAGCTTTGTATTTTCAGGAATGCACA 1572 TTGTCCCCAAAGATGAATGAACTCGTAAGTGTACCTTCCCTGACCTGAGAACACCCT 1452 GTTAGGACCAGACAGCAGATTGCCTGAAACTTCCAATTCCCTTCTTGGACTTCTGTATGC GACCTTTAAACCTAGGCTATACTGGGCAAACCTGGCCACCGTGCTGGGGGATAAGGTCAAT 1332 CTGCTCTGTCTGAGGTAGGCGGAGCAGGTGACCAGCTCCAGTTCTCTGGTTCAGCCTGGA 1212 CATCCTCAGCAAATGACCCTAGGACCAGGCCCTGGACTGCTGGTAGATGCTCTTCTCCAT 644 GCCTGCTCGGGAAGTATTCAGGGGCAGAATTCTCTGTGAACATGAAGAGATGAATCACAC TTGTCCCCACAGATGAATGAACTCGTAAGTGTACCTTCCCTGACCTGAGAACACCCT GTTAGGACCAGACAGCAGATTGCCTGAAACTTCCCAATTCCCTTCTTGGACTTCTGTATGC GACCTTTAAACCTAGGCTATACTGGGCAAACCTGGCCACCGTGCTGGGGGATAAGGTCAAT ATTCTGGGTTCTCCTGGCTCATTCCTCAAAACATCCCTGTACAAAAAGGACAACCAAAAA ATTCTGGGTTCTCCTGGCTCATTCCTCAAAACATCCCTGTACAAAAAGGACAACCAAAAA 1272 GCTCTTGGCTGCAGTTAACTGTCCTGCTTGGATTCACTGTGTAGAGCCACTGAGCGATCC Conservative 0; Mismatches 0 Gaps 1512 1392 284 344 464 524 404 0

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REFERENCE
AUTHORS
                                                        RESULT 3
BQ560868
LOCUS
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JOURNAL
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Best Local :
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BQ937887.1 GI:22353365
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Hiosotience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14017 row: n column: 21
High quality sequence stop: 543.
                                                                                                                                                                                                                                                                                             90;
                  BQ560868 537 bp mF
H4067A01-5 NIA Mouse 7.4K cDNA Clone
H4067A01 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ937887 940 bp n
AGENCOURT_8951807 NCI_CGAP_Co24 Mus
IMAGE:6476852 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
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                                                                                                                                              TCTCTTAAGCACTCGCAAAACAGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTC
                                                                                                                                                                                                                                                          AGTGTGTGCACGGAGGCTGGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGCCA 469
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                                                                                                                                                                                                                                                                                                                                                                                      169
                                                                                                                                                                                                                                                                                          5.3%; Solitarity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/dlome="IMACE:6476852"
/clone=1"="NCI_CGAP_CO24"
/clone=1"="NCI_CGAP_CO24"
/lab_host="OHIOB (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
a 277 c 288 g 200 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                          Score 90;
Pred. No.
                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                    DB 14,
J. 1.8e-33;
O;
                                                      mRNA
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                                     Set
                                   Mus musculus cDNA clone
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                                                        linear
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VERSION
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BB849097
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ORGANISM
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KEYWORDS
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Best Local
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                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                      531
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EST.
                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Rodentia;
                                                                                                                                                                                                                                           BB849097 RIKEN full-length enriched, adult inner ear cDNA clone F930006G02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity
67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yong Qian Contact: Yong Qian Contact: Yong Qian Laboratory of Genetics Laboratory of Genetics National Institutes of Health National Institute on Aging/National Institutes of Health National Drive, Suite 3000, Baltimore, MD 2124-6820, USA Email: cdoneelgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details. Plate: H4067 row: A column: 01
Seg primer: -21M13 Reverse
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Ishii Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
                                                                                                         Mammalia; Eutheria;
1 (bases 1 to 424)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA clone set
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,P.R., Stagg,C.A., Bassey,U.,
Luo,A.G. and Ko,M.S.H.
Assembly, verification, and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
Eukaryota; Metazoa;
                                                                                                                                                                                                                    BB849097.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 537
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                                                                                                                                                                                  house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTGTGTGCACGGAGGCTGGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGCCA 469
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL/6"
/db_xref="niaEST:H4067A01-5"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="mixed"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NIA Mouse 7.4K cDNA Clone
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:21461753
                                                                                                                                                                                                                    GI:17090551
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Rodentia;
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Pred. No.
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ssey,U., Aiba,K., Hamatani,T., Kargul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and initial annotation
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                                                                                                                          Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : SalI; Site_2: NotI; This of 7,407 clones from more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 537
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                                                                                                                                              Euteleostomi;
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Kargul,G.J.,
                                                                                                                             Murinae;
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ACCESSION
VERSION
KEYWORDS
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LOCUS
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SOURCE
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                                                                                                                                                                                                                                                                                                373 AGTGTGTGCACGGAGGCTGGGGGGGGTCCTGCGACCACCTGCATGTCTGC
                                                                                                                                                                                                                                                                                                                                           410 AGTGTGTGCACGGAGGCTGGGGGAGTCCTGCGACCACCTGCATGTCTGC 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Layashifay, Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                  BB374499 315 bp mRNA linear EST 13-JUL-2000
BB374499 RIKEN full-length enriched, 16 days embryo head Mus
musculus cDNA clone Cl30075G16 3' similar to AF126063 Mus musculus
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encyclopedia: real-time sequence clustering for construction nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (200 Please visit our web site (http://genome.gsc.riken.go.jp) fo further details.
                                          BB374499.1
                                                                                                          connective tissue
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Contact: Yoshihide
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RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                  mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
/note="pooled tissues ; (tissue_type=cerebellum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="F930006G02"
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ORGANISM
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Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                           prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
                                                                                     was cloned
                                                                                                                                                                                                                        prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
/note="Si+"
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/dev_stage="16 days
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/db_xref="taxon:10090"
/clone="C130075G16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RIKEN full-length enriched,
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Sciurognathi; Muridae;
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,K., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                                                                                                                                                                                                                                                                                                                                              Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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Tel: 81-45-503-9212
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Contact: Yoshihide Hayashizaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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e mouse tissues
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                                                                                                                                                                                                                                                                                                                                                                      Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Konno, H., Fukunishi, Y., Shibata, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 369)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Hayashizaki,Y
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                                                                                                                                                                                                                                                                                                                      tissues.
                                                                                                                    CDNA"
/note="pooled cell lines
(cell_line=CRL-2116 JC),
                                                     /tissue_type="kidney"
/cell_line="CCL-142 RAG"
                                                                                                                                                                          /db_xref="taxon:10090"
/clone="G430141015"
                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                            one_lib="RIKEN full-length enriched, kidney CCL-142
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Pred. No.
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4.1e-06;
; (cell_line=CRL-1751 WEHI 164), (cell_line=RCB-0035 WEHI-3),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Itoh, M., Carninci, P., Sugahara
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JOURNAL COMMENT
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AI225477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 418)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
AI225477
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                                                                                                                                                                                                                                                                                                                                                                                                             MGI:935757
                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Theising, B., Wylie, T., Lennon, G., Soares, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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(cell_line=RCB-0559 K-1 F1), (cell_line=CRL-1283 B16
melanoma), (cell_type=B cells, cell_line=CRL-1702 WEHI 231
), (cell_type=Leydig cells, cell_line=CRL-2065 MLTC-1),
(cell_type=Nullipotent stem cell, cell_line=CRL-2070 NE),
(tissue_type=bladder, cell_line=RCB-0544 MBT-2),
(tissue_type=bone marrow, cell_type=stroma cell,
cell_line=CRL-2028 SR-4987), (tissue_type=colon,
cell_line=CRL-1028 SR-4987), (tissue_type=colon,
cell_line=CRL-1124 SCA-9 clone 15), (strain=BALB/C,
cell_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,
cell_type=B cells, cell_line=CRL-1669 BCL] clone 13.20-3B3
a modified polylinker; 1st strand cDNA was prepared from pregnant mouse uterus, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ), (strain=C3H, tissue_type=brain, BC3H1)"
                                                                                                                                                                                                           /clone="IMAGE:1498153"
/clone_lib="Soares_NMPu"
                                                                                                                                           /lab_host="DH10B"
                                                                                                                                                                 /dev_stage="adult"
                                                                                                                                                                                               /sex="female"
                                                                                                                    note="Organ: uterus; Vector: pT7T3D-Pac (Pharmacia) with
                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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100.0%; Pr
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu
Marra, M., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU-HHMI Mouse EST project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
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Mammalla; Eutheria; Rodentia; Sciurognathi
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Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -28ml3 rev2 ET from High quality sequence stop: 478.
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                                                                                   vector. Library
Bento Soares and
98 c 100
                                                                        constructed Bonaldo."
                                                                                                                                                                                                                                           /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                               /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                            /sex="male"
                                                                                                                                                                                                                                                                                                       /clone_lib="Soares_mammary_gland_NbMMG"
                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:1195358"
                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
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DB 9; Length 488;
4.4e-06;
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BF138093
BF138093.1 GI
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Email: cgapbs r@mail.nih.gov
Tissue procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 792)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 966)
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35; Conserv
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                                                                                                                               mRNA sequence.
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plate: LLAM9254 row: f column:
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Location/Qualifiers
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10000"
/clone="IMAGE:4012801"
/clone_11b="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
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/strain="CZECH II"
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IMAGE:4021308 5',
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vt97c08.rl Soares_mammary_gland_
IMAGE:1179086 5', mRNA sequence_
AA717584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                      WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                               1 (bases 1 to 426)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                              Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov http://image.llnl.gov h column: 13
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                        MGI:636934
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primer: -28m13 rev2 ET from Amersham
h quality sequence stop: 416.
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llarity 100.0%;
Conservative
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/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:4021308"
/clone_lip="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mac
Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M.
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Mammalia; Eutheria; Primates;
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imer: T7.
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Directional<sup>®</sup>
139 c
                                                                                                   /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone_lib-"HOA (Human Osteoarthritic Cartilage)"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1179086"
                                                           /tissue_type="cartilage"
/lab_host="E.coli DH10 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
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with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
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                                     /note="Vector: psport I; Site_1: SalI; Site_2: NotI
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                                                                                                   K-EST0028180 S2SNU668s1 Homo 5', mRNA sequence. BM751866
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vērtebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 489)
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Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M.
                                                                         EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        709 Swedeland Road, P.O. Tel: 610-270-7245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sanjay_kumar-l@gsk.com
                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="HOA (Human Osteoarthritic Cartilage)"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: No
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2002)
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                         Homo sapiens
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Plate: 2 row: D column: 09
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173 c 159 g 82 t
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/db_xref="taxon:9606"
/clone="$2$NU668$1-2-D09"
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/cell_line="SNU-668"
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Euteleostomi;
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Eukaryota;

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ORIGIN
Search completed: July.28, 2003, 18:02:02 Job time: 3040.91 secs
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Best Local Similarity
Matches 32; Conserv
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                                                                                                            291 GTACCCCTGGTGCTGGATGGCTGTGGCTGCTG 322
                                                                                                                                                              375 GTACCCCTGGTGCTGGATGGCTGTGGCTGCTG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCML510 row: p column: 07
High quality sequence stop: 499.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 618)
                                                                                                                                                                                                                         1.9%; Score 32; DB 12; ilarity 100.0%; Pred. No. 0.00014; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                         95 a
                                                                                                                                                                                                                                                                                                                                                              /Clone="IMAGE:4691574"
/Clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgcctggcc); Site_2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCCAAGGCGGCCAATG-dT(30)BN-3' (where B = A,
C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NHH_MGC Library."
95 a 194 c 213 g 116 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                           Length 618;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Title:
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Maximum DB seq length: 2000000000
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Gapop 60.0 , Gapext 60.0
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175
1 AGTCCAGGAACTTGAGCTTT......GCCTAGAATAAACACCCAAA 175
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

c 45	4	43	4	4	c 40	w	38	c 37	36	ω	ω	c 33	w	w	c 30	29	28	N	c 26	N	c 24	23	22	N	c 20	19	18	17	16	٠,	c 14	<u>_</u>	۔ د	10	9	8	7		ი 5	4	ω	N		No.	Result	
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113164	012988 HOW	10879 Homo s	L66989/ Mouse	02/289 Homo sa	9432 Homo	391285 Homo	109876 Rattu	068306 Homo	122991 Rattu	097209 Rattus n	001725 Homo	3666	15932 Mus	3197 Drosoph	36059 Huma	084409 Mus mu	024074 Homo sap	44809 Homo s	008677 Homo sa	120233 Rattus	115134 Rattus	445431 Human E	129134 Rattus	006215 Drosophi	000692 Homo sap	004735 Dros	002717 Dros	17886 Drosop	32620 Mus mu	14696 Ratt	0334	105337 HOMO 8	002393 Homo	015962 Homo s	F126063 Mus mu	69906 Mus mus	L731698 Mouse [	F100778 Mus mu	210325 Sequenc	210324 Sequence	F259981 Rattus	095418 Rattus n	26895 Rattus	escription		

## ALIGNMENTS

REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AC126895	RESULT L
Rattus. 1 (bases 1 to 137964) Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	Rattus norvegicus	Rattus norvegicus.	HTG; HTGS_PHASE1.	AC126895.1 GI:21724040	AC126895	***, 49 unordered pieces.	Rattus norvegicus clone CH230-301E4, *** SEQUENCING IN PROGRESS	AC126895 137964 bp DNA linear HTG 24-JUL-2002		

not known and their order in this sequence record

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Submitted (24-JUL-2002) Human Genome of Molecular and Human Genetics, Bay Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 137964)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 137964) Worley, K.C. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryan Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, Chen, C., Chen, Z., Chowdhry, I., Christopoulos, C.
                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                      Center project name: GZHG
Center clone name: CH230-301E4
Center clone name: CH230-301E4
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of rea Assembly program: Phrap; version 0-930329
Consensus quality: 89474 bases at least 040
Consensus quality: 93422 bases at least 030
Consensus quality: 95506 bases at least 020
NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 49 contigs. The true order of the pieces
                                                                                                                                                                                                                                                            web site: http://www.hgsc.bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                              Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.o
                                                                                                                                                                                                                                                                                                                                                    Genome Center
                                                                                                                                                                                                                                                                                                                                                                                        Genome Sequencing
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L., Byrd, N.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ayele, M., Banks, T.,
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COMMENT

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* arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence * This second as it is available and the accession number will * be preserved.
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Rattus norvegicus clone CH230-7C10,
51 unordered pieces.
AC095418
AC095418.3 GI:21717893
HTG: HTGS DHACE1
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1 (bases 1 to 226303)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
                                                                                                    Rattus norvegicus
                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                    Norway rat.
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                                                             Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                AGTCCAGGAACTTGAGCTTTGTATTTTCAGGAATGCACATCTCTTAAGCACTCGCAAAAC
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34027 c 35229 g
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/db_xref="taxon:10116"
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9238: contig of 3934 bp in 16
9238: gap of unknown length
97339: contig of 5001 bp in 16
97339: contig of 5001 bp in 16
97439: gap of unknown length
103534: contig of 6095 bp in 16
103634: gap of unknown length
107080: contig of 3446 bp in 16
107180: gap of unknown length
115201: gap of unknown length
121237: contig of 5936 bp in 16
121237: gap of unknown length
121237: gap of unknown length
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99.3%;
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128010: gap of unknown
                                                                       Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission

Simmitted (11-UUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 10, 2002 this sequence version replaced gi:17941885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (17-SEP-2001) Human Genome of Molecular and Human Genetics, Bayl Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C.
Direct Submission
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Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990339 Consensus quality: 18550 bases at least Q40 Consensus quality: 190362 bases at least Q30 Consensus quality: 190362 bases at least Q30 Consensus quality: 193076 bases at least Q30
                                                                                                                                                                                                                                                          Center project Information Center project name: GCDF Center clone name: CH230-7C10 Summary Statistics
                                                                                                                                                                           Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye:
                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Baylor College of Medicine Center code: BCM
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Baylor College of Medicine,
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<sup>(</sup>see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 51 contigs. The true order of the pieces
is not known and their order in this sequence record is NOTE: Estimated insert size may differ from sequence length

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as soon as it be preserved.
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Zhang,R., Averboukh,L., Z
Coffey,R.J., Pardee,A.B.
Identification of rCop-1,
                                                                                                    Rattus norvegicus
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                          Dempsey, P.J.,
    protein family
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Sequence 17
AR210324
AR210324.1
                                                                                                                                                        l (bases 1 to 1734)
Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.
WISP polypeptides and nucleic acids encoding same
Patent: US 6387657-A 17 14-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as a negative regulator for cell transformation Mol. Cell. Biol. 18 (10), 6131-6141 (1998) 98414629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (24-APR-2000) Cell Biology, Vanderbilt-Ingram Cancer
Center, 649 MRB II, Nashville, TN 37232, USA
Location/Qualifiers
                                                                                                                                                                                                                               Unknown
                                                                                                                                                                                                                                             Unknown
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NGRRYLDGETFKPUCKYLCKCDDGGFTCLPLCSEDVTLPSWDCTRPKRLQYPGKCCPE
WYCDDGYTPALQRSAAQGHOLSALYTPASADAPWPNMSTAWGPCSTTCGLGIATRYSN
QNRFCQLEIQRRLCLPRPCLAARSHSSWNSAF"
                                                                                                                                 Location/Qualifiers
1. .1734
                                                                                                         /organism="unknown"
491 c 495 g
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/db_xref="GI:7739781"
/translation="MRGSPLIRLLATSFLCLLSMVCAQLCRTPCTCPWTPPQCPQGVP
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/db_xref="taxon:10116"
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Pred. No.
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Sequence
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Direct Submission
Submitted (23-OCT-1998) Molecular Oncology,
Submitted (23-OCT-1998) CA 94080, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 1734)
Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.
WISP polypeptides and nucleic acids encoding same
Patent: US 6387657-A 18 14-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                              family that are up-regulated in wnt-1-transformed cells a aberrantly expressed in human colon tumors Proc. Natl. Acad. Sci. U.S.A. 95 (25), 14717-14722 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee,J., Brush,J., Taneyhill,L.A., Deuel,B., Lew,M., Watanabe,(Cohen,R.L., Melhem,M.F., Finley,G.G., Quirke,P., Goddard,A.D., Hillan,K.J., Gurney,A.L., Botstein,D. and Levine,A.J., WISP genes are members of the connective tissue growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 1734)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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AF100778
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                                                                                                                                                                                                                                                              South San Francisco, CA
Location/Qualifiers
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495 c 491 g
/product="connective tissue WISP-2"
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                                    /codon_start=1
                                                      /gene="Wisp2"
                                                                           257...1012
                                                                                         /gene="Wisp2"
                                                                                                                                               /cell_type="epithelial"
/tissue_type="mammary"
                                                                                                                                                                 /cell_type="~~'
                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                'note="transformed
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Pred. No.
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growth factor related protein WISP-2
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Goddard,A.D.,
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TITLE
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                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                    where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 TCTGGCAGGCCAGGGCCTTTCTCTTCAGCATGAGA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 25, 2002 this sequence version replaced gi:21213601.
During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong
                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-161B3 is from the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (24-MAY-2002) Wellcome Trust Sanger Institute, Hinxton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mouse DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                        database can be found at
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                                                                                                                             15405
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491 c 495 g 393 t
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/db_xref="GI:4028579"
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20.0%; 5C
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       Score 35; DB; Pred. No. 1.6
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                                                      Length 61072;
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Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 211865 bases at least Q40
Consensus quality: 213403 bases at least Q30
Consensus quality: 214139 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
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Insert size: 234243; 1.8% error; agarose-fp
Quality coverage: 6.29x in Q20 bases; sum-o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coverage: 5.90x in Q20 bases; agarose-fp
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Mus musculus chromosome 2 clone RP23-217C2,
PROCRESS ***, 21 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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35071 39671: contig of 4601
39672 39771: gap of 100 b
39772 46360: contig of 6589
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4001 4100: gap of 100 bp
4101 15267: contig of 11167 bp in length
15268 15367: gap of 100 bp
15368 34970: contig of 19603 bp in length
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                                                      ) 87499: gap
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46360: contig of 6589 k
460: gap of 100 bp
49809: contig of 3349 k
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213978 2167
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119774 119873:
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87500. .98601
                                                                                                                                                                                                             /note="assembly_fragment:01170
fragment_chain:3"
98702. .105522
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35071. .3
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fragment_chain:1"
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4101. .15267
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/note="assembly_fragment:01951
fragment_chain:4"
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fragment_chain:2"
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8 216757: contig of 2780
Location/Qualifiers
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fragment_chain:4"
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fragment_chain:2"
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fragment_chain:2"
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fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51672: gap of 100 bp
169686: contig of 18014 bp in length
69786: gap of 100 bp
200095: contig of 30309 bp in length
00195: gap of 100 bp
113877: contig of 13682 bp in length
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134552: contig of 14679 bp in length
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REFERENCE
AUTHORS
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LOCUS
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AUTHORS
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ORGANISM
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VERSION
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Mus musculus connective tissue
(Ctgfl) mRNA, complete cds.
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Kumar,S., Hand, A.T., Connor, J.R., Dodds, R.A., Ryan, P.J., Trill,J.J., Fisher, S.M., Nuttall, M.E., Lipshutz, D.B., Zou, C., Hwang, S.M., Votta, B.J., James, I.E., Rieman, D.J., Gowen, M. and
                                                                                                                                                                                                                                                                         Direct Submission
Submitted (04-FEB-1999)
SmithKline Beecham, 709
                                                                                                                                                                                                                                                                                                                                                                                       of osteoblast functions J. Biol. Chem. 274 (24), 99287915
                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1739)
Kumar, S. and Zou, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Identification and cloning of a connective tissue growth factor-like cDNA from human osteoblasts encoding a novel regulator
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fragment_chain:6"
213978. .216757
/note="similar to the Mus musculus WISP-2 protein encoded by the sequence presented in GenBank Accession Number AF100778; putative growth factor; CTGF-L; contains IGF binding (IGFBD), Von Willebrand Factor type C (VWC) repearant thrombospondin type I (TSP1) domains; member of the
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| 51573 c 51904 g
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242. .997
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                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                  /tissue_type="lung"
l. .1739
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                                                                                                                                                                                                                                                                         Bone & Cartilage Biology, UW 2109,
Swedeland Rd., King of Prussia, PA
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growth factor-like protein precursor
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Query Match
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EB 1rren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Balren, B., Linton, L., Beckerly, R., Bogushavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Bogushavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Colling, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domlan, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Hewland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McBan, P., McGurk, A., McKernan, K., McLaughlin, J., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C., H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramainian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W., J., Zimmer, A. and Zody, M.
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SEQUENCE,
AC015962
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                                                                                                                                                                                                                                                                  Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 1, 2000 this sequence version replaced gi:6957735.
All repeats were identified using Repeatwasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/Repeatwasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalla; Lucio-14540)

1 (bases 1 to 145540)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Birren,B., Chromosome 18, clone RP11-111D6
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HTG; HTGS_PHASE1; HTGS
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                                                         Center project name:
Center clone name: 11
                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center
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WRRRYLDGETFKFNCBVLCRCDDGGFTCLPLCSEDVBLPSWDCPRPBRIQVPGRCCPPE
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NQNRBCQLEIQRRLCLSRPGLASRSHGSWNSAB;"
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                                                                                                                                                                              http://www-seq.wi.mit.edu
      vector:
                                    Summary
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Matches

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* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
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Insert size: 141840; sum-of-contigs
Quality coverage: 5.5 in Q20 bases; agarose-fp
Quality coverage: 3.1 in Q20 bases.
NOTE: This is a 'working draft' sequence. It currentl
consists of 38 contigs. The true order of the pieces
is not known and their order in this sequence record
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7423 7522: gap of 100 bp 17523 9048: contig of 1526 bp in 9049 9148: gap of 100 bp 10173: contig of 1025 bp in 10174 10273: gap of 100 bp 10274 11873: gap of 100 bp 111774 11875: contig of 1603 bp 11
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56 23665: gap of 100 bp

16 25713: contig of 2048 bp

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32825: contig of 2923 t
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35852: gap of
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2307: contig of 1596
5407: gap of 100 bp
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37965: contig of 2113 i
38065: gap of 100 bp
41361: contig of 3296 i
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29802: contig of 2786 bp
29902: gap of 100 bp
32825: contig of 2923 bp
2925: gap of 100 km
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11288: contig of 1928 bp
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15396: contig of 1820 bp
5496: gap of 100 bp
16981: contig of 1485 bp
081: gap of 100 c
19160:
                                                                                51777: contig of 3990 1

1877: gap of 100 bp

56131: contig of 4254 1

6231: gap of 100 bp

60894: contig of 4663 1
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44463: contig of 3002 l
4563: gap of 100 bp
47687: contig of 3124 l
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85327 85426: gap of 100 bp
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92751 92850: gap of 100 bp
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115237; contig of 9309 bp
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108177: cont
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                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                preserved
                                                                                                           as soon as
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31332 61893

31231 contig of 61792 contig of 88918 contig of

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Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, Japan (E-mail:hattori/hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 176,107 genomic DNA of 18q12 published Only in DataBase (2000) 2 (bases 1 to 176107) 10 (bases 1 to 176107) 11 (bases 1 to 176107) 12 (bases 1 to 176107) 13 (bases 1 to 176107) 15 (bases 1 to 176107) 16 (bases 1 to 176107) 17 (bases 1 to 176107) 17 (bases 1 to 176107) 18 (bases 1 
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Center project name: Humbraft18
Center clone name: Rp11-699C17
Center clone name: Rp11-699C17
Center clone name: Rp11-699C17
Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 163826 bases at least Q40
Consensus quality: 169603 bases at least Q30
Consensus quality: 172435 bases at least Q20
Insert size: 174307; sum-of-contigs
Quality coverage: 5.63x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
------ Project Information
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56232. .60894
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31232 31331: gap of 100 bp
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61793 61892: gap of 100 bp
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/note="assembly_fragment"
61893. .88918
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31332. .61792
                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="18"
                                                       /clone="RP11-699C17."
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149956: contig of 5665
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119559: contig of 10046 bp in length
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98085: contig of 9067 bp in length
185: gap of 100 bp
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167491: cont
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camaratta, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Gage, D., Galagan, J., Collymore, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, L., Johnson, R., Johnson, R., Landers, T., Lehocz, V., Landers, R., Lander
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K.,
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1 (bases 1 to 176612)
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98186. .109413
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89019. .98085
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175010. .176107
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119660. .128623
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37813 c 39266 g 50228 t
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128724. .136240
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109514. .119559
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167592. .170792
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164773. .167491
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50057. .156749
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Birren,B., Nusbaum,C., Lander,E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                               46327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: L12328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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131664 17661:
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                   Conservative
                                                                                                                                                                                                                                                                                               /clone="RP11-699C17"
/clone_lib="RPCI-11 Human Male BAC"
/37044 c 41351 g 51790 t 100 others
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/db_xref="taxon:9606"
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176612: contig of 44949 bp in length
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                                                          13.1%; Score 23; DB 2; 100.0%; Pred. No. 0.027;
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REFERENCE
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                                                                                                                                           CE 3 (bases 1 to 18556)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Laroque, K., Lanazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nayyen, C., Nicol, R., Norbu, C., Necta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Talmer, A., and Zodv, M., Town, C., Strauss, C., Sanbek, I., Zimmer, A., and Zodv, M., Young, G.,
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                                                                                    Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (26-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                   Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:17063224. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A. Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
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                                                                                                                                                                                           Smit, A.F.A. & Green, P. (1996–1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                           Center code: WIBR
                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Research
Contact: sequence_submissions@genome.wi.mit.edu
                                       Web site: http://www-seg.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: Plasmid: n/a; 100% of read Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 consensus quality: 161237 bases at least 030 consensus quality: 164560 bases at least 020 consensus quality: 165460 bases at least 020
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Center clone name: 303_K_3
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Insert size: 165891; sum-of-contigs
                                                                                                                                                                                                                                                                                      103268 103367: gap of
103368 126955: cont
                                                                                                                                                                                                                                                                                                                                       80882 80981:
                                                                                                                                                                                                                                                                                                                                                                                                            40872 40971: gap of
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/note="assembly_fragment"
                    5365.
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14365: contig of 1270 bp in length
14465: gap of 100 bp
16284: contig of 1819 bp in length
16384: gap of 100 bp
18855: contig of 2471 bp in length
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40871: contig of 14561 bp
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10004: gap of 100 bp
11421: contig of 1417 to
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103267; contig of 22286 bp in
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Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Biange,K., Blankanburg,K., Bonnin,D.,
Bouck,J., Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
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Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
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Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Goorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
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Wulliams,G., Williamson,A., Wieczyk,R., Wooden,S., Worley,K.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:19339033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-JUL-2002) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
Direct Submission
Submitted (11-MAR-2002) Human Genome Sequencing Center, Depar Submitted (11-MAR-2002) Human Genome Sequencing Center, Depar of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 173702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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Chemistry: Dye-terminator Big Dye: 100% of re Assembly program: Phrap; version 0.990329 Consensus quality: 113417 bases at least Q40 Consensus quality: 117596 bases at least Q30 Consensus quality: 120896 bases at least Q20
                                                                                                                                                                                                                                                                                    Center project name: GOWB
Center clone name: CH230-202L22
                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
-----Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                            Sequencing vector: Plasmid;
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JOURNAL REFERENCE

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AUTHORS

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 71 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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1424: gap of unknown l
2953: contig of 1529 b
3053: gap of unknown l
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HICP; cell-associated activity; ss; cell proliferation; fibrotic disorder.						Ovary cancer relat		Probe #23874 used	occus abyssi	ທ	Drosophila melanog	Genomic sequence #	Drosophila melanog Human immune/haema	Mechanical stress	Human nervous syst	Drosonhila melanog	Human Jurkat cell	Human membrane spa	Human DNA encoding	Arabidopsis thalia	Human MDDT encodin	Polypeptide-dihydr		Human signal pepti		Human polynucleoti	Arabidopsis thalia	Mouse WISP-2 PCR p	Nucleotide sequenc	Human adenosine re		nella typhi liwar call	DNA encoding a 60		Human adenosine re

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WPI; 1999-562060/47. P-PSDB; AAY27434. Castellot JJ; (TUFT ) TUFTS 19-MAR-1998; 18-MAR-1999; 23-SEP-1999 W09947556-A2 Rattus qs COLLEGE 98US-0044273 99WO-US05999

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100.0 69.1 30.9 20.0 10.3 10.3 10.3

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AAZ07516 ABL59575 ABN30189 AAX76488 AAD32418 AAD32413 ABL91207 ABL92605 ABL91770 AAF21412

Rat HICP polypepti Rat OST23 gene fra Rat spliced transc Mouse WISP-2 prote Chlamydia pneumoni Chlamydia pneumoni Chlamydia pneumoni Human.polynucleoti Human low adenosin

Nucleic acid sequences encoding rat heparin-induced CCN-like protein, used in methods to identify modulators or in diagnostic applications

Score

Length

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Description

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RESULT 2
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The present invention describes a method (M1) hormone receptor ligands (I) and osteoregenera test cell population (CP) comprising cells exp
                                                                        Identifying parathyroid he agents involves detecting regulated by parathyroid |
                                                                                                                                                                        (CURA-)
                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This cDNA encodes a rat heparin-induced CCN-like protein (HICP) protein. Agents that stimulate or inhibit HICP protein activity or expression, antisense HICP nucleic acid molecules and HICP angibodies, can be used to modulate cell-associated activity. HICP modulators can be used to treat disorders characterized by aberrant HICP protein activity or expression. Probes capable of hybridizing to HICP mRNA or antibodies specific for HICP can be used to detect HICP activity in a biological sample. HICP can be used to treat disorders, such as a cardiovascular or fibrotic can be used to treat disorders, such as a cardiovascular or fibrotic
                                                   Claim
                                                                                                                                                 Horesovsky GJ, Noel LS,
                                                                                                                                                                                                            19-SEP-2000; 2000US-233579P
                                                                                                                                                                                                                                    19-SEP-2001; 2001WO-US29548
                                                                                                                                                                                                                                                                                                            Rattus
                                                                                                                                                                                                                                                                                                                                   osteopenia;
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                                                                                                                                                                                                                                                                                                                                                  bone
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                                                                                                                                                                                                                                                                                                                                             OST; osteoregenerative; parathyroid hormone; therapy; parathyroid hormone receptor ligand; formation disorder; bone resorption disorder;
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                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                 osteopetrosis; gene;
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                                                22; 90pp; English
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Pred. No. 3e-79;
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New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription a genome, useful for detecting tissue-, pathology-, and

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Best Local (
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splice
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02-MAY-2001;
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                                                                                                                                                                                                   20-JUL-2001; 2001WO-IB01903
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                                                                                                                                                                                                                                                                                                                  mouse; rat; splice transcript; detection; RNA transcriptome; oligonucleotide library;
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2001US-287724P
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                                                                                                  Faigler
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                                                                                                                                                                                                                                                                                                                                  RNA transcript;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cc set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. Cc The oligonucleotide libraries are useful for detecting mRNAs from a cc biological sample, in expression profiling studies, in qualitatively or cc quantitatively characterising the corresponding transcriptome, and in cc detecting RNA transcripts and splice variants of human or animal cc transcriptomes. The libraries may also be used as specialised mini cc particular biological or pathological state, and so allowing the cc particular biological or pathology-specific genes such as those genes condition; to detect developmental specific pathological condition; to detect developmental specific genes such as those genes condition; to detect developmental specific genes; and to detect RNA cc transcripts and splice variants of a transcriptome of a particular disorder. ABN27253 to ABN59589 represent coligonucleotide sequences from rats, humans and mice, which are used in the sequence data for this patent did not form part of the printed constraints, but was obtained in electronic format directly from WIPO cat from wince the pathological pathological or the printed constraints of the p
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Best Local :
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29-OCT-1997;
03-FEB-1998;
    Botstein:
Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              connective tissue growth factor; cancer; melanoma; arteriosclerosis; leukaemia; lymphoid malignancy; haematopoiesis-related disorder; leukaemia; lymphoid malignancy; haematopoiesis-related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a
                                                                                                                                                                                                                                                              06-MAY-1999
                                                                                                                                                                                                                                                                                                          W09921998-A1
                                                                                                                                                                                                                                                                                                                                                        Mus
                                                                                                                                                                                                                                                                                                                                                                                               tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion kidney disorder; bone-related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation; testicular-related disorder; angiogenesis; immunological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse WISP-2 protein nucleotide sequence SEQ ID NO:17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX76488 standard;
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                                                                        (GETH ) GENENTECH INC.
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llarity 100.0%;
Conservative
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  Cohen R
Levine
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97US-0063704.
98US-0073612.
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                                                                                                                                                                                                                98WO-US22991.
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  e RL,
  Goddard A,
Pennica D,
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Pred. No.
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Roy MA,
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RESULT 5
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ID AAD32413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                     Chlamydiaceae family; chronic infection; persistent infection; pyk; nlp Cpn0585; regulatory pathway; biosynthetic pathway; ompA; ompB; hsp60; lipopolysaccharide; cardiovascular system; respiratory tract; therapy; genital tract; reproductive system; atherosclerotic tissue; macrophage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    products can also be used for detection and diagnosis especially of individuals with neoplastic cell growth or proliferation. The products can be used in the production of transgenic or knock-out animals. Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-337420/28
             18-AUG-2000;
                                                   17-AUG-2001; 2001WO-AU01021.
                                                                                                                                                                                                                                                                                               Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                     multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia pneumoniae AR039 omcB/ompB gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD32413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 178-179; 284pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Wnt-1 induced secreted polypeptides, WISP-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB;
                                                                                        21-FEB-2002
                                                                                                                            WO200214516-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity 100 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1734 BP;
                                                                                                                                                                                                                                                                                                                                   sclerosis; conjunctiva; prophylaxis; antibacterial; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; DNA; 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGGCAGGCCAGGGCCTTTCTCTTCAGCATGAGA 1645
               2000AU-0009540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                 /*tag= a
/product= "Chlamydia pneumoniae AR039 omcB/ompB protein"
/note= "CDS does not include stop codon"
                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                        ..1168
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100.0%; Pr
... 0;
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; Pred. No. 5.10
0; Mismatches
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RESULT 6
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XX ABLS
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                 Chlamydial infection; antigen; immunogen; vaccine; diagnosis; human respiratory disease; cardiovascular disease; atherosclerosis; coronary artery disease; carotid artery stenosis; myocardial infarction; cerebrovascular disease; aortic aneurysm; claudication; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiovascular system, respiratory tract, genital tract, reproductive system or conjunctiva), macrophage, or a cell associated with atherosclerotic tissue or associated with multiple sclerosis brain tissue. The composition is useful for treatment and/or prophylaxis of a chronic infection caused by an organism of the chlamydiaceae family in a patient. Antigen associated with the persistent phase of the developmental cycle of an organism of the Chlamydiaceae family, is useful in the manufacture of a medicament, for treating and/or preventing Chlamydiaceae infection in a patient. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene such as pyk, nlpD, Cpn0585, a gene belonging to same regulatory/
blosynthetic pathway and ompA, ompB, hsp60, a gene involved in
lipopolysaccharide blosynthesis. It is also useful for modulating the
the level and/or functional activity of an expression product of these
genes, where the gene is present in an epithelial cell (selected from
                                   mat_peptide
                                                                                            sig_peptide
                                                                                                                                                                                                                                                                      Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia pneumoniae
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ABL91207 standard;
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                                                                                                                                                                                                                                                                                                                            strain CWL029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL91207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1227 TCCAGGAACTTGAGCTTT 1210
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DB; AAE20302.
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18; Conserv
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                                                                                                                                                                                                                                                                   pneumon tae
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                                   /*tag=
67..166
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1..66
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                                   .1668
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Pred. No
                                                                                                                                                                                                                                                                                                                            frame;
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                                                                                                                                                                                                                                                                                                                            gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene.
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RESULT 7
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XC ABL
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them. The proteins are predicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia pneumoniae is a common cause of respiratory disease in humans, and is also involved in the development of cardiovascular diseases such as catherosclerosis, coronary artery disease, carotid artery stenosis, myocardial infarction, cerebrovascular disease, aortic aneurysm, claudication and stroke. The proteins and nucleic acids of the invention may be used in vaccines and pharmaceutical compositions for the prevention or treatment of chlamydial infections, particularly Chlamydia pneumoniae infections. The proteins may also be used in the detection of Chlamydia pneumoniae, and the nucleic acids may be used in the detection of Chlamydia pneumoniae, and the nucleic acids may be used in the detection of Chlamydia pneumoniae, and the nucleic acids may be used in the detection of chlamydia pneumoniae gene expression. The present sequence represents a specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
                                                                                                                           Query Match
Best Local
                                                                                                 Matches
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11-JUL-2000;
21-JUL-2000;
07-AUG-2000;
18-AUG-2000;
                                                                                                                                                                                                  Sequence 1671 BP; 488 A; 342 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel Chlamydia pneumoniae protein useful in the manufacture of a medicament for treatment or prevention of infection due to Chlamydia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae (strain CWL029), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences ABB90526-ABB90715 represent novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preferably Chlamydia pneumoniae, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABB90549
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1227
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                     3 TCCAGGAACTTGAGCTTT
                                                                                                 18;
                                                                                                                           Similarity
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TCCAGGAACTTGAGCTTT 1210
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2000GB-0019368.
2000GB-0020440.
2000GB-0022583.
2000GB-0027549.
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                                                                                                                      10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
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                                                                                                 0;
                                                                                                                           Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resent novel proteins from Chlamydia ABL91184-ABL91373 represent DNA enco
                                                                                                 Mismatches
                                                                                                                                                                                                  370 G;
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                                                                                                                                                                                                  471 T; 0 other;
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23;
                                                                                                                                                   24;
                                                                                                 0
                                                                                                                                                Length 1671;
                                                                                                 Indels
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                                                                                                 Gaps
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antigen; antibacterial; immunostimulant; immune response; Chlamydia-specific T-cell response; gene; ds. Chlamydial infection; Chlamydia; vaccine; detection; diagnosis; Chlamydia 05-JUN-2002

pneumoniae DNA sequence SEQ

ID

NO:378

(first entry)

ABL92605 standard; DNA; 1671

ВÞ

0;

ABL92605

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ABL91770/C
ID ABL917
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AC ABL917
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AC ABL917
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AC Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccines. Compounds from the present invention can be used for eliciting an immune response, specifically stimulating a Chlamydia-specific T-cell response or inhibiting the development of a Chlamydia infection in an animal. Methods from the present invention can be used: for detecting the presence of Chlamydia in a patient; to stimulate and/or expand T cells specific for a Chlamydia protein; and for treatment of a Chlamydia infection. ABL92394 to ABL92709 and ABB94096 to ABB94374 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes compositions comprising a Chlamydia Capl protein and methods for the diagnosis and therapy of Chlamydia infection Chlamydia DNA and protein sequences from the present invention can have antibacterial and immunostimulant activities, and can be used in
     Kreutzer R,
                                                   (RIBO-) RIBOPHARMA .AG
                                                                                                    09-JAN-2001;
                                                                                                                                                     09-JAN-2001;
                                                                                                                                                                                                      11-APR-2002
                                                                                                                                                                                                                                                    DE10100586-C1
                                                                                                                                                                                                                                                                                                                                                                          Plasmodium;
                                                                                                                                                                                                                                                                                                                                                                                                       Human; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polynucleotide SEQ ID NO 113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL91770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL91770 standard; DNA; 2031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1671 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 333; 537pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel compositions comprising Chlamydia treatment of Chlamydia infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fling SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUL-2000;
23-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-2001; 2001WO-US23121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200208267-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-179901/23
                                                                                                                                                                                                                                                                                                  sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCAGGAACTTGAGCTTT 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCAGGAACTTGAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                   HCV; gene expression; oligoribonucleotide;
virus; viroid; cytokine; prion; antisense of
virucide; protozoacide; antibacterial; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0620412
2001US-0841132
                                                                                                    2001DE-1000586
  Limmer S,
                                                                                                                                                     2001DE-1000586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             488 A; 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probst P,
     Rost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ე
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ore 18; DB;
red. No. 23;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370 G;
     Hadwiger P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bhatia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cap1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein and its use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                          oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                  tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                  pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
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AAF21412/c
Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. Plasmodium or viruses/virolds, pathogenic on humans, animals or plants) or against cytokine, 1d, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang increases stability and thus intracellular concentration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for inhibiting expression of a target gene (ABL91658-ABL91797) in a cell by introducing at least one oligoribonucleotide that has a double-stranded structure consisting of at
                                                                                                                                                                                                                                                                     respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation; chronic chartensin; emphysema; pulmonary transplantation;
                                                                                                                                                                                                                                                                                                                                              numan; airway disorder; bronchoconstriction; lung inflammation;
surfactant depletion; respiratory; bronchodilator; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting gene
by introducing of
                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                        respiratory obstruction; pulmonary obstruction; surfactant hypoproduction; pulmonary vasoconstri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Page 83-84;
                                                                                                             06-APR-1999;
                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                        Human low adenosine antisense oligonucleotide related sequence #2979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF21412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF21412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             terminal bases
                                       Nусе JW;
                                                                 (UYEC-)
                                                                                                                                     24-MAR-2000;
                                                                                                                                                                  26-OCT-2000
                                                                                                                                                                                             WO200062736-A2
                                                                                                                                                                                                                                                                                                                                                                 Low adenosine antisense oligonucleotide; pho
human; airway disorder; bronchoconstriction;
                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAR-2001
                                                                                                                                                                                                                                                                                                                                  immunosuppressive; antiasthmatic; analgesic; hypotensive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125
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                                                                    UNIV
                                                                                                                                                                                                                                                    SS
                                                                                                                                                                                                                                                                  obstructive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAGAGTACTCTCCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; DNA; 2104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAGAGTACTCTCCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                    EAST CAROLINA
                                                                                                                                       2000WO-US08020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e expression in double-stranded
                                                                                                           99US-0127958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           514 A; 549 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.3%; 5c.
100.0%; Pr
                                                                                                                                                                                                                                                                pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells, useful for e.g. treating tumors, d complementary oligoRNA having unpaired
                                                                                                                                                                                                                                                                  disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           561 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             407
                                                                                                                                                                                                                                                                                                                                                                             phosphorothicate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                        potensive; cytostatic;
impeded respiration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other;
                                                                                                                                                                                                                                                                                                                                                                             allergy;
                                                                                                                                                                                                                                                                  n rejection;
bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0

WPI; 2000-679539/66

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RESULT 10
AAA352
ID AAA352
XX AAA352
XX AAA352
XX AAA352
XX Human
DE Human
XX Human
KW Phosph
KW allerg
KW antlal
KW lung antlal
KW respir
KW pulmon
KW respir
XX O
OS Homo s
XX O
PN WO2000
XX 24-FEB
XX 24-FEB
XX 24-FEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunosuppressive, antiasthmatic, hypotensive and cycostatic activities. CC The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with activating peptide factors and malignancies, such as stimulating and cactivating peptide factors and transmitters, thanscription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, binding receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, binding proteins and malignancy associated proteins. The artisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially summarry obstruction and/or lung inflammation, allergy(ies) and or protein are associated with a disease or condition selected from nulmonary was constituted in the activities and disease or condition selected from nulmonary was constituted in the selected from 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothicate; impaired respiration; infilammation; allergy; allergic disease; bronchoconstriction; inhibiter; antinfilammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic figrosis; emphysema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (CDE), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAR18434 to AAR21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the content of t
03-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligonucleotides and compositions (I) comprising them. In the anticoligonucleotides the A is replaced by a 'Universal' or alternative (I) can have respiratory, bronchodilator, antiinflammatory, analyse
                                                                                                                                                                                                                                                                                                                                                                      pulmonary hypertension; chro
cancer; leukaemia; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human adenosine receptor related polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA35290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA35290 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2104 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating
                                                                                                                                                                                     WO200009525-A2
                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1185 GCAGAGTACTCTCTCTG 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 GCAGAGTACTCTCCTCTG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 1393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
99WO-US17712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              524 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         describes low adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1592pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2104
                                                                                                                                                                                                                                                                                                                                                                                                                       chronic obstructive pulmonary disease; COPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               obstructions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Length 2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (A) content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2nd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO:164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the antisense
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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CDS

Location/Qualifiers 59..2089

/\*tag=

Homo

sapiens

cytostatic; immunosuppressive; antidiabetic; ne antiinflammatory; antirheumatic; antiarthritic;

bowel disease;

multiple

human; protein kinase C-delta;

PKC-delta; antipsoriatic;

<u>,,</u>

neuroprotective;
ic; hepatotropic;

hepatitis; cancer;

pancreatitis;

protein kinase C-delta (PKC-delta) encoding cDNA.

Antisense; Human 

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RESULT 11
AAC84222/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cc asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive cpulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONS reduces side effects. The A-containing ONS break down with the crelease of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present the invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences convention. N.B. Sequences given in the disclosure of the present invention to AAA3392) are specifically claimed ONS from the present convention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the disclosure of the present convention when the previous convention the present convention where the previous convention are specifically claimed one that the disclosure of the present convention when the previous convention are specifically claimed one that the sequences given in the disclosure of the present convention the present previous convention and the previous convention are specifically claimed one that the sequences given in the disclosure of the present convention are specifically sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired alivways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                  AAC84222 standard;
                                                                                                                                                                                                                                                                               19-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-205971/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYEC-) UNIV EAST CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAGAGTACTCTCCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGAGTACTCTCCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2104 BP; 524 A; 581 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 1308; 1343pp; English.
                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0095212
                                                                                                                                                                                                                                                                                                                                                                  cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.3%;
                                                                                                                                                                                                                                                                                                                                                                  2104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             582 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             417 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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ARASULT 12
AAA75901/G
ID AAA75
XX AAA75
AC AAA75
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The antisense oligonucleotides are useful for modulating the expression of human PKC-delta in cells or tissues, especially adipose tissues which express human PKC-delta, for inhibiting hyperproliferation of cells and treating or preventing an abnormal proliferative condition such as leukemia. They are also useful for reducing an inflammatory response of human cells and treating an animal having a disease or condition associated with tumour necrosis factor-alpha (TNT-alpha), especially overexpression of TNT-alpha, such as inflammatory or autoimmune disease or a condition which is infectious, diabetes, inflammatory bowel disease, multiple sclerosis, pancreatitis, rheumatoid arthritis, hepatitis, atopic dermatitis or allograft rejection and for reducing the blood glucose level in a human. The present sequence represents the cDNA encoding the human PKC-delta polypeptide.
                                                                                                                Chlamydia
                                                                                                                                                                                                                                                                                                                                      3901/c
AAA75901 standard; DNA; 2111 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense oligonucleotide for modulating human protein kinase C-delta and treating diseases such as cancer, diabetes, comprises nucleotides specifically hybridizable with nucleic acid encoding the protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200070091-A1
                                                                                                                                                                    Cysteine-rich membrane protein; Chlamydia infection; bronchitis; community acquired pneumonia; upper respiratory tract infection;
                                                                                                                                                                                                                        DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-025027/03.
P-PSDB; AAB48037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAY-2000; 2000WO-US13170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-NOV-2000
                                                                                                                                                                                                                                                               22-JAN-2001
                                                                                                                                                                                                                                                                                                 AAA75901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ybridize with
                                                                                                                                                                                                                                                                                                                                                                                                                                 1185 GCAGAGTACTCTCCTCTG 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Page 70-74; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAGAGTACTCTCCTCTG 142
                                                                                                                pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            provides antisense oligonucleotides that specifically h human protein kinase C-delta (PKC-delta) polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
                                                                                                                                                                                                                          60 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0313930
                                                      Location/Qualifiers
                   /product= "membrane-rich protein"
                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "PKC-delta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                524 A; 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.3%;
                                                                                                                                                                                                                          cysteine-rich membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18;
Pred. No.
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                                                                                                                                                                  upper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                582 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                417 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
AAS56353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 18
                                                                                                                           21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a Chlamydia 60 kDa cysteine-rich membrane protein. The membrane-rich polynucleotide and polypeptide are useful for preventing or treating Chlamydia infection, such as community pneumonia, upper respiratory tract infections, bronchitis and sinusitis. They are also useful for diagnosing Chlamydia infection by assaying a body fluid of a mammal. The polypeptide is useful for vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding a 60kda from Chlamydia, useful as a vaccine Chlamydia infection in mammals -
Haselbeck R, Yamamoto RT,
                                                                                          22-DEC-
16-FEB-
                                                                                                                                                                                                                                                                                                                   WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                      Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                          antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella typhi DNA for cellular proliferation protein #386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2111 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-618918/59.
P-PSDB; AAB18820.
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                                                                                                                                                                                                                                         21-MAR-2001;
                                                                                                                                                                                                                                                                              27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                            Antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS56353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS56353 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AVET ) AVENTIS PASTEUR LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1999;
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                                                        (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1365 TCCAGGAACTTGAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Fig 1; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TCCAGGAACTTGAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            ds;
                                                                                                                                                                                                                                                                                                                                                                                        ds; prokaryotic cellular proliferation
antibacterial; drug design.
                                                                                        2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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                                                                                                                                                                                   2000US-191078P
2000US-206848P
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                                                                                                                                                                                                                                         2001WO-US09180
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 Ohlsen
Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
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                 KL,
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                 Zyskind
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Pred. No.
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                 Wall
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23;
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proxaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CE Escherichia coli, Staphylcoccus aureus, Salmonelia typhi, Klabsiella CC invention is also useful for the identification of potential new targets of invention is also useful for the identification of potential new targets to identify proteins used in proliferation, to express these proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in intional drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

CC a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

CC note: The sequence data for this patent did not form part companies the protection of the printed specification, but was obtained in electronic format directly from WIPO at the process of the printed specification in the companies of the printe
    RESULT 14
AAH57492
ID AAH57
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XX AH57
XX Human
XX Human
XX Human
XX Human
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XX Homo
XX Mo200
XX MO200
XX Homo
XX WO201
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                                                                                                                                                                                                                                                                                                                                                                                                                            Human; tissue specific; diagnosis; brain; hearty skeletal muscle; lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; metabolic disease; developmental disease; cytostatic; immunomodulatory; neuroprotective; gene therapy; cancer; immunopsthology; neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
  New cell and tissue specific polynucleotides useful prognosis or monitoring of treatments for disorders
                                                                     WPI; 2001-291057/30
                                                                                                               Sornasse T,
                                                                                                                                                           (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                    02-NOV-2000; 2000WO-US30396
                                                                                                                                                                                                                                                                                                                                            WO200132927-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human liver cell specific cDNA sequence SEQ ID NO:332.
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                                                                                                                                                                                                                                                                                                10-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 CTCGCAAAACAGGAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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                                                                                                                  Watson
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                    Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatio; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasconstriction; asthma; RDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy proteins (II) encoded by then are used in high throughput so
                                                                                                                                                                                                                                                                                                                                                       surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distriess syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                              WPI; 2000-679539/66.
                                                                                              Nусе JW.
                                                                                                                            (UYEC-)
                                                                                                                                                                             06-APR-1999;
                                                                                                                                                                                                           24-MAR-2000; 2000WO-US08020
                                                                                                                                                                                                                                             26-OCT-2000
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                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                           cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human low adenosine antisense oligonucleotide related sequence #2991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH57161 to AAH57576 represent cell and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated with a cancer, immunopathology or neuropathology
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                                                                                                                            EAST CAROLINA
J W.
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Pred. No.
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Low adenosine (A) content antisense oligonucleotides which trigger adenosine receptors during metabolism, useful e.g. cancers and respiratory obstructions -  ${\sf cancers}$ 

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CC The present invention describes low adenosine (A) content antisense CC oligonucleotides and compositions (I) comprising them. In the antisense CC oligonucleotides the A is replaced by a 'Universal' or alternative base. CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, communosuppressive, antiasthmatic, hypotensive and cytostatic activities. CC The antisense oligonucleotides and (I) can be used to down-regulate the CC expression and or activity of target polypeptides associated with CC lung/respiratory disorders and malignancies, such as stimulating and CC activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and CC chemokines, endogenously produced specific and non-specific enzymes, CC binding proteins, adhesion molecules and their receptors, cytokine and CC chemokine receptors, adenosine receptors, bradykinin receptors, cytokine and CC receptors, CNS and peripheral nervous and non-nervous system peptide CC transmitters, defensins, growth factors, vasoactive peptides and CC receptors, binding proteins and malignancy associated proteins. The CC including respiratory obstruction (especially pulmonary obstruction and/or lung inflammation, allergyies) CC and/or surfactant hypoproduction which are associated with a disease or CC condition selected from pulmonary vasoconstriction, inflammation, condition selected from pulmonary vasoconstriction, inflammation, condition, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary CC pulmonary transplantation rejection, pulmonary infections, bronchitis, cand/or cancer. AAF18434 to AAF21543 represent human polynucleotide condition of the present human polynucleotide conditions.
Sequence 38644 BP; 9551 A; 10265 C; 10290 G; 8538 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 1400-1409; 1592pp; English.
                                                                                                               the present invention.
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밁 QV Search completed: July 28, 2003, 15:54:59 Job time: 47.9617 secs Matches Query Match
Best Local Similarity 16814 GCAGAGTACTCTCCTCTG 16797 125 GCAGAGTACTCTCCTCTG 142 18; Conservative 10.3%; Score 18; DB 100.0%; Pred. No. 25 tive 0; Mismatches DB 21; Length 38644; 25; Indels 0, Gaps

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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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       nucleic search, using sw model
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length: 2000000000
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1 AGTCCAGGAACTTGAGCTTT......
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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Sequence 18, Application US/09182145B
Patent No. 6387657
Patent No. 638767

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RESULT 2 US-09-182-145-18/c

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CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: IDEAN, Nicholas M.
TITLE OF INVENTION: Antisense Oligonucleotide Modulation of Human Protein
TITLE OF INVENTION: Kinase C-delta Expression
FILE REFERENCE: ISPH-0357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 18
LENGTH: 1734
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SEQ ID NO 1
LENGTH: 2104
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                                                                                                                                                                                                      AUTHORS: Aris, J. P.
AUTHORS: Basta, P. V.
AUTHORS: Holmes, W. D.
AUTHORS: Ballas, L. M.
AUTHORS: Moomaw, C.
AUTHORS: Rankl, N. B.
AUTHORS: Blobel, G.
AUTHORS: Loomis, C. R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/313,930 CURRENT FILING DATE: 1999-05-18 NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIÇ FILE REFERENCE: P1176R2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Roy, Margaret Ann APPLICANT: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hillan, Ke
APPLICANT: Lawrence,
APPLICANT: Levine, Ar
DATABASE ACCESSION NUMBER: L07860 DATABASE ENTRY DATE: 1993-11-02
                                       ISSUE: 2
PAGES: 171-181
DATE: 1993-08-19
                                                                                                                   TITLE: Molecular and biochemical characterization of a TITLE: recombinant human PKC-delta family member JOURNAL: Biochim. Biophys. Acta
                                                                                                                                                                                                                                                                                                                                                                               UBLICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (59)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                      VOLUME: 1174
                                                                                                                                                                                         AUTHORS: Burns, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                                                                                            Sequence 2, Application US/08966316 Patent No. 5932445
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OTHER INFORMATION: Sequence is synthesized
Patent No. 6387657
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TENGTH: 24
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                                                                                                                                                                                               GENERAL INFORMATION:
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APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gurney, Austin L. APPLICANT: Hillan, Kenneth J. APPLICANT: Lawrence, David A. APPLICANT: Levine, Arnold J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: P1176R2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial sequence
                                                                                       APPLICANT: Mathur, Preete
TITLE OF INVENTION: SIGNAL PEPTIDE
NUMBER OF SEQUENCES: 18
                                                                        CORRESPONDENCE ADDRESS
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                       STREET: 3174 POI
CITY: Palo Alto
COUNTRY:
               STATE:
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6387657
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              CA
                                            E: İncyte Pharmaceuticals,
3174 Porter Drive
                                                                                                                                   Murry, Lynn E.
                                                                                                                                            Au-Young, Janice
Reddy, Roopa
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                             ; SOFTWARE: FastSEQ for Windows V. SEQ ID NO 55; LENGTH: 463; TYPE: DNA; ORGANISM: Chlamydia trachomatis US-09-556-877-55
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Best Local S
Matches 16
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Matches
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Patent No. 6432916
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                    APPLICANT: Maisonneuve, Jeff
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C5
                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-TELECOMMUNICATION INFORMATION: 650.855-0555
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IMMEDIATE SOURCE:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: Herewith
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILLE COLLEGE 1457779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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                                                                    Similarity
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Skeiky, Yasir
Fling, Steve
                    AAGGGACAGCAGAGTA 132
                                                                                                                                                                                   FastSEQ for Windows Version 3.0/4.0
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AAGGGACAGCAGAGTA 397
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                                                      9.1%; Score 16;
100.0%; Pred. No.
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100.0%; Pred. No.
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Sequence 58, Application US/09620412C
Patent NO. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INF
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
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CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 55
LENGTH: 463
TYPE: DNA
ORGANISM: Chlamydia trachomatis
US-09-620-412C-55
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; Sequence 55, Application US/09620412c
; Patent No. 6448234
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; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-556-877-58
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SEQ ID NO 58
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C5
CURRENT APPLICATION NUMBER: US/99/556,877
CURRENT FILING DATE: 2000-04-19
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nes 16; Conserv
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o. 6432916
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Fling, Steve
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Pred. No.
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; SEQ ID NO 22
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-556-877-22
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                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 22 LENGTH: 601
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Best Local Similarity
                                   Query Match
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                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/288,594A CURRENT FILING DATE: 1999-04-08 NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                             TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE TREATMENT TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION FILE REFERENCE: 210121.46SC1
                                                                                                                                                                                                                                          APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Fling, Steven P.
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CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
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APPLICANT: Skeiky, Yasir
APPLICANT: Fling, Steve
APPLICANT: Malsonneuve, Jeff
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                                                                          TYPE: DNA ORGANISM: Chlamydia trachomatis
Local Similarity
nes 16; Conserv
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NNT: Probst, Peter
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100.0%; Pr
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Pred. No.
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Pred. No.
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NUMBER OF SEQ ID NOS: 305
SOFTWARE: FastSEQ for Windows Ver
SEQ ID NO 25
LENGTH: 696
TYPE: DNA
ORGANISM: Chlamydia trachomatis
US-09-556-877-25
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US-09-556-877-25/c
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; ORGANISM: Chlamydia trachomatis
US-09-620-412C-22
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US-09-620-412C-22/c
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Best Local S
Matches 16
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CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTMARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 22
LENGTH: 601
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APPLICANT: Steven P. Fling
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, App. No. 643291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/09620412C Patent No. 6448234
                                                               Sequence 25, Application US/09288594A Patent No. 6447779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Fling, Steve
APPLICANT: Maisonneuve, Jeff
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 20121.46905
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT FILING DATE: 2000-04-19
 APPLICANT:
                            APPLICANT: Probst, Peter
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Bhatia, Ajay
Skeiky, Yasir A.W.
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Steven P. Fling

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

FILE REFERENCE: 210121.469C7

CURRENT APPLICATION NUMBER: US/09/620,412C

CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 363

SOFTWARE: FASTSEQ FOR Windows Version 3.0/4.0

SEQ ID NO 25

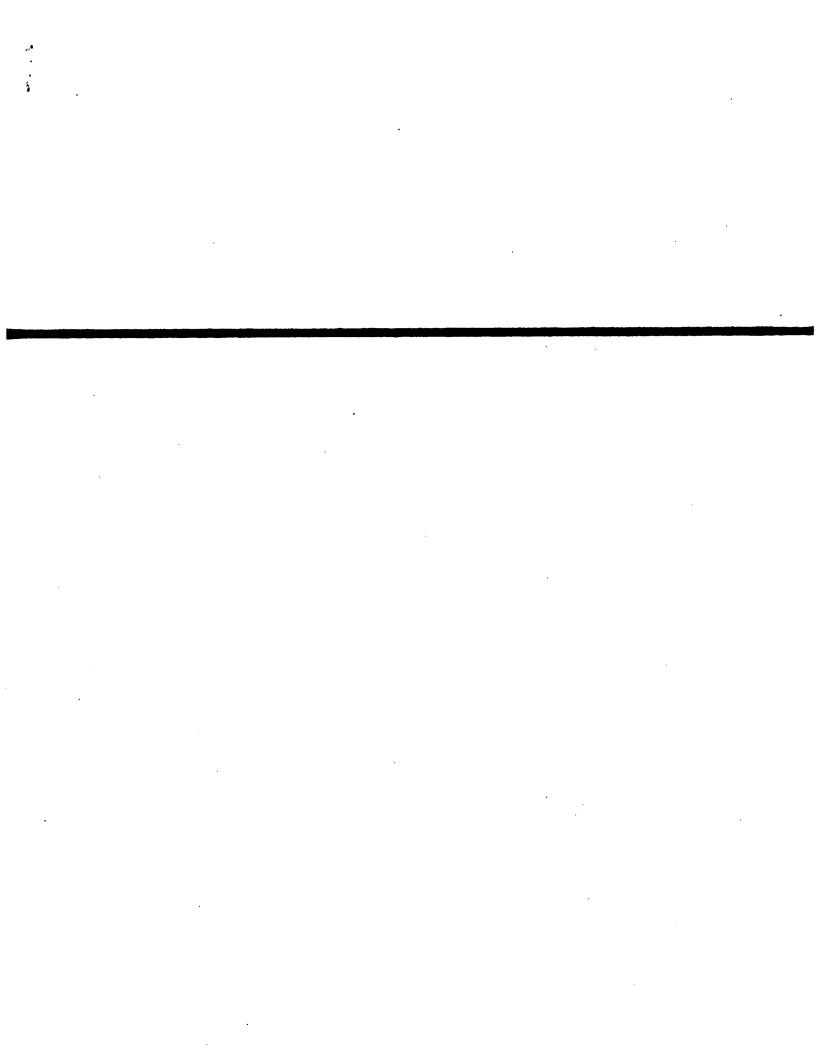
SEQ ID NO 25

LENGTH: 696

TYPE: DNA

ORGANISM: Chlamydia trachomatis

US-09-620-412C-25
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; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE TREATMENT
; TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C1
; CURRENT APPLICATION NUMBER: US/09/288,594A
; CURRENT FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-288-594A-25
Search completed: July 28, 2003, 15:58:55 Job time: 10.5631 secs
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Ce 1, Application tation No. US2002011 RAL INFORMATION: RAPLICANT: John J. TITLE OF INVENTION NUMBER OF SEQUENCE CORRESPONDENCE ADDI ADDRESSEE: LA STREET: Beston STATE: Massa COUNTRY: Boston STATE: Massa COUNTRY: USA ZIP: 02109 COMPUTER READABLE MEDIUM TYPE: COMPUTER READABLE MEDIUM TYPE: COMPUTER: IBN OPERATING SYX SOFTWARE: PAT CURRENT APPLICATION TILLED AND APPLICATION APP		
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Heling Date: Hoppy disk Computer: IBM PC Compation Date: Patention US/10010408 and USES DER OF SEQUENCES: 13 SEEP OF SEQUENCES: 13 SEEP OF SEQUENCES: 13 SEEP OF SEQUENCES: 12 STATE: MASSACHUSELS: 28 State Street CITY: Boston STATE: MASSACHUSELS COUNTRY: USA ZIP: 02109  UTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATION DATA: APPLICATION NUMBER: US/1 FILING DATE: 07-Dec-2001 CLASSIFICATION UMBER: US/1 FILING DATE: WARDLOWN ENTAFIELD NUMBER: US/1 FILING DATE: UNFORMATION: REFERENCE/DOCKET NUMBER: US/1 FILING DATE: G617)227-7400 TELEFAX: (617)227-7400 TELEFAX: (617)742-4214  UN FOR SEQ ID NO: 1:		
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RESULT 3
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; Publication No. US20030068678A1
· GENERAL INFORMATION:
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APPLICANT: No. US20030091973A11 II, L. Staton
APPLICANT: Raha, Debasish
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-09-19 NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/233,579 PRIOR FILING DATE: 2000-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/956,622A CURRENT FILING DATE: 2001-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Method of Identifying Osteoregenerative Agents Using TITLE OF INVENTION: Differential Gene Expression FILE REFERENCE: 21402-445
                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 439
TYPE: DNA
ORGANISM: Rattus norvegicus
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TYPE: nucleic acid
STRANDEDNESS: single
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Query Match
Best Local Similarity
Watches 35; Conserve
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                                        SEQ ID NO 18
LENGTH: 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 156
SEQ ID NO 17
LENGTH: 1734
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                                                                                                                                                 CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145E
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
PRIOR PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
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                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/112,267
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: P1176R2
                                                                                      NUMBER OF SEQ
                                                                                                                PRIOR FILING DATE:
                                                                                                                                      PRIOR APPLICATION NUMBER: EARLIER
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CURRENT FILING DATE: 2002-03-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: P1176R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
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Hillan, Kenneth J.
Lawrence, David A.
Lewine, Arnold J.
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Hillan, Kenneth J.
Lawrence, David A.
Levine, Arnold J.
Pennica, Diane
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Wood, William I.
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musculus
                                                                                                           EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   David A.
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Pred. No.
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                                                                                                              APPLICATION NUMBER: US 60/081,695 DATE: 1998-04-14
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SEQ ID NO 378
LENCTH: 1671
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
US-09-841-132-378
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US-09-815-242-9990
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Matches
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                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR PILING DATE: 2000-05-23 PRIOR FILING DATE: 2000-05-23 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIO
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CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
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APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
                                                                                                             PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-12-27
                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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                                                               NUMBER OF SEQ
                                                                                           PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
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                                 FastSEQ for Windows Version 4.0
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Trawick, John D.
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Yamamoto, Robert T.
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Zyskind, Judith W.
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                                                                                           2001-02-16
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100.0%; Pred. No.
tive 0; Mismatc
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; Mismatches
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; NAME/KEY: misc_feature
; LOCATION: (1)...(2586)
; OTHER INFORMATION: n = A,T,C
US-09-815-242-9990
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US-10-027-632-114289
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                    Sequence 114290, App GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastS
SEQ ID NO 114289
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CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
                                                                                                                APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Polymorphisms
FILE REFERENCE: 108827.129
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28 PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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Pred. No.
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                                                                                                                                               and Mapping of Single Nucleotide in the Human Genome
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APPLICATION NUMBER: US 60/198,676 FILING DATE: 2000-04-20

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                                                                                                                                    FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(3186778)

OTHER INFORMATION: n = A,T,C

US-10-027-632-174961
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US-10-027-632-114290
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-09-28
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Best Local S
Matches 18
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SEQ ID NO 114290
LENGTH: 3073
                                                                     Matches
                                                                                                        Query Match
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SOFTWARE: FastSEQ
SEQ ID NO 174961
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CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR APPLICATION NUMBER: US 60/218,006
OR FILING DATE: 2000-07-12
OR APPLICATION NUMBER: US 60/198,676
OR FILING DATE: 2000-04-20
OR APPLICATION NUMBER: US 60/193,483
OR FILING DATE: 2000-03-29
OR APPLICATION NUMBER: US 60/185,218
OR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
FILING DATE: 1999-09-28
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               47 AGCACTCGCAAAACAGGA 64
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18; Conserv
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AGCACTCGCAAAACAGGA 805023
                                                                     Conservative
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Pred. No.
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Pred. No.
                                                                     Mismatches
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US-10-112-267-110/c
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                                                                                    SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7073
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7073, Application US/09783590 Patent No. US20020110850A1
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Best Local S
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SEQ ID NO 110
LENGTH: 24
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PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/081,695
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/081,695
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
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                                                                                                                                                                                                                                                                                 APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
FILE REFERENCE: PO-16.2C1
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dillon, Patrick J. APPLICANT: Haseltine, William
                                                                                                                               PRIOR FILING DATE: 1994-11-21
                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                          PRIOR APPLICATION NUMBER: 08/346,731
                                                                                                                                                                                               PRIOR FILING DATE: 1995-04-12
                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 08/420,856
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CURRENT FILING DATE: 2002-03-27
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APPLICANT: WOOd, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
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                                           TYPE: DNA
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ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: 1-24
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                                                             ENGTH:
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Ruben, Steven M.
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Hillan, Kenneth J.
Lawrence, David A.
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Pennica, Diane
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o. US20030068678A1
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Pred. No.
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; LCCATION: (1)...(451)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-12392
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                                                                                                                                                                                           Sequence 204519, Application US/10027632 GENERAL INFORMATION:
APPLICANT: Wang, David G.
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Best Local 9
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12392
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                               CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
                                                                                                                                    TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US/09/235,076 PRIOR FILING DATE: 1999-01-20
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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nes 17; Conserv
APPLICATION NUMBER: US 60/193,483 FILING DATE: 2000-03-29
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; Sequence 204521, Application; GENERAL INFORMATION:
; GENERAL INFORMATION: David G.; TITLE OF INVENTION: Identi; TITLE OF INVENTION: Polymo
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                                                                                          RESULT 15
US-10-027-632-204521/c
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US-10-027-632-204520
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LENGTH: 627
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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Best Local Similarity
Matches 17; Conserv
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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CURRENT FILING DATE: 2002-04-30
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PRIOR APPLICATION NUMBER: US 60/156,358
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Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome

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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2003 Compugen Ltd.
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## ALIGNMENTS

RESULT 1

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	REFERENCE AUTHORS TITLE JOURNAL MEDLINE COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	BQ195526/c LOCUS DEFINITION
Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA 7el: 319 335 8250 Fax: 319 335 9565 Email: msoares@blue.weeg.uiowa.edu The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A	Rattus.  1 (bases 1 to 762)  Bonaldo,M.F., Lennon,G. and Soares,M.B.  Bonaldization and subtraction: two approaches to facilitate gene discovery  Genome Res. 6 (9), 791-806 (1996)  97044477  Contact: Soares, MB	BQ195526.1 GI:20371077 BQ195526.1 GI:20371077 EST. Norway rat. Norway rat. Rattus norvegicus Eukharyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	BQ195526 762 bp mRNA linear EST 30-APR-2002 UI-R-CN1-cmg-k-07-0-UI.s1 UI-R-CN1 Rattus norvegicus cDNA clone UI-R-CN1-cmg-k-07-0-UI 3', mRNA sequence.

FEATURES source

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tail. The sequence tag present in the cDNA between the NotI site and the Oligo-dT track served to identify it as a clone from the normalized cervix library cDNA Library Preparation: M.B. Soares ! Clone distribution: clones will be available through Research
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                     bladder, normalized rat curvix, normalized rat brown adipose, normalized rat tundus, and normalized rat brown adipose, normalized rat tundus, and normalized rat trace rat salivary gland. It was constructed according to the procedure described by Bonaldo, Lennon & Soares (Genome Research Genome 6: 791-806, 1995). For construction of the CNI library, plasmid DNA from the pool of normalized libraries was electroporated into completent backeria for the production of single-stranded circular DNA. This was then used as a tracer in a subtractive hybridization with a driver population. By a pool of about 34,000 clones from the final driver population. By a pool of about 29,000 clones from subtracted libraries CAO-BAS, R-CAO-BAS, R-CAO-
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CN1
library is a subtracted library derived from the following
pool of seven normalized rat libraries: normalized rat
seminal vesicles, normalized rat, penis, normalized rat
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non-normalized libraries that make
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AGGAAGGCTCCACACCTCTGGCAGGCCAGGGCCTTTCTCTTCAGCATGAGAAAGACAAAGG 120
                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB374499 RIKEN full-length enriched, 16 days embryo head Mus BB374499 RIKEN full-length enriched, 16 days embryo head Mus musculus cDNA clone Cl30075G16 3' similar to AF126063 Mus musculus connective tissue growth factor-like protein precursor (Ctgfl) mRN
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Car, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., It Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N. Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusa
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BB374499.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resulting pool represented about 2,000 clones from the pool of normalized libraries, CNO, that makes up the tracer. The corresponding plates are R-CNO-BIR, R-CNO-BIL, R-CNO-BIG,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ρ
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176 c 1
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TAG_LIB-UI-R-CN1
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100.0%;
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%; Pred. No. 5.7e-70;
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                                                                                          Itoh, M.,
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                                                                                                                                                           Local
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Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Target of Physical Research (RIKEN)
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RIKEN Mouse ESTs (Konno,H., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinayawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, Yamanaka, I., Tagawa, A., Takahiki, A., Watanabe, S., Yamamura, Yamanaka, I., Yamanaka, Yamanaka, I., Yamanaka, I., Yamanaka, I., Yamanaka, I., Y
                                                                                                                                                                Similarity
TCTGGCAGGCCAGGGCCTTTCTCTCAGCATGAGA 111
                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                           87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                           primer adapter of sequence [5' GAGAGAGAGATTATTAATTAATCCCCCCCCCCCC 3']. cDNA was cloned into the xhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C130075G16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="head"
/dev_stage="16 days embryo"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RIKEN full-length enriched, 16
                                                                                                                                                                                                                                                                                      80 c
                                                                                                                                                       20.0%;
                                                                                                                     0,
                                                                                                                                                       Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                       67 g
                                                                                                                     Mismatches
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                                                                                                                                                   DB 10; 1
1.1e-07;
                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                         Length 315;
                                                                                                                 Indels
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COMMENT
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BB792544
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2009)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB792544 RIKEN full-length enriched, kidney CCL-142 musculus cDNA clone G430141015 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing pipeline with 384 multicar
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB792544.1 GI:16961776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         further details.
e mouse tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y. and Hayashizaki, Y
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                                                                                                                                                                   /note="pooled cell lines; (cell_line=CRL-1751 WEHI 164), (cell_line=CRL-2116 JC), (cell_line=RCB-0035 WEHI-3), (cell_line=RCB-0545 OHTA), (cell_line=RCB-0545 OHTA), (cell_line=RCB-1283 B16 (cell_line=RCB-1283 B16 melanoma), (cell_type=B cells, cell_line=CRL-1702 WEHI 231), (cell_type=Leydig cells, cell_line=CRL-2065 MLTC-1), (cell_type=Nullipotent stem cell_cell_line=CRL-2070 NE),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                     (tissue_type=bladder, cell_line=RCB-0544 MBT-2),
(tissue_type=bone_marrow, cell_type=stroma cell,
                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="kidney"
/cell_line="CCL-142 RAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="G430141015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RIKEN full-length enriched, kidney CCL-142
CRI-2028 SR-4987), (tissue_type=kidney,
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1 (bases 1 to 418)

1 (bases 1 to 4
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35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
Contact: Marra M/Mouse EST Project
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                             /note-"Organ: uterus; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pregnant mouse uterus, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1498153"
/clone_lib="Soares_NMPu"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="adult"
/lab_host="DH10B"
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1.1e-07;
                                                            DB 9; #Length 418;
                              1.2e-07;
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Best Local :
                                                                    ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution info
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9254 row: f column: 02
High quality sequence stop: 705.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
1 (bases 1 to 307)
                                                                                                                                                                                BB220676 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A530061F23 3′ similar to AF126063 Mus musculus connective tissue growth factor-like protein precursor (Ctgfl) mRNA
                                                                                                          EST.
                                                                                                                                                                                                                                                                                                                                                                                                                      . Similarity 35; Conser
                                                                                                                          BB220676.1 GI:8889288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BF138093
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                                                                                      house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: SalI; transgenic model WNT-1, expression driver MMTV-LTR enhancer; Cloned unidirectionally Primer: OldT. Library constructed by Life Technologies.

Investigator providing samples: Gilbert Smith, NIH" 204 c 205 g 190 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:4012801"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
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Pred. No. 1.5e-07;
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303.
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y., and Hayashiayi,Y.
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Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
T., Tsunoda,Y., Matahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.,
Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M., and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
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Unpublished (2000)
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Fax: 81-45-503-9216
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                                                                                                                                                                                                   modified pBluescript KS(+) after bulk excision from Lambda
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/dev_stage="adult"
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/db_xref="taxon:10090"
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High quality sequence stop: 299
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-MT0193-
151200-565-e02&t3=2000-12-15&t4=1)
Seq primer: puc 18 forward
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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BB367824 Ilnear EST 12-JUL-2000 BB367824 RIKEN full-length enriched, 16 days embryo head Mus musculus cDNA clone C130039K03 3' similar to AP126063 Mus musculus connective tissue growth factor-like protein precursor (Ctgfl) mRNA

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REFERENCE
AUTHORS
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Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-(
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RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)
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URL:http://genome.gsc.riken.go.jp/
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High-efficiency full-length cDNA cloning.
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Automated filtration-based high-throughput plasmid preparation ystem. Genome Res. 9 (5), 463-470 (1999)
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nno, H., Aizawa, K.
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                              cap-trapper. Second strand cDNA was
primer adapter of sequence [5'
                                                                                                                         prepared by using trehalose themmo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                         contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="head"
/dev_stage="16 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="C130039K03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RIKEN full-length enriched, 16 days embryo
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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BamHI sites.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0124 row: I column: 0:
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1M0124I03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0124I03 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: plasmid ends
High quality sequence stop: 538
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Seq primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Res
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                       polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                        musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
  purified.
                    with adaptors complementary to the insert adaptors and
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                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0124103"
                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Mouse 10kb plasmid UUGC1M library"
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The sheared, adaptored mouse DNA was annealed to
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AW660658 546 bp mRNA linear 99634 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKBN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAC end sequences of Library PTB
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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and selected for ampicillin resistance."
a 107 c 92 g 177 t
                                                                                                                                                                                                  /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
65 c 187 g 226 t 7 others
                                                                                                                                                                                                                                                           /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-072N12.R"
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                                                                                                                                     house mouse
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                                                                                                                                                                                        DNA sequence.
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ACCESSION
              Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
                                                                                                                               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 591)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, UTel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 546)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                           RPCI-24-265L18.TV RPCI-24
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AW660658.1
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FORWARD: AGGAAACAGCTATGACCAT
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Other_GSSs: RPCI-24-265L18.TJB
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ilarity 100.0%;
Conservative (
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135 c 147 g 104 t
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/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pooled"
/lab_host="DH10B"
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McKown,C.G.,
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BE778127/c
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Clones are derived from the mouse BAC library.RPCI-24. For BAC library availability, please contact pletter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/oxderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 265 row: L column: 18

Seq primer: T7

Class: Page:                                                                                                                                 CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9511 row: p column: 13
High quality sequence stop: 635.
Location/Qualifiers
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BE778127
BE778127.1 GI:10199325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 932)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Fax: 301 838 0208
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/note="Vector: pTAKBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTAKBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTAKBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTAKBAC1; Site_2: BamH1; Site_2: BamH1; Sites using MboI partially digested male C57BL/6JDNA."
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3866748"
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/clone="RPCI-24-265L18"
/clone_11b="RPCI-24"
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/strain="C57BL/6J"
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322 GAAGGCTCCACACCTCTGG 304
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                               63 GAAGGCTCCACACCTCTGG 81.
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19; Conserv
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National Institutes of Health, Mammalian
Unpublished (1999)
                                                                   Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 145
High quality sequence stop: 179.
Location/Qualifiers
1. .957
                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://imagge.llnl.gov
Plate: LLAM11349 row: m column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
BI334722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI334722 957 bp mRNA linear EST 30-JUL-20 602999615F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5141931 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 957)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                      252
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                                                                   Conservative
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                                                                                                                                                  /tissue_type="cervical carcinoma cell line"
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/note="Organ: cervix: Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
262 c 193 g 249 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="retinoblastoma"
/lab_host="DH10B (phage=resistant)"
/note="0rgan: eye; Vector: pCMV-SPORT6; Site_1:
Site_2: Sall; Cloned unidirectionally. Primer:
Average insert size 1.75 kb. Library construct
Technologies."
197 c 258 g 293 t
                                                                                                                                                                                                                                                                       /clone="IMAGE:5141931"
/clone_lib="NIH_MGC_12"
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/db_xref="taxon:9606"
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Pred. No.
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45;
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45;
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                                                                                                 Length 957;
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Direct Submission
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
sequefggenoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS.
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Saccharomyces kluyveri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   keywords for description of this sequence and
the other extremity of this insert.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuveglise,C., Bon,E., Lepingle,A., Wincker,P., Artiguenave,F., Gaillardin,C. and Casaregola,S.
Genomic exploration of the hemiascomycetous yeasts: 9.
Saccharomyces kluyveri
FEBS Lett. 487 (1), 56-60 (2000)
20584719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.
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                                                                                                  Conservative
                                                                                                                                                                                                                                                                /evidence-not_experimental complement(<1073. >1138)  
/note-"similar to Saccharomyces cerevisiae ORF YMR015c [
ERG5; C-22 sterol desaturase]"
                                                                                                                                                                                                                                                                                                                                                                                  /note="end : T3"
<193. .>807
<193. .>807
/note="similar to Saccharomyces cerevisiae ORF YMR014w [
weak similarity to s.pombe hypothetical protein SPAC4F10
                                                                                                                                                                                                                  /evidence=not_experimental
165 c 285 g 266
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/clone="AU0AA012G07"
/clone_lib="AU0AA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Saccharomyces kluyveri"
/strain="CBS 3082"
                                                                                           10.9%; Score 19; DB 17; 100.0%; Pred. No. 48; tive 0; Mismatches (
                                                                                                0,
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Search completed: July 28, 2003, 18:02:13 Job time: 318.442 secs

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Result No. $\alpha$ C 0000 O Score Query Match 36296 83021 84001 117840 129090 135817 147990 162486 163258 Length DВ 10 AF126063 AR210337 AX076919 AX464186 AR210320 AR210323 AR210323 AR210323 AR210323 AR21039352 AR210901782 AR21090173 AC012010 AC122105 AC123106 AC122105 AC122105 AC122105 AC122105 AC122105 AC122105 AC122384 AC123884  AC123884 AC12 AC126895 AC095418 AC126895 AC126895 AC1259981 AR210324 AR210325 AF100778 AL731698 AL669906 IJ AC126895 Rattus no AC026895 Rattus no AC126895 Rattus no AF259981 Rattus no AF259981 Rattus no AF259981 Rattus no AF26923 Sequence AF210323 Sequence AF210780 Homo sapi AF210780 Homo sapi AF210781 Homo sapi AF210782 Homo sapi AF210782 Homo sapi AF210782 Homo sapi AF210782 Homo sapi AF210782 Homo sapi AF210783 Sequence AF2782 Homo sapi AF210781 Homo sapi AF210781 Homo sapi AF210781 Homo sapi AF210781 Mus muscu AF21884 Mus muscu AF21884 Homo sapi AF21884 Homo sapi AF21884 Homo sapi AF21884 Homo sapi AF21884 Homo sapi AF21884 Homo sapi AF21884 Homo sapi AF218856 Homo sapi AF218856 Homo sapi AF218856 Homo sapi AF218856 Homo sapi AF218856 Homo sapi AF218856 Homo sapi AF21886 Homo sapi Description

## ALIGNMENTS

REFERENCE AUTHORS	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AC126895	RESULT 1
Rattus.  1 (bases 1 to 137964)  Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,	Madrudia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	Rattus norvegicus.	HTG; HTGS_PHASE1.	AC126895.1 GI:21724040	AC126895	***, 49 unordered pieces.	Rattus norvegicus clone CH230-301E4, *** SEQUENCING IN PROGRESS	AC126895 137964 bp DNA linear HTG 24-JUL-2002		

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Carron, T. F., Carter, M., Cavasos, S.R., Chacko, J., Chavez, D. Chen, G., Chen, R., Chen, Z., Chowdhry, I., Chacko, C., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathornes, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Falls, T., Ferraguto, D., Flagy, N., Havlak, P., Hawes, A., Hernandez, J., Hogues, M., Holloway, C., Hollins, B., Falls, T., Howard, S., Huth, M., Haylak, P., Hawes, A., Hernandez, J., Jackson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlson, E., Lui, J., Liu, W., Loulseged, H., Lozado, R., Juna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Morgan, M., Morris, S., Moser, M., Nolabata, K., Morgan, M., Morris, S., Moser, M., Nolabo, R., Pece, A., Payton, B., Pecey, J., Perez, L., Peters, L., Pickens, R., Pace, A., Payton, B., Pecey, J., Perez, L., Peters, L., Peters, E., Sonatke, T., Sparks, A., Stanley, H., Stone, H., Sodergren, E., Sonatke, T., Sparks, A., Tonson, R., Wang, Q., Wartin, S., Warren, R., Washington, C., Watlington, S., Wulley, K., Wulley, K., Wulley, K., Wulley, K., Wulley, K., Walley, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (24-JUL-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 137964)
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 49 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 137964)
                                                                                                                                                                                                                                Center project name: GZHG
Center clone name: CH230-301E4
Center clone name: CH230-301E4
Center clone name: CH230-301E4
Chemistry: Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 89474 bases at least 040
Consensus quality: 93422 bases at least 030
Consensus quality: 936506 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.
Contact: hgsc-help@bcm.tmc.edu
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* is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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                                                                                          Rattus norvegicus clone CH230-7C10, 51 unordered pieces.
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                        Rattus norvegicus
                                                  Norway rat.
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/db_xref="taxon:10116"
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Douthwaite, K. J. Draper, H. Dugan-Rocha, S. Durbin, K.J.,

Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,

Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,

Falls, T., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,

Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,

Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,

Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,

Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,

Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,

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Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,

Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,

Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,

Kratisson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,

Karlsson, E., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,

Lozado, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,

Lozado, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,

Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,

Maneshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,

Manes, G., Matchell, T., Mohabbat, K., Morgan, M., Mortis, S.,

Noser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N.,

Nguyen, N., Nickerson, E., Nwokenkwo, S., Oghh, M., Okwuonu, G.,

Oragunye, N., Ovledo, R., Pace, A., Payton, B., Peery, J.,

Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y.,

Rodergren, E., Sonaike, T., Sparks, A., Tamerisa, N., Thomas, S.,

Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,

Wang, S., Wallianson, A., Walezyk, R., Woden, S.,

Willianson, A., Walezyk, R., Woden, S.,

Willianson, A., Walezyk, R., Woden, S.,
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Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, TSA
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Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Navlor Plaza, Houston, TX 77030, USA
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Chen, J., Charlet, Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, R., 
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Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barboria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bonnin,D., Bimage,K., Blankenburg,K., Bonnin,D., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bimage,K., Blankenburg,K., Bimage,K., B
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                                                                                                                     Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryan Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).

length length

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NOTE: This is a 'working draft' sequence. It currently consists of 51 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K. J.,
Earnhart, C., Edgar, D., Elwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hatt, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Holloway, C., Hollins, B.,
Hernandez, O., Huber, J., Hulyk, S., Hume, J., Jackson, L. E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Jackson, L. E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Jackson, L. E.,
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Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Jackson, L.,
Karlsson, E., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Lozado, R., J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Lozado, R., J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maneshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mavhiney, E., McLeod, M.P., Meador, M., Mel, G., Metzker, M.,
Noderyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwonou, G.,
Scher, S., Soot, E., Pu, L., Quiles, M., Ren, Y.,
Rives, M., Rojubokan, I., Shooshtari, N., Sisson, I.,
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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.,
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Barbaria, J., Benton, J., Briava, M., Brown, E., Brown, M., Bryant, N.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
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Consensus quality: 96506 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently
consists of 49 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N. but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
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/db_xref="taxon:10116"
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Rattus norvegicus
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
Unclassified.

1 (bases 1 to
Botstein,D.A.,
Lawrence,D.A.,
                                                                                                     AR210324
Sequence
AR210324
AR210324.
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Mol. Cell
98414629
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2 hang, R., averboukh, L., Zhu, W., Zhang, H., Jo, H., Coffey, R.J., Pardee, A.B. and Liang, P.
10 Identification of rCop-1, a new member of the CC as a negative regulator for cell transformation Mol. Cell. Biol. 18 (10), 6131-6141 (1998)
                                                           Unknown
                                                                        Unknown
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NGRRYLDGETEKPNCKYLCRCDDGGFTCLPLCSSDVTLPSWDCPRFKRIQVPGKCCPE
WYCDGGYTPAJORSAAQHQLSALVTPASADAPWPNWSTAWGPCSTTCGLGIATRYSN
QNRFCQLEIQRRLCLPRPCLAARSHSSWNSAF*
1 491 c 480 g 384 t
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262. .1014
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/protein_id-"AAF69011.1"
/db_xref-"G1:7739781"
/translation-"MRGSPLIRLLATSFLCLLSMVCAQLCRTPCTCPWTPPQCPQGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organ1sm="Rattus norvegicus"
/db_xref="taxon:10116"
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99.1%;
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 Cohen, R.L.,
Levine, A.J.
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Rodentia;
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Pred. No. 7e-50;
Mismatches
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6387657
               Goddard, A.D.,
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Roy, M. Ann. an
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   Hillan,K.
d Wood,W.I
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Sequence
AR210325
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1734)
Pennica,D., Swanson,T.A., Welsh,J.W., Roy,M.A., Lawrence,D.A., Lee,J., Brush,J., Taneyhill,L.A., Deuel,B., Lew,M., Watanabe,C., Cohen,R.L., Melhem,M.F., Finley,G.G., Quirke,P., Goddard,A.D., Hillan,K.J., Gurney,A.L., Botstein,D. and Levine,A.J.
                                                                                                                                                 (Wisp2) mRNA, complete AF100778 AF100778.1 GI:4028578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WISP
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1 (bases 1 to 1734)

1 (bases 1 to 1734)

Botstein, D.A., Cohen, R.L., Goddard, A.D., Gurney, A.L., Hillan, K.J., Botstein, D.A., Levine, A.J., Pennica, D., Roy, M.Ann. and Wood, W.I.
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Mus musculus connective tissue
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                                                                                                             musculus
                                                                                                                         musculus.
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polypeptides and nucleic acids encoding
nt: US 6387657-A 18 14-MAY-2002;
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ilarity 100.0%;
Conservative
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5.8e-37;
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                                                                                                                                                                                                                                                                                                                                                        AL731698
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                             Submitted (24-MAY-2002) Wellcome Trust Sanger Institute, Hinxto Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 61072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90;
                                                                                            On May 25, 2002 this sequence version replaced gi:21213601. During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                        Wallis,J.
                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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MGRRYLDGETFKPNCRVUCRCDGGFTCLFLCSBDVRLDSWDCPRPRRIOVPGRCCPE
WVCDQAVMQPAIQPSSAQGHQLSALVTPASADGFCPNMSTAWGPCSTTCGLGIATRVS
NQNRFCQLEIQRRLCLSRPCLASRSHGSWNSAF*
491 c 495 g 393 t
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257. .
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GI:4028579"
/translation="MRGNPLIHLLAISFLCILSMVYSQLCPAPCACPWTPPQCPPGVP
                                                                                                                                                                                                                                                                                                                                                                                              sequence from clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAC96320.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="transformed by Wnt-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="mammary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="epithelial"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_line="C57MG"
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Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 211865 bases at least; Q40
Consensus quality: 213403 bases at least; Q30
Consensus quality: 214139 bases at least; Q20
Insert size: 214757; sum-of-contigs
Insert size: 234243; 1.8% error; agarose-fp
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                                                                                                                                                                                                                                                                                                                                              Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 25, 2002 this sequence version replaced gi:18181793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG;
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                                                                                                                                                                                                     Center project name: bM217C2
                                                                                                                                                                                                                                 Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                       Center: Wellcome Trust Sanger Institute Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-JUL-2002) Wellcome Trust Sanger Institute, Hinxton
Cambridgeshire, CB10 1SA, UK. E-mail enqûiries:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 216757)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   database can be found at
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/db_xref="taxon:10090"
/chromosome="2"
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15368 c 15033 g ]
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100.0%; Pr
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35071 39671: contig of 4601 bp
35072 39771: gap of 100 bp
39672 39772 46360: contig of 6589 bp
46361 46460: gap of 100 bp
46461 49809: contig of 3349 bp
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213978 21675;
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65990 66089: gap of 100 bp
66090 84635: contig of 18546 bp in length
84636 84735: gap of 100 bp
84736 87399: contig of 2664 bp in length
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                                                     /note="assembly_fragment:00812
fragment_chain:1"
35071. .39671
                                                                                                                                                                 4101.
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                                                                                                                                                                                                 clone_end:SP6
                 fragment_chain:1"
                                                                                                             15368.
                                                                                                                           fragment.
                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="2"
                                                                                                                           /note="assembly_fragment:00814
fragment_chain:1"
                                     note="assembly_
                                                                                                                                                                                                                  note="assembly_fragment:03429/
                                                                                                                                                                                                                                                                           /clone="RP23-217C2"
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200095; contig of 30309 k
00195; gap of 100 bp
213877; contig of 13682 b
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                                                                                                                                                                                                                                                                                                                                                                                       216757:
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69686: contig of 18014 bp in
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                                                                                                                                                                 .15267
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18: contig of 4506 bp
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contig of 14679 h
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                                  fragment:03544
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Mus musculus connective tissue (Ctgfl) mRNA, complete cds. AF126063
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                                                                                                                                                        GGGCCTGGTTTGTCAGCCTGGGGCAGGCCC
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fragment_chain:2"
84736. .87399
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51573 c 51904 g
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fragment_chain:6"
213978. .216757
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fragment_chain:5"
145909. .151572
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fragment_chain:3"
98702. .105522
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fragment_chain:5"
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fragment_chain:5"
151673. .169686
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fragment_chain:4"
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fragment_chain:4"
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fragment_chain:3"
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fragment_chain:2"
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fragment_chain:6"
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fragment_chain:2"
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fragment_chain:2"
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ragment_chain:3"
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                                  p mRNA linear
growth factor-like
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2.3e-37;
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                 Sequence 38
AR210337
AR210337.1
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J. Biol. Chem. 274 (24), 17123-17131 (1999)
99287915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 1739)
Kumar, S. and Zou, C.
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Kumar, S., Hand, A.T., Connor, J.R., Dodds, R.A., Ryan, P.J.,
Trill, J.J., Fisher, S.M., Nuttall, M.E., Lipshutz, D.B., Zou, C.,
Hwang, S.M., Votta, B.J., James, I.E., Rieman, D.J., Gowen, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                   AR210337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"similar to the Mus musculus WISP-2 protein encoded by the sequence presented in GenBank Accession Number AF100778; putative growth factor; CTGF-L; contains IGF binding (IGFBD), Von Willebrand Factor type C (VWC) repeat and thrombospondin type I (TSP1) domains; member of the CCN (CTGF/Cyr61/Nov) family; lacks the fourth carboxy-terminal (CT) domain present in other members of the CCN family
                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAD18058.1"
/db_xref="G1:4337060"
/db_xref="G1:4337060"
/db_xref="G1:4337060"
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/translation="Miscapelihilidaiseic/IlsmvysQlCpApCaCpwTppQCppGSCEV
LVLDGCGCCRVCARRLGESCDHLHVCDPSQGLVCQPGAcApSGRAVCLFEEDDGSCEV
LVLDGCFTKNPCRVLCRCDDGGFTCLPLCSEDVRLPSWDCPRPRRTQVPGRCCPE
WCCDQAVMQPAIQPSSAQGHQLSALVTPASADGPCPNWSTAWGPCSTTCGLGIATRVS
NQNRFCQLEIQRRLCLSRSPCLASRSHASWNSAF"
1 480 c 489 g 395 t
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1. .1739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="connective tissue growth factor-like
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                    GI:21512542
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Swedeland Rd., King of Prussia, PA
                                                                     738
                                                   38 bp
6387657
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19406,

PAT 20-JUN-2002

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SOURCE
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Unknown.
                     Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E., Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L. Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31 from AX076919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and WISP polypeptides and nucleic acids encoding same Patent: US 6387657-A 38 14-MAY-2002;
                                              Baker, K.P.,
                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                               Eukaryota;
                                                                                            Homo sapiens
                                                                                                                             AX464186.1
                                                                                                                                                           AX464186
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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           Wood, W.L.
                                                                                                      human
                                                                                                                                                                                                                                                                                                                                                                               Genentech,
                                                                                                                                                                                                                                                                                                                                                                                       Polypeptidic compositions and method Patent: WO 0105836-A 31 25-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                Wood, W.I
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            and Zhang, Z
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                       Watanabe,C.K.,
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                                                                                Euteleostomi;
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Best Local S
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32; Conserv
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Submitted (11-AUG-1998)
SmithKline Beecham, 709
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Kumar, S., Hand, A.T., Connor, J.C., Dodds, R.A., Ryan, P.J.,
Trill, J.G., Fisher, S.M., Slemmon, J.R., Lipshutz, D.B.,
Bartholomew, V., James, I.E., Rieman, D.J., Gowen, M. and Lee, J.C.
Identification and cloning of CTGF-L from human osteoblasts, a
novel cysteine rich protein containing an IGF binding domain
Bone 23 (5), S240 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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Homo sapiens connective tissue of
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                                                                                     WGRLYREGETFQPHCSIRCRCEDGGFTCVPLCSEDVRLPSWDCPHPRRVEVLGKCCPE
WVCGQGGLGTQPLPAQGPQFSGLVSSLPPGVPCPEWSTAWGPCSTTCGLGMATRVSN
QNRFCRLETGRRLCLSRCPPESRGRSPQNSAF"
1 418 c 389 g 241 t
                                                                                                                                                                                                                                                                precursor"
                                                                                                                                                                                                                                                                                                                              the fourth carboxy-terminal domain members of the CCN family"
                                                                                                                                                                        /protein_id="AAC70350.1"
/protein_id="AAC70350.1"
/db_xref="GI:3462836"
/translation="MyGTPKYHLLAFSLLCLLSKVRTQLCPTPCTCPWPPPRCPLGVP
/translation="MyGTPKYHLLAFSLLCLLSKVRTQLGPTPCTCPWPPPRCPLGVP
LVLDGCGCCRVCARRLGEPCDQLHVCDASQGLVCQPGAGPGGRGALCLLAEDDSSCEV
                                                                                                                                                                                                                                                                                    /product="connective tissue
                                                                                                                                                                                                                                                                                                                                                                     /note="CTGF-L; encodes IGF binding (IGFB), V factor type C (VWC) and thrombospondin type domains; member of the CCN (CTGF/Cyr61/nov)
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/db_xref="taxon:9606"
/chromosome="20"
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418 c 390 g 24
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AUTHORS
Search completed: July 28, 2003, 21:14:43 Job time: 1766.67 secs
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## ALIGNMENTS

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XX C Castellot JJ 23-SEP-1999 W09947556-A2 Rattus sp. Heparin-induced CCN-like protein; HICP; cell-associated activity; ss; cardiovascular disorder; aberrant cell proliferation; fibrotic disorder. Rat HICP polypeptide encoding cDNA 26-NOV-1999 AAZ07516; AAZ07516 standard; (TUFT ) TUFTS 18-MAR-1999; 19-MAR-1998; (first entry) COLLEGE. 98US-0044273 99WO-US05999 cDNA; 1708 ВP

a

Nucleic acid sequences encoding rat heparin-induced CCN-like protein, used in methods to identify modulators or in diagnostic applications

WPI; 1999-562060/47. P-PSDB; AAY27434.

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 Rat HICP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heparin-induced CCN-like protein; cardiovascular disorder; aberrant
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proliferation; fibrotic disorder
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cardiovascular disorder; aberrant
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GATGACGGTGGCTTCACC
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applications
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                            TGCGACCACCTGCATGTCTGCGACCCCAGCCAGGGCCTGGTTTGTCAGCCTGGGGCAGGC
CCTGGCGGCCATGGGGCTGTGTGTCTCTTG
                                                                                                                                                                                                                                                                                                                 33.1%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                     BP;
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                                                                                                                                                                                                                                                                                                                 Score 210; DB 20;
Pred. No. 9.9e-93;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                   74 G; 44 T;
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210; 0

Gaps

60

497 120 437

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RESULT 6
AAX76489/c
ID AAX76489 s
XX
AC AAX76489;
AC AAX76489;
XX
DT 06-AUG-199
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Best Local S
Matches 90
                                                                                                                                                                                                                                                                    The invention provides a rat heparin-induced CCN like protein (HICP) protein. Agents that stimulate or inhibit HICP protein activity or expression, antisense HICP nucleic acid molecules and HICP antibodies, can be used to modulate cell-associated activity. HICP modulators can be used to treat disorders characterized by aberrant HICP protein activity or expression. Probes capable of hybridizing to HICP mRNA or antibodies specific for HICP can be used to detect HICP activity in a biological sample. HICP can be used to treat disorders, such as a cardiovascular or fibrotic disorder, characterized by aberrant cell proliferation. The present sequence represents a cDNA encoding the Yon Willebrand C (VWC) a domain of the HICP polypeptide.
           06-AUG-1999
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-562060/47
P-PSDB; AAY27436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heparin-induced CCN-like protein; HICP; cell-associated activity; ss; cardiovascular disorder; aberrant cell proliferation; fibrotic disorder; von Willebrand C domain; VWC.
                                                                                                                                                                                                                                                                                                                                                                                                                                     used
                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Castellot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09947556-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat HICP VWC
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                                                                                                                                                                                                        90;
                                                                                                                                                                                                                                                                                                                                                                                                                                  acid sequences encoding rat heparin-induced CCN-like protein, methods to identify modulators or in diagnostic applications
                                                                                                                                                                                                                   Similarity
                                                                                                                          CTGTGCCGCTGTGATGACGGTGGCTTCACC 635
                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; cDNA;
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Page 103;
                                                                                                                                                                                                                                                    B₽;
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                                                      DNA;
                                                                                                                                                                                                                                                   A; 47 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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                                                                                                                                                                                                                                                                                                                                                                                                            108pp; English.
                                                                                                                                                                                                                 Score 90; pred. No.
                                                      ВР
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hes 0;
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RESULT 7
AAX76488
ID AAX7

AAX76488

standard; DNA; 1734

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CC Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
                                                                                                                            Best Loc
Matches
                                                                                                                                                           Query Match
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29-OCT-1997;
03-FEB-1998;
                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue-growth disorder; skin disorder; desmoplasia; fibrot kidney disorder; bone-related disorder; osteoporosis; trau connective tissue disorder; catabolic state; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-337420/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Botstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tu connective tissue growth factor; cancer; melanoma; arteriosclero leukaemia; lymphoid mallgnancy; haematopoiesis-related disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Wnt-1 induced secreted polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      testicular-related disorder; angiogenesis; immunological disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse WISP-2 protein complementary nucleotide sequence
                                                                                                                                           госат
    532
                                                               592
                                                                                               410
                                                                                                                            Similarity
90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DA,
AGTGTGTGCACGGAGGCTGGGGGGAGTCCTGCGACCCACCTGCATGTCTGCGACCCCAGCCA
                                                               AGTGTGTGCACGGAGGCTGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGCCA
                                                                                                                                                                                          753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 179-180;
                                                                                                                              Conservative
                                                                                                                                                                                         BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cohen RL,
Levine AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0081695.
97US-0063704.
98US-0073612.
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                                                                                                                                                                                          159
                                                                                                                                                                                          A.
                                                                                                                                           100.0%;
                                                                                                                                                           14.28;
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Pennica D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284pp; English.
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                                                                                                                            0;
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Pred. No.
                                                                                                                                                                                          238
                                                                                                                              Mismatches
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Roy MA, W
                                                                                                                                           DB 20; I
. 5.3e-34;
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                                                                                                                                                                                          other;
                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arteriosclerosis;
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                                                                       В
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                                                                                                                                                                                                                                                                                          The present invention describes Wnt-1 induced secreted polypeptides, CC WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and WISP-3 have homology to connective tissue growth factor (CTGF). CC and WISP-3 have homology to connective tissue growth factor (CTGF). CC Products from the present invention can be used to treat WISP-related CI disorders such as breast, ovarian, and colon cancer or melanoma. The CI color to treat other diseases e.g. benign and malignant tumours, color to treat other diseases e.g. benign and malignant tumours, color to treat diseases e.g. benign and malignant tumours, color to treat other diseases e.g. benign and malignant tumours, color to the products can also be lastocoelic disorders, had an analysis and other glandular, macrophagal, epithelial, stromal, and color blastocoelic disorders, hadmatopoissis-related disorders, kidney colored disorders, skin disorders, adematopoissis-related disorders, kidney colored with the color treated disorders, and inflammatory, colored with most of the colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored colored color
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29-OCT-1997;
03-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAY-1999
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 178–179; 284pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Wnt-1 induced secreted polypeptides, WISP-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Botstein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  testicular-related disorder; angiogenesis; immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WISP-2 protein nucleotide sequence
                                                                                                                                                         l Similarity
·90; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY17651
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                     GGGCCTGGTTTGTCAGCCTGGGGCAGGCCC
                                                                           AGTGTGTGCACGGAGGCTGGGGGAGTCCTGCGACCTGCATGTCTGCGACCCCAGCCA
                                                                                                                                                                                                                                            1734
                                                                                                                 AGTGTGTGCACGGAGGCTGGGGGAGTCCTGCGACCACCTGCATGTCTGCGACCCCAGCCA
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Levine AJ,
                                                                                                                                                                                                                                         B₽;
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97US-0063704.
98US-0073612.
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                                                                                                                                                                                                                                       A; 491
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                                                                                                                                                         0;
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                                                                                                                                                                            Score 90;
Pred. No.
                                                                                                                                                                                                                                       495
                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; melanoma; arteriosclerosis;
                                                                                                                                                                                                                                     G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gurney AL, Hi.
Roy MA, Wood
                                                                                                                                                                                                                                     393 T; 0 other;
                                                                                                                                                                            5.2
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                                                                                                                                                                                             Length 1734;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillan K;
ood WI;
                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorder;
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                                                                                                                                                       Gaps
                                                                             477
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RESULT 8
AAX76501
                                                                                                                                                                                                                                              CC Products from the present invention can be used to treat WISP-related CC disorders such as breast, ovarian, and colon cancer or melanoma. The CC products can be used to treat other diseases e.g. benign and malignant tumours, CC leukaemia and lymphoid malignancies, neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, and Collastocoelic disorders, haematopoiesis-related disorders, kidney CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney CC disorders, bone-related disorders such as osteoporosis, trauma such as CC burns, incisions, and other wounds, connective tissue disorders, catabolic states, testicular-related disorders, and inflammatory, CC angiogenic and immunologic disorders including arteriosclerosis. The CC products can also be used for detection and diagnosis especially of CC individuals with neoplastic cell growth or proliferation. The products can be used in the production of transgenic or knock-out animals.

CC anlibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
                                                                                           Query Match
Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-APR-1998;
29-OCT-1997;
03-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour; connective tissue growth factor; cancer; melanoma; arteriosclerosis; leukaemia; lymphoid malignancy; haematopoiesis-related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion; kidney disorder; bone-related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WIS and WISP-3 have homology to connective tissue growth factor (CTGF).
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                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Botstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX76501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Wnt-1 induced secreted polypeptides, WISP-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Botstein DA,
Lawrence DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9921998-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          testicular-related disorder; angiogenesis; immunological disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1999-337420/28
WISP-2
                                                                                           Similarity 32; Conser
                                                                                                                                                                                      738
                                                                                         5.0%; Silarity 100.0%; Conservative 0;
                                                                                                                                                                                    BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein nucleotide sequence clone SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Levine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cohen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0081695.
97US-0063704.
98US-0073612.
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                                                                                                                                                                                      104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ר RL,
א AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                    A;
                                                                                                                                                                                      272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goddard A,
Pennica D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284pp;
                                                                                                                                                                                    ç;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                              Score 32;
Pred. No.
                                                                                           Pred. No. 1.
Mismatches
                                                                                                                                                                                    238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                      ç;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gurney AL,
Roy MA, W
                                                                                                                                                                                      124
                                                                                                                                      DB 20;
                                                                                                                 1.3e-05;
                                                                                                                                                                                    ∓;
                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wood
                                                                                                                                                                                      other;
                                                                                                                                    Length 738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID NO:38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
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                                                                                           Gaps
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AAX76487/6487 standard; DNA; 750 BP XX AAX76487;

AC AAX76487;

AC AAX76487;

AC AAX76487;

AC AAX76487;

AC AAX76487;

AC AAX76487;

AC AAX76487;

AC AAX76487;

AC AAX76487;

AC AAX76487;

AC AAX76487;

AC AAX76487;

AC AAX76487;

AC AAX76487;

AC AAX76487;

AC AAX76487;

DT 06-AUG-1999 (first entry)

XX WNT-1 induced secreted protein factor of the connective tissue growth factor of the connective tissue growth factor of the connective tissue disorder; skin deconnective tissue disorder; skin deconnective tissue disorder; can connective tissue disorder; skin deconnective tissue disorder; can be used to treat tissue growth factor of the connective tissue disorder; can be used to treat tissue growth factor we can be used in the production can be used to induced seconnective tissue disorders, skin disorders, deam to the connective tissue to treat the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue to the connective tissue tissue to the connective tissue tissue to the connective tissue tis
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                                                                                                                                                                                                                                                                                                                                                                     The present invention describes Wnt-1 induced Secreted polypeptides, CC WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-2, WISP-2 CC and WISP-3 have homology to connective tissue growth factor (CTGF). CC Products from the present invention can be used to treat WISP-related CC disorders such as breast, ovarian, and colon cancer or melanoma. The CC products can be used to treat arteriosclerosis, The products can also be used to treat other diseases e.g. benign and manignant tumours, CC leukaemia and lymphoid malignancies, neuronal, glial, astrocytal, and blastocoelic disorders, haematopoiesis-related disorders, kidney CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney CC disorders, bone-related disorders, truma such as the bolic states, testicular-related disorders, and inflammatory, CC catabolic states, testicular-related disorders
                                                                                                                                   Query Match
Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumous connective tissue growth factor; cancer; melanoma; arteriosclerosis leukaemia; lymphoid mallipnancy; haematopoiesis*related disorder; tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion kidney disorder; bone-related disorder; osteoporosis; trauma; burn; connective tissue disorder; catabolic state; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Wnt-1 induced secreted polypeptidės,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         testicular-related disorder; angiogenesis; immunological
624
                                                                                                                                                                           Similarity
GTACCCCTGGTGCTGGATGGCTGTGGCTGCTG
                                GTACCCCTGGTGCTGGATGGCTGTGGCTGCTG
                                                                                                                               5.0%,
                                                                                                                                                                                                                                                                              A; 242 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complementary nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goddard A,
Pennica D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284pp;
                                                                                                                                   Score 32; DB; Pred. No. 1.3
                                                                                                                                                                                                                                                                              274 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gurney AL, Hill Roy MA, Wood
                                                                                                                                                                                                                                                                              109
                                                                                                                                                                        DB 20;
1.3e-05
                                                                                                                                   1.3e-05;
ss 0;
593
                                                                 406
                                                                                                                                                                                                                                                                              T;
                                                                                                                                                                                                                                                                                 other;
                                                                                                                                                                                                     Length 750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillan
ood WI;
                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WISP-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arteriosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fibrotic lesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IJ
                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO:14.
                                                                                                                                   Gaps
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RESULT 11 AAA30048

AX I

AAA30048 standard; cDNA; 1266 BP

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RESULT 10
AAX28435
                                                                    Matches
                                                                                    Query Match
Best Local
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EBAF-8 homologue;
                                                                                                                                                                   This sequence encodes the EGF-like homologue PRO261.
The invention relates to antibodies (Ab) that bind to any of the polypeptides (I) designated PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246 or EBAF-2. The Ab, or other agents that inhibit expression and/or activity of (I) are used: (i) to inhibit growth of tumours; and (ii) as diagnostic/prognostic reagents for detection or quantification of (I) in cells or tissues, by standard immunoassays, wi overexpression being indicative of cancer. For therapeutic use, the Ab may be conjugated to a toxin, chemotherapeutic agent or radioisotope. Genes expressing (I), many of which are growth factor homologues, are overexpressed in some cases of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-NOV-1997;
17-SEP-1997;
17-SEP-1997;
18-SEP-1997;
18-SEP-1997;
15-OCT-1997;
17-OCT-1997;
17-OCT-1997;
                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 Antibodies against specific proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-229532/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody; PRO187; PRO533; PRO214; EBAF-2; inhibitor; tumour growth; FGF-8 homologue; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX28435 standard; DNA; 1257
                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 22; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9914327-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-1997;
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                                                                l Similarity
32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY05285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D, Goddard
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D,
              GTACCCCTGGTGCTGGATGGCTGTGGCTGCTG
GTACCCCTGGTGCTGGATGGCTGTGGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homologue
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                       BP; 215 A; 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0059263.
97US-0062125.
97US-0062285.
97US-0062287.
97US-0062816.
97US-0063704.
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97US-0059117.
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                                                                                    5.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gurney
                                                                  0;
                                                                                    Score 32;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Α,
                                                                    Mismatches
                                                                                                                                       385 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO240;
cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillan
                                                                                                                                                                                                                                                                                                                                                                                                                 overexpressed
                                                                                                                                       241 T; 0 other;
                                                                                                      DB
                                                                                    1.3e-05;
                                  406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO211; PRO230; PRO261; PRO246; EGF-like homologue;
158
                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawrence
                                                                                                   Length 1257;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     'n
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                                                                    0,
                                                                    Gaps
                                                                                                                                                                                                                                             with
                                                                    0;
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RESULT 12
AAS21403
ID AAS21
XX
AC AAS21
XX
AC AAS21
XX
DT 24-OC
XX
DE Human
XX
KW Human
KW Human
                                                                                                                                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a human PRO261 nucleotide sequence. PRO261 is a CC growth factor. The invention relates to isolated antibodies which bind to CC a polypeptide. The "PRO" polypeptides are encoded by genes which are over CC expressed in the genome of tumour cells. Vectors and host cells CC comprising the nucleic acid encoding the antibodies are used in the CC production of the antibodies. The antibodies and nucleic acids encoding them are used for diagnosing a tumour in a mammal. The antibodies are CC used for inhibiting the growth of tumour cells and identifying compounds CC that inhibit a biological or immunological activity of and/or expression CC of a pRO187, pRO533, pRO214, pRO240, pRO211, pRO246 or CC mediated prodrug therapy (ADEPT) by conjugating the antibody to a CC mediated prodrug therapy (ADEPT) by conjugating the antibody to a CC drug. The antibodies can be fluorescently labelled and monitored by light conscripts, flow cytometry or fluorimetry for diagnosis and prognosis of temporare.
                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO26 PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; cell growth; proliferation; growth factor; ADEPT; antibody dependent enzyme mediated prodrug therapy; ss.
breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
              Human secretory and transmembrane; PRO; mammalian; cancer;
                                            Human cDNA sequence encoding for PRO261 polypeptide
                                                                              24-OCT-2001
                                                                                                             AAS21403;
                                                                                                                                           AAS21403 standard;
                                                                                                                                                                                                                                                                                                                                                  Sequence 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 7; Fig 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated antibodies which bind to specific polypeptides used for diagnosis and treatment of neoplastic cell growth and proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-SEP-1998;
10-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-SEP-1999;
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                                                                                                                                                                                                                                                                                    Local Similarity les 32; Conserv
                                                                                                                                                                                                                         136
                                                                                                                                                                                                                                                     375
                                                                                                                                                                                                                                      GTACCCCTGGTGCTGGATGGCTGTGGCTGCTG 406
                                                                                                                                                                                                                      GTACCCCTGGTGCTGGATGGCTGTGGCTGCTG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gurney AL,
                                                                                                                                                                                                                                                                                    Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                  BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0099803.
98WO-US18824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US20594
                                                                                                                                                                                                                                                                                                                                               216 A; 418
                                                                                                                                           CDNA; 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200pp; English.
                                                                                                                                                                                                                                                                                                                   5.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillan
                                                                                                                                                                                                                                                                                 Score 32; DB; Pred. No. 1.3
                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                               C; 390 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ž,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO240; PRO211; PRO230; PRO261; PRO246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy MA,
                                                                                                                                                                                                                                                                             DB 2+,
3. 1.3e-05;
0;
                                                                                                                                                                                                                                                                                                                                               242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood WI,
                                                                                                                                                                                                                                                                                                                Length 1266;
                                                                                                                                                                                                                                                                                    Indels
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01-DEC-1999;
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02-DEC-1999;
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02-DEC-1999;
09-DEC-1999;
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20-MAR-2000;
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30-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                          30-MAR-2000;
17-MAY-2000;
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2000WO-US03565.
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2000WO-US05004.
2000WO-US05601.
2000WO-US07377.
2000WO-US07532.
2000WO-US03439.
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Smith V, Baker KP, Beresini M, Deacconst ME, Goddard A, Godows! Stewart TA, Deforge L, Desnoyers L, Filva A, Godowski PJ, Gurney AL, Sh Tumas D, Watanabe CK, Wood WI, Filvaroff E, L, Sherwood S; 2; Gao Σ

P-PSDB; 2001-408281/43. DB; AAU12331.

Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. breast, prostate, cervical

Claim 3; Fig 319; 813pp; English.

PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCS), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing interactions.

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                                                                                                                                 It was found that the pRO genes are amplified in the genome of tumour cells. The gene amplification is expected to be associated with the overexpression of the gene product and contributes to tumourigenesis. Therefore, antagonists of PRO proteins are useful for the treatment of benders such as neuronal, gilal, astrocytal, hypothalamic, glandular epithelial, inflammatory and immunologic discrete.
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08-SEP-1999;
13-SEP-1999;
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02-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                              useful
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05-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH )
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                                                                                                                                                                                                                                                                                                                                                                                                       antibody that binds to a PRO polypeptide,
ful for diagnosing and treating cancers -
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375 GTACCCCTGGTGCTGGATGGCTGTGGCTGCTG
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                                                             Similarity
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99US-0145698.
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The invention relates to novel human angiogenesis-associated protein designated PRO proteins (AAB33064-B53097), and to nucleic acids ence PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion protein compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detec mutations in a PRO gene, or the expression level of a PRO gene within

detecting within a

WPI; 200 P-PSDB;

2001-090793/10. DB; AAB53084.

Godowski PJ,

AJ, Baker J, Gurney Pitti RM,

KP, Ferrara N, AL, Hillan KJ, Watanabe CK, V

N, Gerber H, I, Kuo SS, Ma Williams PM,

Mark

Marsters SA;

WI;

Goddard A; rk MR, Wood

NF,

New isolated nucleic acid for producing a PRO polypeptide, genetic disorders and treating cardiovascular, endothelial angiogenic disorders, such as atherosclerosis, wounds or co

cancer

proteins

encoding

and

analyzing or

Claim

Fig 41; 293pp;

English.

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RESULT 1.
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01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crohn's disease; psoriasis; endometriosis; Alzheimer's disease; Huntington's disease; gene therapy; transgenic animal; ss.
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02-DEC-1999;
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30-NOV-1999;
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15-SEP-1999;
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99US-01410373
99US-0144568
99US-0145688
99WO-US20111
99WO-US210594
99WO-US21697
99WO-US218413
99WO-US28413
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                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-182-145-38
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LENGTH: 1734
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APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
                                                                                                   SEQ ID NO 38
LENGTH: 738
    Query Match
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CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-04-14
                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
                                                                                                                                                                                                                                                                                                           APPLICANT: ROY, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
                                                                                                                                                            EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-04-14
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APPLICANT: Wood, William I.
FITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
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Hillan, Kenneth J.
Lawrence, David A.
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Length 738;
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NUMBER OF SEQ 1
; SEQ ID NO 13
; SEQ ID NO 13
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                                                                              APPLICANT: ROY, Margaret Ann
APPLICANT: WOOd, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER ---
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                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/09182145B Patent No. 6387657
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Best Local
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                                                                                                                                                                                                                                                                                                    APPLICANT: Botstein,
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APPLICANT: Wood, William I.
                                                  EARLIER
                                                                   CURRENT
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                                   EARLIER
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              APPLICATION NUMBER: US 60/073,612
                             APPLICATION NUMBER: US 60/063,704 FILING DATE: 1997-10-29
                                                                 APPLICATION NUMBER: US/09/182,145B FILING DATE: 1998-10-29
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Hillan, Kenneth J.
Lawrence, David A.
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Pennica, Diane
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1998-02-04
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Pred. No.
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disorder via the administration of a PRO protein, PRO nucleic acid, or PRO agonist or antagonist; a retroviral gene therapy vector comprising a PRO agonist or antagonist; a retroviral gene therapy vector comprising a PRO agonist caid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced analogenesis via the administration of a PRO protein, or an agonist or antagonist thereof. PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO agonists and PRO antagonists may be used as therapeutic agents to treat cardiovascular, endothelial or angiogenic disorders, such as therapeutic spents to treat cardiovascular, endothelial or angiogenic disorders, such as therapeutic spents to treat cardiovascular, or an agonist and a section and properties, wounds, cancer, Alzhelmer's disease, Huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate colls with sequence identity to PRO proteins, to map genes encoding PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential
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diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
cytostatic; gene therapy; vaccine; ss.
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inappropriate PRO expression such as cardiovascular, endotherial or anglogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24438 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the present invention.
                                                        Goddard A;
                                                                                                                                                                                                                                                                                                                         The present invention describes nucleic acids encoding PRO polypeptides
                                                                                                                                                                                                                                                                                                                                        useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                      Gerber H, Hillan KJ, Goddi
Kuo SS, Paoni NF, Smith V;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 GTACCCCTGGTGCTGGATGGCTGTGGCTGCTG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 GTACCCCTGGTGCTGGATGCCTGTGCTGCTG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.0%; Score 32; DB
100.0%; Pred. No. 1.3
live 0; Mismatches
                                                        Ferrara N,
Klein RD,
                                                                                              Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: July 28, 2003, 15:54:57
Job time : 167.775 secs
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                                                                             Godowski PJ, Gurney AL, K
Watanabe CK, Williams PM,
                                                        Baker KP,
Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 32; Conservative
                  (GETH ) GENENTECH INC.
                                                                                                                                      WPI; 2000-412154/35.
                                                                                                                                                              P-PSDB; AAB24402.
                                                        Ashkenazi AJ,
δλ
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